



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 150258

TO: Ruixiang Li
Location: REM/4D75/4C70
Art Unit: 1646
Friday, April 15, 2005

Case Serial Number: 10/664667

From: Toby Port
Location: Biotech-Chem Library
REM1-A59
Phone: 272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Li,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

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STIC-Biotech/ChemLib

150258

From: Li, Ruixiang
Sent: Friday, April 08, 2005 11:20 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.10/664,667

Please do a standard search on:

- (i). SEQ ID NOS: 4, 5, and 6 against commercial nucleic acid databases;
- (ii). SEQ ID NO: 5 against commercial amino acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

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APR - 8 2005
STIC-Biotech/ChemLib
(STIC)

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 11:57:53 ; Search time 5363.18 Seconds
(without alignments)
17643.956 Million cell updates/sec

Title: US-10-664-667-4
Perfect score: 2486
Sequence: 1 taatacagactcactataggg.....agtgtaacctaaattcaatt 2486

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2311.4	93.0	3509	3 BC038795	Homo sapi
2	1360.2	54.7	2822	3 AK052873	Mus muscu
3	1333.4	53.6	3583	3 AK085901	Mus muscu
4	747.8	30.1	771	5 BQ425502	AGENCOURT
5	590.2	23.7	647	2 AW970780	EST382863
6	539.8	21.7	982	2 BF159363	601770339
7	534.4	21.5	819	4 BG863804	602798701
8	520.2	20.9	599	1 AA292507	zt30b10.r
9	516.2	20.8	812	4 BG916782	602816031
10	515	20.7	3855	3 AK040883	Mus muscu
11	507.4	20.4	509	2 AW009250	ws79g09.x
12	486.4	19.6	690	2 BB636845	BB636845
13	477.4	19.2	482	4 BM669843	UI-E-DX1-
14	476	19.1	479	5 BM993280	UI-H-DT0-
15	474.2	19.1	633	1 AA524536	ng45g03.s
16	468.4	18.8	471	5 BX281802	BX281802
17	465.8	18.7	680	7 CN258480	CN258480
18	457.6	18.4	753	4 BG916963	602816251
19	455	18.3	558	1 AA131133	zt016b04.r
20	451.2	18.1	468	1 AA443637	zw35f07.s
21	451	18.1	451	2 BE326280	hw01dl1.x
22	439.4	17.7	441	1 AA716422	zg64c06.s
23	424.4	17.1	869	2 BF158974	601766476
24	416.8	16.8	420	2 AW167811	xg56f07.x

C 25	399.4	16.1	401	1 AI989794	AI989794 ws27c09.x
C 26	398.2	16.0	577	7 W93698	W93698 zd96c01.s1
C 27	398	16.0	398	1 AI204695	AI204695 qd44f06.x
C 28	391.4	15.7	393	1 AI206303	AI206303 qr26g08.x
C 29	385.2	15.5	461	2 BE149368	BE149368 RCl-HT025
C 30	382.2	15.4	472	1 AA815396	AA815396 ai61c08.s
C 31	378.8	15.2	395	2 AW102822	AW102822 xd38f11.x
C 32	362.4	14.6	2724	9 AY411734	AY411734 Mus muscu
C 33	359	14.4	368	1 AA195671	AA195671 zr32g12.r
C 34	357	14.4	381	2 AW104260	AW104260 xd70g09.x
C 35	355.6	14.3	2724	9 AY411732	AY411732 Homo sap1
C 36	349.8	14.1	443	1 AI131316	AI131316 qc18a07.x
C 37	344.6	13.9	373	1 AI686439	AI686439 tw99f07.x
C 38	322.4	13.0	640	7 CO351740	CO351740 DR_AOV_NR
C 39	314.6	12.7	400	7 W93749	W93749 zd96c01.r1
C 40	310.8	12.5	377	1 AA235322	AA235322 zt30b10.s
C 41	310.2	12.5	467	1 AA131081	AA131081 zol6b04.s
C 42	282.4	11.4	310	7 Z44115	Z44115 HSC1SG111.n
C 43	277.2	11.2	1719	2 BF144122	BF144122 601788812
C 44	274	11.0	2593	9 AY411733	AY411733 Pan trogl
C 45	267.8	10.8	311	1 AA195672	AA195672 zr32g12.s

ALIGNMENTS

RESULT 1	BC038795	3509 bp	mRNA	linear	HTC 19-NOV-2003
LOCUS	BC038795	Homo sapiens	leucine-rich repeat-containing G protein-coupled receptor 6,	mRNA (cDNA clone IMAGE:5220507), with apparent retained intron.	
DEFINITION	BC038795.1	GI:24433474			
ACCESSION	BC038795				
VERSION	BC038795.1				
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 3509)				
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99	(26),	16899-16903	(2002)
MEDLINE	22388257				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 3509)				
AUTHORS	Strausberg,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-OCT-2002)				
REMARK	National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov				

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 64 Row: n Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis

This clone has the following problem: retained intron.

FEATURES
source

Location/Qualifiers
1. .3509
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5220507"
/tissue_type="Pancreas, Spleen, adult pooled"
/clone_lib="NIH MGC_120"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

	Query Match	93.0%;	Score 2311.4;	DB 3;	Length 3509;	
	Best Local Similarity	99.7%;	Pred. No. 0;			
	Matches 2326;	Conservative	0;	Mismatches	6;	Indels 1; Gaps 1;
QY	71	GGCTCCGTGGAGCGGAGCCAGGGTCTTGAGCCTGCCGCTCATCCAGCCTCTCTGTGCC	130			
Db	1063	GGGGGCATGGAGCGGAGCCAGGGTCTGAGCCTGCCGCTCATCCAGCCTCTCTGTGCC	1122			
QY	131	CTAGCGGCTCCAAACACACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTG	190			
Db	1123	CTAGCGGCTCCAAACACACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTG	1181			
QY	191	AGCTCCCTGCAAGCCCTTGATCTTAGCTGGAAAGCCATCCGGTCCATCCACCTTGAGGCC	250			
Db	1182	AGCTCCCTGCAAGCCCTTGGATCTTAGCTGGAAAGCCATCCGGTCCATCCACCTGAGGCC	1241			
QY	251	TTCTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACACACTG	310			
Db	1242	TTCTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACACACTG	1301			
QY	311	CCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAAACCTTGCTCTCTCC	370			
Db	1302	CCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAAACCTTGCTCTCTCC	1361			
QY	371	CAGGCCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCCTATGCGCTAC	430			
Db	1362	CAGGCCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCCTATGCGCTAC	1421			
QY	431	CAGTGTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCAGTGGAGGCT	490			
Db	1422	CAGTGTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCAGTGGAGGCT	1481			
QY	491	GAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAGGCCCTCTGGGCCTCTTGCCAGA	550			
Db	1482	GAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAGGCCCTCTGGGCCTCTTGCCAGA	1541			
QY	551	CAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCA	610			

Db	1542	CAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCA	1601			
QY	611	AAGCCACACCCACAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTAC	670			
Db	1602	AAGCCACACCCACAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTAC	1661			
QY	671	CTCTTTGAAAGCTGGGGCATCCGCCCTGGCGTGTGGGCCCATCGTGTCTCTCCGTGCTC	730			
Db	1662	CTCTTTGAAAGCTGGGGCATCCGCCCTGGCGTGTGGGCCCATCGTGTCTCTCCGTGCTC	1721			
QY	731	TGCAATGGACTGTGTCTGCTGACCGTGTTCGTGGCGGGCCTGCCCCCTGCCCCCGGTC	790			
Db	1722	TGCAATGGACTGTGTCTGCTGACCGTGTTCGTGGCGGGCCTGCCCCCTGCCCCCGGTC	1781			
QY	791	AAGTTTGTGTAGTGCATTGACGGCGCCAACACTTGTACTGGCAATTTCTGTGGCCCTT	850			
Db	1782	AAGTTTGTGTAGTGCATTGACGGCGCCAACACTTGTACTGGCAATTTCTGTGGCCCTT	1841			
QY	851	CTAGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCCGTGGAG	910			
Db	1842	CTAGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCCGTGGAG	1901			
QY	911	ACGGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTCGGAGGCATCGGTG	970			
Db	1902	ACGGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTCGGAGGCATCGGTG	1961			
QY	971	CTGCTGCTCACTCTGGCCCGCAGTGCAGTGCAGCGTCTCCGTCTCTGTGTCCGGGCCCTAT	1030			
Db	1962	CTGCTGCTCACTCTGGCCCGCAGTGCAGTGCAGCGTCTCCGTCTCTGTGTCCGGGCCCTAT	2021			
QY	1031	GGGAAGTCCCTCCCTGGGCAGCGTTCCGAGCAGGGGTCTTAGGTCCTTGGCACTGGCA	1090			
Db	2022	GGGAAGTCCCTCCCTGGGCAGCGTTCCGAGCAGGGGTCTTAGGTCCTTGGCACTGGCA	2081			
QY	1091	GGGCTGGCCGCGCACACTGCCCTGGCCCTCAGTGGGAGAATACGGGGCCTCCCACTCTGC	1150			
Db	2082	GGGCTGGCCGCGCACACTGCCCTGGCCCTCAGTGGGAGAATACGGGGCCTCCCACTCTGC	2141			
QY	1151	CTGCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTG	1210			
Db	2142	CTGCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTG	2201			
QY	1211	ATGATGAACCTCTTCTGTTTCTTGTCTGGCCGGTGCCTACATCAAATGTACTGTGAC	1270			
Db	2202	ATGATGAACCTCTTCTGTTTCTTGTCTGGCCGGTGCCTACATCAAATGTACTGTGAC	2261			
QY	1271	CTGCCGCGGGGCGACTTTGAGGCCGTGTGSSACTGCGCCATGGTGAGGCACTGGCCCTGG	1330			
Db	2262	CTGCCGCGGGGCGACTTTGAGGCCGTGTGSSACTGCGCCATGGTGAGGCACTGGCCCTGG	2321			
QY	1331	CTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCTCCTCAGCTTCGCTCCATG	1390			
Db	2322	CTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCTCCTCAGCTTCGCTCCATG	2381			
QY	1391	CTGGGCCTCTTCCCTGTACGCCCGGAGGCCGTCAAAGTCTGTCTCTGCTGGTGGTGTGCCC	1450			
Db	2382	CTGGGCCTCTTCCCTGTACGCCCGGAGGCCGTCAAAGTCTGTCTCTGCTGGTGGTGTGCCC	2441			
QY	1451	CTGCCTGCCTGCCTCAACCCACTGTCTGTACTGTCTTCAAACCCCACTTCCGGGATGAC	1510			
Db	2442	CTGCCTGCCTGCCTCAACCCACTGTCTGTACTGTCTTCAAACCCCACTTCCGGGATGAC	2501			
QY	1511	CTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGTGCGGCCGGG	1570			
Db	2502	CTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGTGCGGCCGGG	2561			
QY	1571	GAGCTGGAGAGAGACTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGAT	1630			
Db	2562	GAGCTGGAGAGAGACTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGAT	2621			
QY	1631	CTCATTTCTGGAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCC	1690			

ORIGIN		homolog [Homo sapiens] (SPTR Q96K69, evidence: FASTY, 85.8%ID, 92.1%length, match=637)"	
Query Match		54.7%; Score 1360.2; DB 3; Length 2822;	
Best Local Similarity		77.6%; Pred. No. 0;	
Matches 1775; Conservative		0; Mismatches 439; Indels 72; Gaps 8;	
QY	136	GGCCTCCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAGCTC	195
Db	474	GGCCTCGACATAACCGGATCAAGGAAATTGGTGC-AGATACCTTCAGCCAGCTGGGCTC	532
QY	196	CCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCCCTTCTC	255
Db	533	CTTGCAAGCTTTAGACCTGAGTTGGAATGCCATCCGTGCCATCCACCCTGAGGCTTTCTC	592
QY	256	CACCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAAACAGCTGACCACACTGCCCCCT	315
Db	593	AACCTTCGATCCTTGGTTAAGCTGGACCTGACTGACAACACAGCTGACCACACTGCCCCCT	652
QY	316	GGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGC	375
Db	653	GGCTGGCTGGGAGGCCTGATGCACCTGAAGCTCAAAGGGAACCTTGGCCCTGTCTCAGGC	712
QY	376	CTTCTCCAAGGACAGTTTCCAAAACTGAGGATCCTGGAGGTGCCTTATG CCTACAGTG	435
Db	713	CTTCTCCAAGGACAGTTTCCAAAACTGAGGATCCTGGAGGTGCCCTACGCCCTACAGTG	772
QY	436	CTGTCCCTATGGGATGTGTGCAGCTTCTTCAAGGCCCTCTGGGCAGTGGGAGGCTGAAGA	495
Db	773	CTGTGCCTACGGCATCTGTGCGAGCTTCTTCAAGACCTCTGGGCAGTGGCAGGCGAGGA	832
QY	496	CCTTCACCTTGATGATGAGAGTCTTCAAAAAAGGCCCTTGGGCCCTCCTTGCCAGACAAGC	555
Db	833	CTTTCATCCAGAGGAAGAGGAGGCACCAAAGAGGCCCTTGGGTCTCCTTGCTGGACAAGC	892
QY	556	AGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCC	615
Db	893	TGAGAACCACTATGACCTAGACCTGGATGAGCTCCAGATGGGACAGAGGACTCAAAGCC	952
QY	616	ACACCCCACTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTT	675
Db	953	ACACCCCACTGTCCAGTGTAGCCCTGTTCAGGCCCTTCAAGCCCTGCGAGCCTCTT	1012
QY	676	TGAAAGCTGGGCACTCCGCCTGGCCGCTGTGGGCCATCGTGTGCTCTCCGTGCTCTGCAA	735
Db	1013	TGAGAGCTGGGCATCCGCCCTGTGTGTGGGCCATCGTGTACTCTCCGTACTCTGTAA	1072
QY	736	TGGACTGGTGTGCTGACCGTGTTCGCTGGCGGGCCCTGCCCCCCTGCCCCCGGTCAAGTT	795
Db	1073	CGGGCTGGTGTGCTGACAGTCTTTGCCAGCGGACCCAGCCCCGCTGTCCCCCGTCAAGCT	1132
QY	796	TGTGGTAGGTGCGATTGCAAGCGCCAAACACCTTGACTGGCATTTCCTGTGGCCTTCTAGC	855
Db	1133	TGTGGTGGTGCGATGGCAGGCGCCAAACGCCCTGTCCGGCATTTCTGTGGTCTCCTGGC	1192
QY	856	CTCAGTCGATGCCCTGACCTTTGGTTCAGTTCTCTGAGTACGAGCCCCGCTGGGAGACGGG	915
Db	1193	CTCGTGGACGCCCTTGACCTATGGTCAGTTTCGCTGAGTATGGAGCCCCGCTGGGAGACGG	1252
QY	916	GCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGGTCCGAGGCATCGGTGCTGCT	975
Db	1253	TCTGGGCTGCCAGGCTACGGGCTTCCTGGCTGTCTCTGGGTTTCAGAGGCGTGGTGTGCT	1312
QY	976	GCTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCCTATGGAA	1035
Db	1313	GCTCACACTGGCGGCCGTGCAGTGCAGCATCTCCGTGACCTGCGTCCGAGCCTACGGGAA	1372
QY	1036	GTCCCCCTCCCTGGGACGCTTCAGCAGGGGTCTTAGGCTGCCCTGGCACTGGCAGGGCT	1095
Db	1373	GGCGCCGTGCGCTGGCAGCGTCCGCGCAGGCGCACTGGGATGCCTGGCGCTGGCCGGCT	1432
QY	1096	G6CCGCGCACTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCTGCC	1155

Db	1433	GGCCGCAGCACTGCCGTGGCCTCGGTGGGAGAGTATGGCGCCTCCCCACTCTGCTGCC	1492
QY	1156	CTACGGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGAT	1215
Db	1493	CTACGCCCCACCCGAGGCGCGCGGCTGCCCTGGGCTTCGCTGTAGCCCTGGTGATGAT	1552
QY	1216	GAACTCCTTCTGTTCCTGGTTCGTGGCCGCTGCGCATGGTGAGGCACGT-GGCTTGGCTCA	1275
Db	1553	GAACTCGCTCTGCTTCTGGTGGTGGCGGCGCTACATCAAGCTCTACTGTGACCTGCC	1612
QY	1276	GCGGGCGACTTTGAGGCCCTGTGGGACTGCGCATGGTGAGGCACGT-GGCTTGGCTCA	1334
Db	1613	ACGGGGTGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGCGCCACGTGGGCTGGCTCA	1672
QY	1335	TCTTCGCAGACGGGCTCCTCTACTGTGCCGTGGGCTTCCTCAGCTTCGCCCTCCATGCTGG	1394
Db	1673	TCTTTGCAGATGGCTCCTCTACTGCCCCGCTGGGCTTCCTCAGCTTTGCCCTATGCTGG	1732
QY	1395	GCCTCTTCCCTGTACGCCCGGAGGCCGTCAAGTCTGCTGCTGCTGGTGGTGTGCCCTGC	1454
Db	1733	GCCTCTTCCCTGTACCCCCGAGGGTGTCAAGTCAGTCCTTCTGGTGGTGGCTCTGC	1792
QY	1455	CTGCTGCTCAACCCACTGCTGTACCTGCTCTTCAACCCCACTTCCGGGATGACCTTC	1514
Db	1793	CTGCTGCTCAACCCACTGCTCTACCTGCTCTTCAACCCCTCACTTCCGGGATGACCTTC	1852
QY	1515	GGCGGCTTCGGCCCGCGCAGGGGACTCAGGCCCCCTAGCCTATGCTGCGCGGGGAGC	1574
Db	1853	GGCGGCTCTGGCCAAGCCCTCGGTCCCCAGGGCCCCCTAGCCTACGCTGCAGCGGTGAGC	1912
QY	1575	TGGAGAAAGACTCCTGTGATTCTACCCAGGSCCTTGGTAGCCTTCTCTGATGTGGATCTCA	1634
Db	1913	TGGAGAAAGACTCCTGCGACTCCACCCCAAGCGCTGGTGGCTTCTCAGATGTGGATCTTA	1972
QY	1635	TTCTGGAAGCTTCTGAAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCCCTCAG	1694
Db	1973	TTCTGGAAGCTTCTGAGGCTGGGAGCCCTCTGGGCTAGAGACCTATGGCTTCCCCCTCAG	2032
QY	1695	TGACCTCTATCTCCTGTGACGACCCAGGGCCCCCAGGCTGGAGGGCAGCCATTGTGTAG	1754
Db	2033	TGACCTCTATCTCCCGACATCAGCCGGGGGTACCAGGCTGGAGGGAACCATTTTGTAG	2092
QY	1755	AGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTGCTGA	1814
Db	2093	AGTCTGATGGNAACCAAGTTTGGGAACCCCAACACCTCCCATGAAGGGAGAACTGCTGCTGA	2152
QY	1815	GGCAGAGGGATCTACCCAGCAGGTGGAGGCTTGTACGGGGTGGCGGCTTTCAGCCCT	1874
Db	2153	AGCAGAGGGAGCCACTTTGGCAGGCTGTGGCTCTTCCGTGGTGGAGCCCTCTGGCCCT	2212
QY	1875	CTGGCTTGGCCTTTGCTTCACACGTGTAATATCCCTCCCCATCTTCTTCCCCCTCTC	1934
Db	2213	CTGGCTCTCTTTGGCCTCTCATTGTGAAATATCCCTCTCTGTTTGTCTCTTCCCCGTCC	2272
QY	1935	TTCCCTTCTCTCTCCCCCTCGGTGAAATGATGGCTGCTTCTAATAAATAACAAACCAAA	1994
Db	2273	-----AATGATGGCTGCTTATAAAGAAAGAACAACTCCA	2306
QY	1995	ACTCAGCAGTGTGATCTATAGCAGGATGGCCAGTACCTGGCTCCACTGATCACCTCTCT	2054
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Db	2410	CACCTTACCCCTGGGCCCTTCTCTGTCTCCAATCCAATACTTCTGACAGAGSCCTGGGAAAT	2469
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Qy 2235 GGACAGT-----GGACAGGGAGACCTCACAGAGAAAGGCCTGGAAAGGTGATTTC 2284

Db 2530 TGATCAGTAAGTGCAGAGTGATGGGGAGGTCTCACAGAGAGCATGACACTGGAAGACAAC TA 2589

Qy 2285 CCGTGTGACTCATGG-----ATAGGATACAAAATGTGTTCCATGTACC 2327

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Qy 2328 ATTAATCTTGACATATGCCATGCTATAAAGACTTCTCTATTAAATAAGCTTTTGGAAAGAGAT 2387

Db 2650 ATTAATCTTGACCTATGCTGTGCCAAAGTGCTTCTCTGTTAAATAACACTTTTGGAAAGACAT 2709

Qy 2388 TAAAAA 2393

Db 2710 TGCATA 2715

RESULT 3

AK085901

LOCUS

DEFINITION

AK085901 3583 bp mRNA linear HTC 03-APR-2004

Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830026M09 product:CDNA FLJ14471 FIS, CLONE MAMMA1001030, WEAKLY SIMILAR TO LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR homolog [Homo sapiens], full insert sequence.

ACCESSION

AK085901

VERSION

AK085901.1 GI:26103061

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

Carninci,P. and Hayashizaki,Y.

AUTHORS

High-efficiency full-length cDNA cloning

TITLE

Meth. Enzymol. 303, 19-44 (1999)

JOURNAL

99279253

MEDLINE

10349636

PUBMED

REFERENCE

2

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

AUTHORS

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

TITLE

Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL

20499374

MEDLINE

11042159

PUBMED

REFERENCE

3

Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

AUTHORS

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

TITLE

Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL

20530913

MEDLINE

11076861

PUBMED

REFERENCE

4

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

AUTHORS

Functional annotation of a full-length mouse cDNA collection

TITLE

Nature 409, 685-690 (2001)

JOURNAL

5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

AUTHORS

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

TITLE

Nature 420, 563-573 (2002)

JOURNAL

6

(bases 1 to 3583)

REFERENCE

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,

Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohaato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/

URL:http://fantom.gsc.riken.jp/

FEATURES

Location/Qualifiers

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polyA_signal

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/note="putative"

polyA_site

3583

/note="putative"

ORIGIN

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Best Local Similarity 77.4%; Pred. No. 0;

Matches 1772; Conservative 0; Mismatches 442; Indels 74; Gaps 10;

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Db 1233 GGCCTCCGACATAACCGGATCAAGGAAATTGGTGC-AGATACCTTCAGCCAGCTGGGCTC 1291

Qy 196 CCTGCAAGCCCTGGATCTTAGCTGGAACGCCCATCCGGTCCATCCACCCCTGAGGCTTCTC 255

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Db 1292 CTTGCAAGCTTTAGACCTGAGTTGGAATGCCATCCGTGCCATCCACCCCTGAGGCTTCTC 1351

Qy 256 CACCCTGCACCTCCCTGGTCAAGCTGGACCTGACACAAACCAGCTGACCACACTGCCCCCT 315

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Qy 316 GGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGC 375

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Qy 376 CTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCTCGAGGTGCCTTATGCCTACCACTG 435

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

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BQ425502
BQ425502.1 GI:21120817
EST.

771 bp mRNA linear EST 23-MAY-2002

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 771)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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VERSION AW970780.1 GI:8160625
KEYWORDS EST.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 647)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 282
Seq primer: Forward.
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ACCESSION BF159363
VERSION BF159363.1 GI:11039462
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 982)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9199 row: n column: 09
High quality sequence stop: 663.
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Stem cell origin."
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/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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1. .982
/organism="Mus musculus"
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Stem cell origin."
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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QY 1193 TTCACCGTGGCCCTGGTGATGAACCTCCTTCTGTTTTCCTGGTCGTGGCCGGTGCCTAC 1252
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DEFINITION mRNA sequence.
ACCESSION BG863804
VERSION BG863804.1 GI:14214342
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 819)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
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Db 541 AAGCTTTGGAAGAGATACACA 561
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DEFINITION mRNA sequence.

ACCESSION BG916782
VERSION BG916782.1 GI:14297258
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 812)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10865 row: m column: 08
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FEATURES

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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match 20.8%; Score 516.2; DB 4; Length 812;
Best Local Similarity 81.3%; Pred. No. 4.9e-115;
Matches 635; Conservative 0; Mismatches 143; Indels 3; Gaps 3;
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QY 452 TGTGCCAGCTTCTTCAAGGCCTCTGGCAGTGGGAGGCTGAAGACCTTCACCTTGATGAT 511
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QY 812 GCAGGCGCCAAACACCTTGACTGGCATTTCTGTGGCTTCTAGCCCTCAGTCGATGCCCTG 871
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RESULT 10
AK040883

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DEFINITION Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530037C04 product:CDNA FLJ14471 FIS, CLONE MAMMA1001030, WEAKLY SIMILAR TO LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR homolog [Homo sapiens], full insert sequence.
ACCESSION AK040883
VERSION AK040883.1 GI:26088131
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 Carninci,P. and Hayashizaki,Y.
AUTHORS High-efficiency full-length cDNA cloning
TITLE Meth. Enzymol. 303, 19-44 (1999)
JOURNAL 99279253
MEDLINE PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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VERSION AW009250.1 GI:5858028
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 509)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 451.
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with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library went through one round of
normalization."

ORIGIN

Query Match 20.4%; Score 507.4; DB 2; Length 509;
Best Local Similarity 99.8%; Pred. No. 6.3e-113;
Matches 508; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1888 TGCTTCACACGTTAAATATCCCTCCCAATCTTCTTCCCTCTCTTCCCTCTCT 1947
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QY 2008 ATCTATAGCAGGATGGCCCAGTACCTGGTCCACTGATCACCTCTCTCTGTGACCATCA 2067
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QY 2248 GGGAGACCTCACAGAGAAAGGCCCTGGAAGGTGATTTCCCGTGTGACTCATGGATAGGATA 2307
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QY 2308 CAAAATGTGTCCATGTACCATTAACTTGACATATGCCATGCATAAAGACTTCCTATTA 2367
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QY 2368 AAATAAGCTTTGGAAGAGATTAAAAAAA 2396
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Db 29 AAATAAGCTTTGGAAGAGATTAAAAAAA 1

RESULT 12
BB636845
LOCUS BB636845
DEFINITION BB636845 RIKEN full-length enriched, adult male aorta and vein Mus
musculus cDNA clone A530037C04 5', mRNA sequence.
ACCESSION BB636845
VERSION BB636845.1 GI:16472635
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 690)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,

Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)

TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the Classroom	Journal of Educational Research	1980, Vol. 83, No. 1, pp. 1-10
2. The Impact of Technology on Education	Journal of Educational Technology	1985, Vol. 10, No. 2, pp. 15-25
3. The Importance of Parental Involvement	Journal of Educational Psychology	1990, Vol. 82, No. 3, pp. 201-210
4. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	1995, Vol. 98, No. 4, pp. 301-310
5. The Role of the School in the Community	Journal of Educational Research	2000, Vol. 103, No. 1, pp. 1-10
6. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2005, Vol. 108, No. 2, pp. 15-25
7. The Importance of Teacher Professionalism	Journal of Educational Research	2010, Vol. 113, No. 3, pp. 201-210
8. The Effect of Teacher Professionalism on Student Achievement	Journal of Educational Research	2015, Vol. 118, No. 4, pp. 301-310
9. The Role of the Teacher in the 21st Century	Journal of Educational Research	2020, Vol. 123, No. 1, pp. 1-10
10. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2025, Vol. 128, No. 2, pp. 15-25

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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.,
and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES

Location/Qualifiers
1. .690
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A530037C04"
/sex="male"
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/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male aorta and vein"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAAATATCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

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Qy	1565	GCCGGGAGCTGGAGAAGAGCTCCTGTGTATCTACCCAGGCCCTGGTAGCCTTCTCTGAT	1624
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Qy	1865	TTTCAGCCCTCTGGCTTGGCCCTTGTCTTCACACGTGTAAATATCCCTCCCCCATTTCTCTC	1924
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DEFINITION	UI-E-DX1-agx-c-12-0-UI.s1 UI-E-DX1 Homo sapiens cDNA clone UI-E-DX1-agx-c-12-0-UI 3', mRNA sequence.
ACCESSION	BM669843
VERSION	BM669843.1 GI:18979740
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 482)
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
PUBMED	8889548
COMMENT	Contact: Soares, MB Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565

|||||
Db 419 AACCAAACTCAGCAGTGTGATCTATAGCAGGATGGCCACAGTACCTGGCTCCACTGATCA 360
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QY 2228 TGATCAGGGCACAGTGGACAGGGACCTCACAGAGAAAGCCTGGAAGGTGATTTCCTCG 2287
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Db 59 TGCATAAAGACTTCTCTATTAAAAATAAGCTTTGGAAGAGATTAAAAA 4

RESULT 15
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DEFINITION ng45903.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937780 3',
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ACCESSION AA524536
VERSION AA524536.1 GI:2265464
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 633)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 619 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 371.

FEATURES
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
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was prepared from 12 pooled bulk tumor samples and primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not

I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library went through one round of
normalization."

ORIGIN
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Best Local Similarity 98.8%; Pred. No. 9e-105;
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QY 1941 TTCCTCTCTCC-CCCTCGGTGAATGATGGCTGCTTTAAACAAATACAACC-AAAACTC 1998
Db 455 TTCCTCTCTCCACCCCTCGGTGAATGATGGCTGCTTTAAACAAATACAACC AAAAATC 396
QY 1999 AGCAGTGTGATCTATAGCAGGATGGCCAGTACCTGGCTCCACTGATCACCTCTCTCCTG 2058
Db 395 AGCAGTGTGATCTATAGCAGGATGGCCAGTACCTGGCTCCACTGATCACCTCTCTCCTG 336
QY 2059 TGACCATCACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCCTCAGCTTCACC 2118
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Db 35 TTCCTATTAAAAATAAGCTTTTGGAGAGAGATTAAAAA 1

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES:

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1	2255.8	90.7	2988	4 US-09-799-451-723	Sequence 723, App
2	439.4	17.7	453	3 US-09-397-787-240	Sequence 240, App
3	355.6	14.3	2724	4 US-09-170-496D-263	Sequence 263, App
4	355.6	14.3	4570	4 US-09-976-594-201	Sequence 201, App
5	352.4	14.2	2724	4 US-09-170-496D-277	Sequence 277, App
6	194	7.8	2612	4 US-09-495-050A-214	Sequence 214, App
7	194	7.8	4203	2 US-08-866-757-1	Sequence 1, Appli
8	194	7.8	4203	3 US-09-153-593-1	Sequence 1, Appli
9	181.8	7.3	723	4 US-09-495-050A-220	Sequence 220, App
10	105	4.2	2703	4 US-09-482-273-75	Sequence 75, Appl
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14	100	4.0	1581	2 US-08-460-898-1	Sequence 1, Appli
15	95.4	3.8	1255	3 US-09-118-442-31	Sequence 31, Appl
16	95.4	3.8	1255	3 US-09-677-064-31	Sequence 31, Appl
17	94.6	3.8	2709	4 US-09-482-273-101	Sequence 101, App
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19	86.6	3.5	826	4 US-09-620-312D-584	Sequence 584, App
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22	85.4	3.4	1984	4 US-09-904-615-46	Sequence 46, Appl
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26	81.8	3.3	696	3 US-09-227-357-69	Sequence 69, Appl
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ALIGNMENTS

RESULT 1

US-09-799-451-723
; Sequence 723, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunging
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 723
; LENGTH: 2988
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2484)
US-09-799-451-723

Query Match 90.7%; Score 2255.8; DB 4; Length 2988;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2268; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db	837	CTCACCCCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAAACCAGCTGACCACACTGCC	896	Db	1917	CATCTTCGCAGACGGGCTCCTACTGTCCCCTGGCCCTTCTCTCAGCTTCGCCTCCATGCT	1976
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QY	373	GGCCTTCTCCAAGGACAGTTTCCCAAAAACCTGAGGATCCTGGAGGTGCCTTATGCCTACCA	432	QY	1453	GCCTGCCTGCCTCAACCCACTGCTGTACCTTCTTCAACCCCCCACTTCCGGGATGACCT	1512
Db	957	GGCCTTCTCCAAGGACAGTTTCCCAAAAACCTGAGGATCCTGGAGGTGCCTTATGCCTACCA	1016	Db	2037	GCCTGCCTGCCTCAACCCACTGCTGTACCTTCTTCAACCCCCCACTTCCGGGATGACCT	2096
QY	433	GTGCTGTCCCCTATGCGGATGTGCCCAGCTTCTTCAAGGCTCTTGGGCAGTGGGAGGCTGA	492	QY	1513	TCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGGGCCGGGA	1572
Db	1017	GTGCTGTCCCCTATGCGGATGTGCCCAGCTTCTTCAAGGCTCTTGGGCAGTGGGAGGCTGA	1076	Db	2097	TCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGGGCCGGGA	2156
QY	493	AGACCTTCACCTTGATGAGGAGTCTTCAAAAAGGCCCTTGGCCCTCCTTGGCAGACA	552	QY	1573	GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGSCCTGGTAGCCCTTCTCTGATGTGGATCT	1632
Db	1077	AGACCTTCACCTTGATGAGGAGTCTTCAAAAAGGCCCTTGGCCCTCCTTGGCAGACA	1136	Db	2157	GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGATCT	2216
QY	553	AGCAGAGAAACCACTATGACAGGACCTTGGATGAGCTCAAGCTGGAGATGGAGACTCAAA	612	QY	1633	CATTCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGSCCTTCCCCCTC	1692
Db	1137	AGCAGAGAAACCACTATGACAGGACCTTGGATGAGCTCAAGCTGGAGATGGAGACTCAAA	1196	Db	2217	CATTCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGSCCTTCCCCCTC	2276
QY	613	GCCACACCCAGTGTCCAGGTAGCCCTTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	672	QY	1693	AGTGACCCCTCATCTCTGTCAAGCAGCCAGGGGCCCCAGGCTGGAGGGCAGCCATTGTGT	1752
Db	1197	GCCACACCCAGTGTCCAGGTAGCCCTTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	1256	Db	2277	AGTGACCCCTCATCTCTGTCAAGCAGCCAGGGGCCCCAGGCTGGAGGGCAGCCATTGTGT	2336
QY	673	CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTTCCTCCGTCTCTG	732	QY	1753	AGAGCCAGAGGGAAACCACTTTGGGAACCCCAACCCCTCCAATGGATGGAGAACTGCTGCT	1812
Db	1257	CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTTCCTCCGTCTCTG	1316	Db	2337	AGAGCCAGAGGGAAACCACTTTGGGAACCCCAACCCCTCCAATGGATGGAGAACTGCTGCT	2396
QY	733	CAATGGACTGGTGTCTGACCGTGTTCGCTGGCGGGCCCTGCCCCCTGCCCCCGGTCAA	792	QY	1813	GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGCTTTCAGCC	1872
Db	1317	CAATGGACTGGTGTCTGACCGTGTTCGCTGGCGGGCCCTGTCCTGTCCTGTCCTGTC	1376	Db	2397	GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGCTTTCAGCC	2456
QY	793	GTTTGTGGTAGGTGCGATTGACGGCGCCAAACACTTGACTGGCATTTCTGTGGCCTTCT	852	QY	1873	CTCTGGCTTGGCCTTGTCTTCAACACGTGTAAATAATCCCTCCCCATTTCTTCTTCCCCCTC	1932
Db	1377	GTTTGTGGTAGGTGCGATTGACGGCGCCAAACACTTGACTGGCATTTCTGTGGCCTTCT	1436	Db	2457	CTCTGGCTTGGCCTTGTCTTCAACCGTGTAAATAATCCCTCCCCATTTCTTCTTCCCCCTC	2516
QY	853	AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	912	QY	1933	TCTTCCCCTTTCCTCTCTCCCCCTCGGTGAAATGATGGCTGTCTTCTTCTTCTTCTTCTTCT	1992
Db	1437	AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	1496	Db	2517	TCTTCCCCTTTCCTCTCTCCCCCTCGGTGAAATGATGGCTGTCTTCTTCTTCTTCTTCTTCT	2576
QY	913	GGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGTTCGGAGGCACTGGTGCT	972	QY	1993	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCCAGTACCTGGCTCCACTGATCACCTCT	2052
Db	1497	GGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGTTCGGAGGCACTGGTGCT	1556	Db	2577	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCCAGTACCTGGCTCCACTGATCACCTCT	2636
QY	973	GCTGCTCACTCTGGCCGAGTGCAGTGCAAGCTTCCGTCTCCGTCTCCGTCTCCGTCTCCGT	1032	QY	2053	CTCCTGTGACCATCACCAACGGGTGCCTTGGCCCTGGCTTTCCCTTGGCCTTCCCTCAGC	2112
Db	1557	GCTGCTCACTCTGGCCGAGTGCAGTGCAAGCTTCCGTCTCCGTCTCCGTCTCCGTCTCCGT	1616	Db	2637	CTCCTGTGACCATCACCAACGGGTGCCTTGGCCCTGGCTTTCCCTTGGCCTTCCCTCAGC	2696
QY	1033	GAAGTCCCCCTCCCTGGGACGCTTCGAGCAGGGTCCCTAGGCTGCCTGGCCTGGCAGG	1092	QY	2113	TTACCTTGTACTGGGCCCTCTTCCCTTGTCAATGCTGAAGCTGTGGACAGAGACCTGGA	2172
Db	1617	GAAGTCCCCCTCCCTGGGACGCTTCGAGCAGGGTCCCTAGGCTGCCTGGCCTGGCAGG	1676	Db	2697	TTACCTTGTACTGGGCCCTCTTCCCTTGTCAATGCTGAAGCTGTGGACAGAGACCTGGA	2756
QY	1093	GCTGGCCGCGCACTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCTTCCCACTCTGCCT	1152	QY	2173	CTTTTGTCTGCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATC	2232
Db	1677	GCTGGCCGCGCACTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCTTCCCACTCTGCCT	1736	Db	2757	CTTTTGTCTGCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATC	2816
QY	1153	GCCCTACGCGCCACCTGAGGGTTCAGCCAGCAGCCCTGGGCTTCAACCTGGCCCTGGTGAT	1212	QY	2233	AGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCCTGGAAAGGTGATTTCCCGTGTGA	2292
Db	1737	GCCCTACGCGCCACCTGAGGGTTCAGCCAGCAGCCCTGGGCTTCAACCTGGCCCTGGTGAT	1796	Db	2817	AGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCCTGGAAAGGTGATTTCCCGTGTGA	2876
QY	1213	GATGAACCTCTTCTGTTCCCTGGTCTGGCCGGTGCCTACATCAAACTGACTGTGACCT	1272	QY	2293	CTCATGGATAGGATACAAAATGTGTTCCATGTACCAATTAATCTTGCATATGCCATGCAT	2352
Db	1797	GATGAACCTCTTCTGTTTCCCTGGTCTGGCCGGTGCCTACATCAAACTGACTGTGACCT	1856	Db	2877	CTCATGGATAGGATACAAAATGTGTTCCATGTACCAATTAATCTTGCATATGCCATGCAT	2936
QY	1273	GCCGCGGGCGCACTTGAGGCCCGTGTGGGACTGCGCCCATGGTGAGGCAGTGGCCCTGGCT	1332	QY	2353	AAAGACTTCCCTATTAAAATAAGCTTTTGGAAAGAGATTAAAAAATAAAAAA	2403
Db	1857	GCCGCGGGCGCACTTGAGGCCCGTGTGGGACTGCGCCCATGGTGAGGCACGTGGCCCTGGCT	1916	Db	2937	AAAGACTTCCCTATTAAAATAAGCTTTTGGAAAGAGATTAAAAAATAAAAAA	2987


```
RESULT 2
US-09-397-787-240
; Sequence 240, Application US/09397787
; Patent No. 6468758
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
; TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.466C2
; CURRENT APPLICATION NUMBER: US/09/397,787
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 240
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-397-787-240

Query Match      17.7%; Score 439.4; DB 3; Length 453;
Best Local Similarity 99.6%; Pred. No. 2.4e-99;
Matches 451; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1329 GGCTCATCTTCGACAGCGGCTCCTCTACTGTCCCGTGGCCCTTCCTCAGCTTCGCGCTCCA 1388
Db 1 GGCTCATCTTCGACAGCGGCTCCTCTACTGTCCCGTGGCCCTTCCTCAGCTTCGCGCTCCA 60

QY 1389 TGCTGGCCCTCTCCCTGTACGCGCCGAGGCGCTCAAGTCTGTCTGCTGGTGTGCTGC 1448
Db 61 TGCTGGCCCTCTTCCTGTACGCGCCGAGGCGCTCAAGTCTGTCTGCTGGTGTGCTGC 120

QY 1449 CCCTGCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCACCTTCGCGGATG 1508
Db 121 CCCTGCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCACCTTCGCGGATG 180

QY 1509 ACCTTCGGCGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGCTGGGCGCG 1568
Db 181 ACCTTCGGCGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGCTGGGCGCG 240

QY 1569 GGGAGCTGGAGAAGAGCTCTGTGATTCTACCCAGGCGCTGGTAGCCTTCTCTGATGTGG 1628
Db 241 GGGAGCTGGAGAAGAGCTCCCGTGATTCTACCCAGGCGCTGGTAGCCTTCTCTGATGTGG 300

QY 1629 ATCTCATTTCTGGAAGCTTCTGAAGCTGGGCGGCCCTGGCTGGAGACCTATGGCTTCC 1688
Db 301 ATCTCATTTCTGGAAGCTTCTGAAGCTGGGCGGCCCTGGCTGGAGACCTATGGCTTCC 360

QY 1689 CCTCAGTGACCCTCATCTCTGTTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGC-AGCCAT 1747
Db 361 CCTCAGTGACCCTCATCTCTGTTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGCAAGCCAT 420

QY 1748 TGTGTAGAGCCAGAGGGGAACCACTTTTGGGAAC 1780
Db 421 TGTGTAGAGCCAGAGGGGAACCACTTTTGGGAAC 453

RESULT 3
US-09-170-496D-263
; Sequence 263, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 263
; LENGTH: 2724
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-263

Query Match      14.3%; Score 355.6; DB 4; Length 2724;
Best Local Similarity 56.2%; Pred. No. 3.6e-78;
Matches 781; Conservative 0; Mismatches 580; Indels 28; Gaps 5;

QY 136 GGCCTCCAACACACCCGCATCTGGGAAATTTGGAGCTNGACACCTTCAGCCAGCTGAGCTC 195
Db 1138 GACCTAAGACATAATGAAATCTACGAAATTTAAAG-TTGACACTTTCAGCAGATTGCTTAG 1196

QY 196 CCTGAAGCCCTGGATCTTAGCTGGAAAGCCATCCGGTCCATCCACCTGAGGCTTCTC 255
Db 1197 CCTCCGATCGCTGAATTTGGCTTGGAAACAAAATTGCTATTATTACCCCAATGCATTTTC 1256

QY 256 CACCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAAACAGCTGACCAACTGCCCCCT 315
Db 1257 CACTTTGCCATCCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTGCTCTTTTCCCTAT 1316

QY 316 GGCTGGACTTGGGGCTTGATGTCATCTGAAGCTCAAAAGGGAACCTTGTCTCTCTCCAGGC 375
Db 1317 AACTGGTTACATGTTTAACTCACTTAAATTAACAGGAAATCATGCCTTACAGAGCTT 1376

QY 376 CTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCCTTATGCCCTACCAGTG 435
Db 1377 GATATCATCTGAAAACCTTCCAGAACTCAAGGTTATAGAAATGCCCTTATGCTTACCAGTG 1436

QY 436 CTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCTCTGGGAGTGGGAGCTGAAGA 495
Db 1437 CTGTGCATTTGGAGTGTGTGAGAAATGCCCTATAAGATTTCTAATCAATGGAATAAAGTGA 1496

QY 496 CTTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTCTGGGCTCCTTGCACAGACAAGC 555
Db 1497 CAACAGCAGTATGGACGACCTTCATAAGAAA-----GATGCTGGAATGTT 1541

QY 556 AGAGAACCACATATGACCAGGACCTGGATGAGCTCCAGCTGGAGAT---GGAGACTCAAA 612
Db 1542 TCAGGCTCAAGATGAACGTGACCTTGAAGATTTCTGCTTGACTTTGAGGAAGACCTGAA 1601

QY 613 GCCACACCCCACTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTTGAGTACCT 672
Db 1602 AGCCCTTCATTCACTGTCAGTGTTCACCTTCCCAGGCCCTTCAAAACCTTGAAACACCT 1661

QY 673 CTTTGAAAGCTGGGCATCCGCCTGGCCGTGGGCCCATCGTGTGCTCTCCGTGCTCTG 732
Db 1662 GCTTGATGGCTGGCTGATCAGAAATGGAGTGGACCATAGCAGTTCTGGCACTTACTTG 1721

QY 733 CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGCCCTGCCCCCTGCCCCCGGTCAA 792
Db 1722 TAATGCTTTGTTGACTTCAACAGTTTTCAGATCC---CCTCTGTACATTTCCCCCATTA 1778

QY 793 GTTTGTGGTAGGTGGGATTCAGGCGCCAAACACCTTGACTGGCATTTCTGTGGCTTCT 852
Db 1779 ACTGTTAATTGGGCTCATCGCAGCAGTGAACATGCTCAGGGAGTCTCCAGTGGCGTGT 1838

QY 853 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC 912
Db 1839 GGCTGGTGTGGATGGCTTCACTTTTGGCAGCTTTCACGACATGGTGCCTGGTGGGAGAA 1898

QY 913 GGGGCTAGGCTGCCGGCCACTGGCTTCCCTGGCAGTACTTGGGTCGGAGGCAATCGGTGCT 972
Db 1899 TGGGGTTGGTTGCCATGTCTGGTTTTTTTGTCATTTTGTCTTCAGAAATCATCTGTTTT 1958

QY 973 GCTGCTCACTCTGGCGCAGTGCAGTGCAGCTCTCCGTCTCTCTGTGTCCGGGCTATGG 1032
Db 1959 CTTGCTTACTCTGGCAGCCCTGGAGCGTGGGTTCTCTGTGAAATATTCTGCAAAATTTGA 2018

QY 1033 GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCCTAGGCTGCCTGGCACTGGCAGG 1092
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Db 2019 AACGAAAGCTCCATTTCTAGCCTGAAAGTAATCAATTTTGCTCTGTGCCCTGCTGGCCCTT 2078
QY 1093 GCTGGCCGCGCACTGCCCTGGCCTCAGTGGGAGAATACGGGCCCTCCCCACTCTGCCT 1152
Db 2079 GACCATGGCCGAGTTCCCTGCTGGGTGGCAGCAAGTATGGCCCTCCCTCTCTGCCT 2138
QY 1153 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGAT 1212
Db 2139 GCCTT-----TGCCTTTTGGGAGCCAGCACCATGGGCTACATGGTCGCTCTCATCTT 2192
QY 1213 GATGAACCTCTCTGTTCCCTGGTCGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCT 1272
Db 2193 GCTCAATTCCCTTTGCTTCCCTCATGATGACCATTGCCATACCAAGCTCTACTGCAATT 2252
QY 1273 GCCCGGGGCGACTTTAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT 1332
Db 2253 GGACAAGGGAGACCTGGAGAAATTTGGGACTGCTCTATGGTAAACACATTGCCCTGTT 2312
QY 1333 CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCCTCAGCTTCGCCCTCCATGCT 1392
Db 2313 GCTCTTCACCAACTGCATCCTAAACTGCCCTGGGCTTCTTGTCCTTCTCCTCTTAAT 2372
QY 1393 GGGCCTCTTCCCTGTCAAGCCCGGAGCCGTCGAAGTCTGTCTGCTGGTGGTGGCCCT 1452
Db 2373 AAACCTTACATTTATCAGTCTGGAAGTAATTAAGTTTATCCTTCTGGTGGTAGTCCACT 2432
QY 1453 GCCTGCCTGCCTCAACCCACTGTGTACCTGCTCTTCAACCCCCACCTTCGGGATGACCT 1512
Db 2433 TCCTGCATGTCTCAATCCCCCTTCTCTACATCTTGTTCAATCCTCACTTTTAAGGAGGATCT 2492
QY 1513 TCGGCGGCT 1521
Db 2493 GGTGAGCCT 2501

RESULT 4

US-09-976-594-201
; Sequence 201, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 201
; LENGTH: 4570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 205542.2
; NAME/KEY: unsure
; LOCATION: 3900, 3919, 3934
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-201

Query Match 14.3%; Score 355.6; DB 4; Length 4570;
Best Local Similarity 56.2%; Pred. No. 4.4e-78;
Matches 781; Conservative 0; Mismatches 580; Indels 28; Gaps 5;
QY 136 GGCCTCCAAACACGCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAGCTC 195
Db 1399 GACCTAAGACATAATGAAATCTACGAAATTAAAG-TTGACACTTTCAGCAGATTGCTTAG 1457
QY 196 CCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCTTCTC 255
Db 1458 CCTCCGATCGCTGAATTGGCTTGGAACAAATTTGCTATTATTCACCCCAATGCAATTTTC 1517

QY 256 CACCTTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTGACCACACTGCCCCCT 315
Db 1518 CACTTTGCCATCCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTGCTTTTCTCTAT 1577
QY 316 GGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGC 375
Db 1578 AACTGGGTTACATGGTTTAACTCACTTAAATAAACAGGAAATCATGCCCTTACAGAGCTT 1637
QY 376 CTTCTCCAAGGACAGTTTCCAAAACTGAGGATCCTGGAGGTGCCCTTATGCCCTACCAGTG 435
Db 1638 GATATCATCTGAAAACTTTCAGAACTCAAGGTTATAGAAATGCCCTTATGCTTACCAGTG 1697
QY 436 CTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCAGTGGGAGGCTGAAGA 495
Db 1698 CTGTGCATTTGGAGTGTGTGAGAATGCCCTATAAGATTCTAATCAATGGAATAAAGGTGA 1757
QY 496 CTTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCCTCCTTGCCAGACAAGC 555
Db 1758 CAACAGCAGTATGGACGACCTTTCATAAGAAA-----GATGCTGGAATGTT 1802
QY 556 AGAGAAACCATATGACCAGGACCTGGATGAGCTCCAGCTGGAGAT---GGAGGACTCAA 612
Db 1803 TCAGGCTCAAGATGAACGTGACCTTGAAGATTCTCTGCTTGACTTTGAGGAAGACCTGAA 1862
QY 613 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 672
Db 1863 AGCCCTTCATTCACTGTCAGTGTTCACCTTCCCAGGCCCTTCAAAACCCTGTGAACACCT 1922
QY 673 CTTTGAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCCATCGTGTGCTCTCCGTGCTCTG 732
Db 1923 GCTTGATGGCTGGCTGATCAGAAATTGGAGTGTGGACCATAGCAGTTCTGGCAGCTTACTTG 1982
QY 733 CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGGCCCTGCCCCCTGCCCCCGGTCAA 792
Db 1983 TAATGCTTTGGTGACTTCAACAGTTTTTCAGATCC--CCTCTGTACATTTCCCCCATTA 2039
QY 793 GTTTGTGGTAGGTGCGATTGACGGCGGCCAAACACCTTGACTGGCATTTCTGTGGCCTTCT 852
Db 2040 ACTGTTAATTGGGGTCATCGCAGCAGTGAACATGCTCACGGGAGTCTCCAGTGCCGTGCT 2099
QY 853 AGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCGCTGGGAGAC 912
Db 2100 GGCTGGTGGATGCGTTCACTTTTGGCAGCTTTCACGACATGTTGTCGCTGCGGGAGAA 2159
QY 913 GGGCTAGGCTGCCGGGCCACTGGCTTCTCTGGCAGTACTTGGGTGGAGGATCGGTGCT 972
Db 2160 TGGGGTTGGTTGCCATGTCAATGGTTTTTTTGTCCATTTTGTCTCAGAATCATCTGTTT 2219
QY 973 GCTGCTCACTCTGGCCGCACTGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCGGGCCCTATGG 1032
Db 2220 CCTGCTTACTCTGGCAGCCCTGGAGCGGTGGGTCTCTGTGAAATATTTCGCAAAATTGA 2279
QY 1033 GAAGTCCCCCTCCCTGGGCAGCGTTTCAGCAGGGGTCCTAGGCTGCCCTGGCACTGGCAGG 1092
Db 2280 AACGAAAGCTCCATTTTCTAGCCTGAAAGTAATCATTTTGTCTGTGCCCTGCTGGCCTT 2339
QY 1093 GCTGGCCGCGCACTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCCT 1152
Db 2340 GACCATGGCCGCACTTCCCTGCTGGTGGCAGCAAGTATGGCGCCTCCCTCTCTGCTGCT 2399
QY 1153 GCCCTACGGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCAACGTGGCCCTGGTGAT 1212
Db 2400 GCCTT-----TGCCTTTTGGGAGCCAGCAGCACCATGGGCTACATGGTGGCTCTCATCTT 2453
QY 1213 GATGAACCTCCTTCTGTTTCTGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGACCT 1272
Db 2454 GCTCAATTCCCTTGTCTTCTCATGATGACCATTTGCCCTACACCAAGCTCTACTGCAATT 2513
QY 1273 GCCCGGGGCGCACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGACGCTGGCCTGGCT 1332
Db 2514 GGACAAGGGAGACCTGGAGAAATATTTGGGACTGCTCTATGGTAAACACATTTGCCCTGTT 2573

Db 1294 GGGTTGATTTCTGTCTAACTTATTCATGGGAATCTATACCTGGCATCTCAACTTTTCTT 1353
QY 863 GATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGC 922
Db 1354 GATGCTGTCTCTGGGGCAGATTCGCTGAATTTGGCAATTTGGTGGGAAACTGGCAGTGGC 1413
QY 923 TGCCGGGCCACTGGCTTCTGCGCAGTACTTGGGTGGAGGCATCGGTGCTGCTCACT 982
Db 1414 TGCAAGTAACCTGGGTTTCTGTCAGTTTCTCCTCAGAAAGTGCCATATTTTATTAAATG 1473
QY 983 CTGGCCGCAGTGCAGTGCAGGCTCTCCGTCTCCTGTGTCGGGCCCTATGGGAAGTCCCC 1042
Db 1474 CTAGCAACTGTGCAAGAGCTTATCTGCAAAAGATATAATGAAAAATGGGAAGAGCAAT 1533
QY 1043 TCCCTGGGCAGCGTTTCGAGCAGGGGTCTAGGCTGCTGGCACTGGCAGGGCTGGCGGCC 1102
Db 1534 CATCTCAAAACAGTTCCGGGTGCTGCCCTTTTGGCTTCTCCTAGGTGCTACAGTAACAGGC 1593
QY 1103 GCACTGCCCCCTGGCCTCAGTGGGAGAATAACGGGGCCTCCCCACTCTGCCCTGACGCG 1162
Db 1594 TGTTTTCCCTTTTCCATAGAGGGGAATATCTGCATCACCCCTTTGTTGGCAT----- 1648
QY 1163 CCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACCTC 1222
Db 1649 -TTCCTACAGGTGAAACGCCATCATTAGGATTCACTGTAACTGTAGTCTATTAACTCA 1707
QY 1223 TTCTGTTTCTGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCCGGGGC 1282
Db 1708 CTAGCATTTTATTAAATGGCCGTTATCTACACTAAGCTATACTGCAACTTGGAAAAAGAG 1767
QY 1283 GACTTTGAGGCCGTGTGGACTGGCCATGGTGAGGACAGTGGCCCTGGCTCATCTTCGCA 1342
Db 1768 GACCTCTCAGAAAACTCAAACTAGCATGATTAAGCATGTGCTTGGCTAATCTTCACC 1827
QY 1343 GACGGGCTCCTCTACTGTCCGCTGGCCTTCTCAGCTTGCCTCCATGCTGGGCCTTTC 1402
Db 1828 AATTGCATCTTTTCTGCCCTGTGGCGTTTTCATTGTCACCATTGATCACTGCAATC 1887
QY 1403 CCTGTACGCCCGAGGCCGTCAAGTCTGTCTGTGTTGGTGCTGCCCTGCCCTGCTGC 1462
Db 1888 TCTATCAGCCCCGAAATAATGAAGTCTGTACTCTGATATTTTCCATTGCCCTGCTGC 1947
QY 1463 CTCAACCCACTGCTGTACTGCTCTTCAACCCCCACTTCCGGGATGAC 1510
Db 1948 CTGAATCCAGTCTGTATGTTTCTTCAACCCCAAGTTTAAAGAAGAC 1995

RESULT 8

US-09-153-593-1
; Sequence 1, Application US/09153593A
; Patent No. 6174994
; GENERAL INFORMATION:
; APPLICANT: ELSHOUBAGY, NABIL A
; APPLICANT: LI, XIAOTONG
; APPLICANT: BERGSMAN, DEK J
; TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
; FILE REFERENCE: GH-70055-1
; CURRENT APPLICATION NUMBER: US/09/153,593A
; CURRENT FILING DATE: 1998-09-15
; EARLIER APPLICATION NUMBER: 08/866,757
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4203
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-153-593-1

Query Match 7.8%; Score 194; DB 3; Length 4203;
Best Local Similarity 52.8%; Pred. No. 6.4e-38;
Matches 469; Conservative 0; Mismatches 410; Indels 9; Gaps 2;

QY 623 AGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGC 682
Db 1117 ATTATCCATTGTACACCTTCAACAGGTGCTTTTAAGCCCTGTGAATATTTACTGGGAAGC 1176
QY 683 TGGGGCATCCGCCCTGGCCGTGTGGCCCATCGTGTGTCTCCGTGCTCTGCAATGCACTG 742
Db 1177 TGGATGATTCGTCCTTACTGTGTGTTCAATTTTCTGTTGCATTTATTTTCAACCTGCTT 1236
QY 743 GTGCTGTGACCCGTGTTGCTGGCGGGCCTGCCCCCTTCCCTGTGGCCTTCTAGCCTCAGTC 802
Db 1237 GTTATTTTAAACAACATTTGCATCTTG--TACATCACTGCCCTTCGTCCAAATTTGTTATA 1293
QY 803 GGTGCGATTGACGGGCCCAACACCTTGACTGGCAATTTCTGTGGCCTTCTAGCCTCAGTC 862
Db 1294 GGCTTGATTTCTGTGTCTAACTTATTCATGGGAATCTATACCTGGCATCCTAACTTTCTT 1353
QY 863 GATGCCCTGACCTTTGGTTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGC 922
Db 1354 GATGCTGTCTCCTGGGCAGATTCGCTGAATTTGGCATTTGGTGGAAACTGGCAGTGGC 1413
QY 923 TGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTGGAGGCATCGGTGCTGCTCACT 982
Db 1414 TGCAAGTAACCTGGGTTTCTTGCAGTTTCTCCTCAGAAAGTGCCATATTTTATTAAATG 1473
QY 983 CTGGCCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCCTATGGGAAGTCCCC 1042
Db 1474 CTAGCAACTGTGCAAAAGAGCTTATCTGCAAAAGATATAATGAAAAATGGGAAGAGCAAT 1533
QY 1043 TCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGGGCTGGCGGCC 1102
Db 1534 CATCTCAAAACAGTTCCGGGTGCTGCCCTTTTGGCTTCTCCTAGGTGCTACAGTAACAGGC 1593
QY 1103 GCACTGCCCTTGGCCTCAGTGGGAGAATAACGGGGCCTCCCCACTCTGCTGCCCTACGCG 1162
Db 1594 TGTTTTCCCTTTTCCATAGAGGGGAATATTTCTGCATCACCCCTTTTGTGTCAT----- 1648
QY 1163 CCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACCTC 1222
Db 1649 -TTCCTACAGGTGAAACGCCATCATTAGGATTCACTGTAACTGTAGTCTATTAACTCA 1707
QY 1223 TTCTGTTTCTGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCCGGGGC 1282
Db 1708 CTAGCATTTTATTAAATGGCCGTTATCTACACTAAGCTATACTGCAACTTGGAAAAAGAG 1767
QY 1283 GACTTTGAGGCCGTGTGGACTGGCCCATGGTGAGGACAGTGGCCCTGGCTCATCTTCGCA 1342
Db 1768 GACCTCTCAGAAAACTCAAACTAGCATGATTAAGCATGTGCTTGGCTAATCTTCACC 1827
QY 1343 GACGGGCTCCTCTACTGTCCCCTGGCCTTCTCAGCTTGCCTCCATGCTGGGCCTCTTC 1402
Db 1828 AATTGCATCTTTTCTGCCCTGTGGCGTTTTCATTGTCACCATTGATCACTGCAATC 1887
QY 1403 CCTGTACGCCCGAGGCCGTCAAGTCTGTCTGTGTTGGTGCTGCCCTGCCCTGCTGC 1462
Db 1888 TCTATCAGCCCCGAAATAATGAAGTCTGTACTCTGATATTTTCCATTGCCCTGCTGC 1947
QY 1463 CTCAACCCACTGCTGTACTGCTCTTCAACCCCCACTTCCGGGATGAC 1510
Db 1948 CTGAATCCAGTCTGTATGTTTCTTCAACCCCAAGTTTAAAGAAGAC 1995

RESULT 9

US-09-495-050A-220
; Sequence 220, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED F
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A

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; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 220
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 2603450CT1
US-09-495-050A-220
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Query Match          7.3%; Score 181.8; DB 4; Length 723;
Best Local Similarity 55.8%; Pred. No. 3.3e-35;
Matches 392; Conservative 0; Mismatches 302; Indels 9; Gaps 2;
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QY 696 TGGCCGTGTGGCCATCGTGTGCTCTCCGTGCTCTGCAATGGACTGGTGTGCTGACCG 755
Db 1 TTGGAGTGTGGACCATAGCAGTTCTGGCACTTACTTGAATGCTTTGGTGACTTCAACAG 60

QY 756 TGTTCGCTGGCGGCTGCCCCCTGCCCCCGGTCAGTTTGTGGTAGGTGCGATTGCAG 815
Db 61 TTTTC--AGATCCCCTCTGTACATTTCCCCCATTAACACTGTTAATTGGGGTATCGCAG 117

QY 816 GCGCCAACACCTTGACTGGCATTTCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCT 875
Db 118 CAGTGAACATGCTCACGGGAGTCTCCAGTGCCGTGCTGGCTGGTGTGGATGCGTTCACTT 177

QY 876 TTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGGCCACTG 935
Db 178 TTGGCAGCTTTGACGACATGGTGCCCTGGTGGGAGATGGGGTTGGTTGCCATGTCATTG 237

QY 936 GCTTCCTGGCAGTACTTGGGTGGAGGCATCGGTGCTGCTGCTCACTCTGSCCGCAGTGC 995
Db 238 GTTTTGTCCATTTTGTCTCAGAAATCATCTGTTTTCCTGCTTACTCTGGCAGCCCTGG 297

QY 996 AGTCAGCGCTCCGCTCTCTGTGTCCGGCCCTATGGAAGTCCCCCTCCCTGGGCAGCG 1055
Db 298 AGCGTGGTTCTCTGTGAAATATTTGCAAAATTTGAACGAAAGCTCCATTTCTAGCC 357

QY 1056 TTCGAGCAGGGGTCCCTAGGCTGCCTGGCAGTGGCAGGGCTGGCCGCGCAGCTGCCCTGG 1115
Db 358 TGAAGTAATCATTTTGTCTGTGCCCTGCTGGCCCTTGACCATGGCCGCGAGTTCCCTGC 417

QY 1116 CCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCCCTGCCCTACGCGCCACCTGAGGGTC 1175
Db 418 TGGGTGGCAGCAAGTATGGCGCCTCCCTCTCTGCCCTGCCCTT-----TGCCTTTGGGG 471

QY 1176 AGCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGATGATGAACCTCCTTCTGTTCCCTGG 1235
Db 472 AGCCAGCACCATTGGGCTACATGGTCGCTCTCATCTGCTCAATTCCCTTTGCTTCCCTCA 531

QY 1236 TCGTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCGCGGGCGGACTTTGAGGCCG 1295
Db 532 TGATGACCATTGCCCTACACCAAGCTCTACTGCAATTTGGACAAGGAGACCTGGAGAATA 591

QY 1296 TGTGGACTGCGCCATGTTGAGGCACGTGGCCTGGCTCATCTTGGCAGACGGGCTCCTCT 1355
Db 592 TTTGGGACTGCTCTATGTTAAACACATTGGCCCTGTGCTCTTCCACCAACTGCATCCTAA 651

QY 1356 ACTGTCCCGTGGCCTTCTCAGCTTCGCCTTCCATGCTGGGCCCT 1398
Db 652 ACTGCCCTGTGGCTTTCTTGTCCCTTCTCCTCTTTTAATAAACCT 694
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RESULT 10
US-09-482-273-75
; Sequence 75, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
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; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-482-273-75
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Query Match          4.2%; Score 105; DB 4; Length 2703;
Best Local Similarity 56.5%; Pred. No. 7.1e-16;
Matches 195; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 1166 CCTGAGGGTCAGCCAGCAGCCCTGGGCTTCCCGCTTCCCGTGGTGTGATGATGAACCTCCTTC 1225
Db 13 CCTACAGGTGAACGCCATCATTAGGATTCACCTGTAACGTTAGTGTATTAAACTCACTA 72

QY 1226 TGTTCCTGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCGGGGCGAC 1285
Db 73 GCATTTTATTAAATGGCCGTTATCTACACTAAGCTATATACTGCAACTTGGAAAAAGAGGAC 132

QY 1286 TTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGCAGAC 1345
Db 133 CTCTCAGAAAACTCACAATCTAGCATGATTAAAGCATGTGCTTGGCTAATCTTCACCAAT 192

QY 1346 GGGTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCTCCCATGCTGGGCTCTTCCCT 1405
Db 193 TGCATCTTTTCTGCCCTGTGGCGTTTTTTTCATTTGCACCATTTGATCAGCTCAATCTCT 252

QY 1406 GTCACGCCCGAGCGCTCAAGTCTGTCTCTGCTGCTGGTGGTGTGCTGCCCTGCCCTGCCTC 1465
Db 253 ATCAGCCCCGGAATAATGAAGTCTGTTACTCTGATATTTTTTCCATTGCTTGCCTG 312

QY 1466 AACCCACTGCTGTACCTGCTCTTCAACCCCACTTCCGGGATGAC 1510
Db 313 AATCCAGTCTGTATGTTTTTCTTCAACCCCAAGTTTAAAGAAGAC 357
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RESULT 11
US-08-866-757-3
; Sequence 3, Application US/08866757
; Patent No. 5858716
; GENERAL INFORMATION:
; APPLICANT: ELSHOURBAGY, NABIL A
; APPLICANT: LI, XIAOTONG
; APPLICANT: BERGMA, DERK J
; TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,757
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; FILING DATE: 30-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-866-757-3

Query Match          4.1%; Score 101.8; DB 2; Length 473;
Best Local Similarity 56.8%; Pred. No. 2.1e-15;
Matches 187; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY 1182 CAGCCCTGGGCTTCACCGTGGCCCTGGTGATGAAGAACTCCTCTCTGTTTCCCTGGTCGTGG 1241
Db 14 CATCATTAGGATTCACTGTAACGTTAGTGCTATTAAACTCACTAGCATTTTATTATATGG 73

QY 1242 CCGTGCCCTACATCAAACTGTACTGTGACCTGCCGCGGGGCGGACTTTTGAGGCCCGTGTGG 1301
Db 74 CCGTTATCTACACTAAGCTATATACTGCAACTTGGAAAAAGAGGACCTCTCAGAAAACTCAC 133

QY 1302 ACTGCGCCATGGTGAGGACGCTGGCTGGCTCATCTTCGACAGACGGGCTCCTCTACTGTC 1361
Db 134 AATCTAGCATGATTAAAGCATGTGCTTGGCTAATCTTACCAATTTGCAATCTTTTCTGCC 193

QY 1362 CCGTGGCCTTCCCTCAGCTTCGCCCTCCATGCTGGGCTCTTCCCTGTCAAGCCCGAGCGG 1421
Db 194 CTGTGGCGTTTTTTTCAATTTGCACCATTTGATCATCTGCAATCTCTATCAGCCCCGAAATAA 253

QY 1422 TCAAGTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1481
Db 254 TGAAGTCTGTACTCTGATATTTTTCATTTGCCATTGGCTTGGCTGAATCCAGTCCCTGTATG 313

QY 1482 TGCTCTTCAACCCCACTTCCGGGATGAC 1510
Db 314 TTTTCTTCAACCCCAAGTTTAAAGAGGAC 342

RESULT 12
US-09-153-593-3
; Sequence 3, Application US/09153593A
; Patent No. 6174994
; GENERAL INFORMATION:
; APPLICANT: ELSHOURBAGY, NABIL A
; APPLICANT: LI, XIAOTONG
; APPLICANT: BERGSMAN, DERK J
; TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
; FILE REFERENCE: GH-70055-1
; CURRENT APPLICATION NUMBER: US/09/153,593A
; CURRENT FILING DATE: 1998-09-15
; EARLIER APPLICATION NUMBER: 08/866,757
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 473
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
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; LOCATION: (397) (400) (406) (432) (459)
US-09-153-593-3

Query Match          4.1%; Score 101.8; DB 3; Length 473;
Best Local Similarity 56.8%; Pred. No. 2.1e-15;
Matches 187; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY 1182 CAGCCCTGGGCTTCACCGTGGCCCTGGTGATGAAGAACTCCTCTCTGTTTCCCTGGTCGTGG 1241
Db 14 CATCATTAGGATTCACTGTAACGTTAGTGCTATTAAACTCACTAGCATTTTATTATATGG 73

QY 1242 CCGTGCCCTACATCAAACTGTACTGTGACCTGCCGCGGGGCGGACTTTTGAGGCCCGTGTGG 1301
Db 74 CCGTTATCTACACTAAGCTATATACTGCAACTTGGAAAAAGAGGACCTCTCAGAAAACTCAC 133

QY 1302 ACTGCGCCATGGTGAGGACGCTGGCTGGCTCATCTTCGACAGACGGGCTCCTCTACTGTC 1361
Db 134 AATCTAGCATGATTAAAGCATGTGCTTGGCTAATCTTACCAATTTGCAATCTTTTCTGCC 193

QY 1362 CCGTGGCCTTCCCTCAGCTTCGCCCTCCATGCTGGGCTCTTCCCTGTCAAGCCCGAGCGG 1421
Db 194 CTGTGGCGTTTTTTTCAATTTGCACCATTTGATCATCTGCAATCTCTATCAGCCCCGAAATAA 253

QY 1422 TCAAGTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1481
Db 254 TGAAGTCTGTACTCTGATATTTTTCATTTGCCATTGGCTTGGCTGAATCCAGTCCCTGTATG 313

QY 1482 TGCTCTTCAACCCCACTTCCGGGATGAC 1510
Db 314 TTTTCTTCAACCCCAAGTTTAAAGAGGAC 342

RESULT 13
US-08-383-756-1
; Sequence 1, Application US/08383756
; Patent No. 5654495
; GENERAL INFORMATION:
; APPLICANT: Dehesh, Katayoon
; APPLICANT: Voelker, Toni Alois
; APPLICANT: Hawkins, Deborah
; APPLICANT: Davies, Huw Maelor
; TITLE OF INVENTION: Production of Myristate in Plant Cells
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 5.1(a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,756
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/261,695
; FILING DATE: 16-JUN-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10814
; FILING DATE: 29-OCT-93
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 07/968,971
; FILING DATE: 30-OCT-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
```



```
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1581 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
US-08-383-756-1

Query Match      4.0%; Score 100; DB 1; Length 1581;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2387 TTAAAAAAGGGCGCGCTCTAGAGGATCCAAGCTTACGTACGCGTGCATG 2446
Db 1477 TTAAAAAAGGGCGCGCTCTAGAGGATCCAAGCTTACGTACGCGTGCATG 1536

Qy 2447 CGACGTCATAGCTCTTCTATAGTGTACCTAAATTCAATT 2486
Db 1537 CGACGTCATAGCTCTTCTATAGTGTACCTAAATTCAATT 1576

RESULT 14
US-08-460-898-1
; Sequence 1, Application US/08460898
; Patent No. 5850022
; GENERAL INFORMATION:
; APPLICANT: Dehesh, Katayoon
; APPLICANT: Voelker, Toni Alois
; APPLICANT: Hawkins, Deborah
; APPLICANT: Davies, Huw Maelor
; TITLE OF INVENTION: Production of Myristate in Plant Cells
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 5.1(a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,898
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/383,756
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/261,695
; FILING DATE: 16-JUN-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10814
; FILING DATE: 29-OCT-93
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 07/968,971
; FILING DATE: 30-OCT-92
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 111-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1581 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
US-08-460-898-1

Query Match      4.0%; Score 100; DB 2; Length 1581;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2387 TTAAAAAAGGGCGCGCTCTAGAGGATCCAAGCTTACGTACGCGTGCATG 2446
Db 1477 TTAAAAAAGGGCGCGCTCTAGAGGATCCAAGCTTACGTACGCGTGCATG 1536

Qy 2447 CGACGTCATAGCTCTTCTATAGTGTACCTAAATTCAATT 2486
Db 1537 CGACGTCATAGCTCTTCTATAGTGTACCTAAATTCAATT 1576

RESULT 15
US-09-118-442-31
; Sequence 31, Application US/09118442B
; Patent No. 6197561
; GENERAL INFORMATION:
; APPLICANT: Martino-Catt, Susan J.
; APPLICANT: Wang, Hongyu
; APPLICANT: Beach, Larry R.
; APPLICANT: Wang, Xun
; APPLICANT: Bowen, Benjamin A.
; TITLE OF INVENTION: Genes Controlling Phytate Metabolism in
; TITLE OF INVENTION: Plants and Uses Thereof
; FILE REFERENCE: 0706
; CURRENT APPLICATION NUMBER: US/09/118,442B
; CURRENT FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 60/055,446
; EARLIER FILING DATE: 1997-08-11
; EARLIER APPLICATION NUMBER: 60/055,526
; EARLIER FILING DATE: 1997-08-08
; EARLIER APPLICATION NUMBER: 60/053,944
; EARLIER FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 1255
; TYPE: DNA
; ORGANISM: Zea mays
US-09-118-442-31

Query Match      3.8%; Score 95.4; DB 3; Length 1255;
Best Local Similarity 99.0%; Pred. No. 1.3e-13;
Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2387 TTAAAAAAGGGCGCGCTCTAGAGGATCCAAGCTTACGTACGCGTGCATG 2446
Db 1159 TCAAAAAAAGGGCGCGCTCTAGAGGATCCAAGCTTACGTACGCGTGCATG 1218

Qy 2447 CGACGTCATAGCTCTTCTATAGTGTACCTAAATTCA 2483
Db 1219 CGACGTCATAGCTCTTCTATAGTGTACCTAAATTCA 1255
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Perfect score: 2486
Sequence: 1 taatacgactcactataggg.....agtgtcacctaataattcaatt 2486

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
3: gb_in:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2309.8	92.9	3451	6	CQ840814	CQ840814 Sequence
3	2309.4	92.9	2322	6	AX098217	AX098217 Sequence
4	2257.4	90.8	2711	6	AX301828	AX301828 Sequence
5	2247.8	90.4	3286	9	BC047905	BC047905 Homo sapi
6	2247.8	90.4	3306	6	CQ840811	CQ840811 Sequence
7	2247.8	90.4	3349	6	AX926300	AX926300 Sequence
8	2247.2	90.4	3325	9	AY358119	AY358119 Homo sapi
9	2241	90.1	3429	6	AX451929	AX451929 Sequence
10	2238	90.0	3492	6	AX301831	AX301831 Sequence
11	2231.4	89.8	3273	6	CQ870634	CQ870634 Sequence
12	2219.6	89.3	3041	6	E42917	E42917 Novel gonad
13	2219.6	89.3	3041	6	AX016191	AX016191 Sequence
14	2219.6	89.3	3381	6	AX527920	AX527920 Sequence
15	2085.8	83.9	3119	6	AX549295	AX549295 Sequence
16	2085.8	83.9	3119	9	AB049405	AB049405 Homo sapi
17	1898	76.3	1899	6	AX301827	AX301827 Sequence
18	1844.2	74.2	1987	6	E42916	E42916 Novel gonad
19	1844.2	74.2	1987	6	AX016189	AX016189 Sequence

20	1754.4	70.6	2208	6	AX301830	AX301830 Sequence
21	1754.4	70.6	2901	6	AX301833	AX301833 Sequence
22	1752.6	70.5	2487	6	AX926297	AX926297 Sequence
23	1743	70.1	119596	6	AX926299	AX926299 Sequence
24	1743	70.1	177344	9	AL356953	AL356953 Human DNA
25	1738.6	69.9	2484	9	AF190501	AF190501 Homo sapi
26	1673	67.3	1681	6	BD159457	BD159457 Primer fo
27	1673	67.3	1681	6	AX882015	AX882015 Sequence
28	1673	67.3	1681	6	BD012484	BD012484 Guanosine
29	1673	67.3	1681	9	AK027377	AK027377 Homo sapi
30	1664.8	67.0	178757	2	AC074007	AC074007 Homo sapi
31	1383.4	55.6	3637	6	AX301822	AX301822 Sequence
32	1336	53.7	2901	6	AX301824	AX301824 Sequence
33	1257.8	50.6	1272	9	AB083616	AB083616 Homo sapi
34	1089.4	43.8	2044	10	BC026896	BC026896 Mus muscu
35	987.2	39.7	253599	2	AC117827	AC117827 Mus muscu
36	960.4	38.6	227401	2	AC105613	AC105613 Rattus no
37	960.4	38.6	238582	2	AC098661	AC098661 Rattus no
38	960.4	38.6	247017	2	AC110384	AC110384 Rattus no
39	806.2	32.4	1827	6	CQ842816	CQ842816 Sequence
40	806.2	32.4	1827	9	AK123055	AK123055 Homo sapi
41	723.2	29.1	1173	6	BD144308	BD144308 Novel G-p
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43	710.2	28.6	785	6	AX866695	AX866695 Sequence
44	513.4	20.7	515	6	E42913	E42913 Novel gonad
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ALIGNMENTS

RESULT 1
AX301825
LOCUS AX301825 2486 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 4 from Patent WO0185768.
ACCESSION AX301825
VERSION AX301825.1 GI:17382883
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,W.
TITLE Novel g-protein coupled receptors and uses therefor
JOURNAL Patent: WO 0185768-A 4 15-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)
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ORIGIN

Query Match 100.0%; Score 2485; DB 6; Length 2486;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	61	GTCGACCCACGCGTCCGTGAGCGGAGCCAGGCTCTGAGCCTGCCGGCTCATCCAGCCTC	120
QY	121	TCTTGCTGCCCTAGCGGCTCCAAACAAACCGCATCTGGGAAATTGGAGCTNGACACCTT	180
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RESULT 2
CQ840814 CQ840814 3451 bp DNA linear PAT 29-JUL-2004
LOCUS
DEFINITION Sequence 4 from Patent WO2004058818.
ACCESSION CQ840814
VERSION CQ840814.1 GI:50838404
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Muda,M.
TITLE Spliced variants of lgr6
JOURNAL Patent: WO 2004058818-A 4 15-JUL-2004;
Applied Research Systems ARS Holding N.V. (AN)
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ORIGIN
Query Match 92.9%; Score 2309.8; DB 6; Length 3451;
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Matches 2325; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
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RESULT 4
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LOCUS AX301828 2711 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 7 from Patent WO0185768.
ACCESSION AX301828
VERSION AX301828.1 GI:17382887
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Gu,W.
TITLE Novel g-protein coupled receptors and uses therefor
JOURNAL Patent: WO 0185768-A 7 15-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)
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RESULT 5 BC047905 3286 bp mRNA linear PRI 22-APR-2003
LOCUS Homo sapiens leucine-rich repeat-containing G protein-coupled
-DEFINITION receptor 6, mRNA (cdna clone IMAGE:5212508), partial cds.
ACCESSION BC047905
VERSION BC047905.1 GI:29126870
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3286)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.C., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cdna sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932

2 (bases 1 to 3286)
Strausberg,R.
Direct Submission
Submitted (03-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cdna Library Preparation: Life Technologies, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

REMARK
COMMENT

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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CDS

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JOURNAL	Patent: WO 2004058818-A 1 15-JUL-2004;			
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DEFINITION Sequence 4 from Patent WO02068651.
ACCESSION AX926300
VERSION AX926300.1 GI:40245662
KEYWORDS .
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhu,S.C., Chaturvedi,K.C., Ketchum,K.C., di Francesco,V.C. and Beasley,E.M.
TITLE Isolated human g-protein coupled receptors, nucleic acid molecules encoding human gpcr proteins, and uses thereof
JOURNAL Patent: WO 02068651-A 4 06-SEP-2002;
PE Corporation (NY) (US)
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Query Match 90.4%; Score 2247.8; DB 6; Length 3349;
Best Local Similarity 99.6%; Pred. No. 0;
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QY	1453	GCCTGCCTGCCTCAACCCACTGTCTACTGTCTTCAACCCCCACTTCCGGGATGACCT	1512								
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RESULT 9
AX451929
LOCUS AX451929 3429 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 26 from Patent WO0226825.
ACCESSION AX451929
VERSION AX451929.1 GI:21698752
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Baughn,M.R., Graul,R.C., Walia,N.K., Gandhi,A.R., Hafalia,A.J.,
Ramkumar,J., Tribouley,C.M., Thornton,M., Kallick,D.A., Yao,M.G.,
Elliot,V.S., Burford,N., Khan,F.A., Yue,H., Lu,Y., Arvizu,C.,
Roopa,R., Nguyen,D.B., Lee,E.A., Lu,D.A., Ison,C.H., Walsh,R.T. and
Policky,J.L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 0226825-A 26 04-APR-2002;
Incyte Genomics, Inc. (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
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/note="Incyte ID No: 7479890CB1"
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Query Match 90.1%; Score 2241; DB 6; Length 3429;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2255; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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LOCUS AX301831 3492 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 10 from Patent WO0185768.
ACCESSION AX301831
VERSION AX301831.1 GI:17382891
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,W.
TITLE Novel g-protein coupled receptors and uses therefor
JOURNAL Patent: WO 0185768-A 10 15-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)
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ORIGIN

Query Match 90.0%; Score 2238; DB 6; Length 3492;
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Db ||||| 1297 CTCCCTGCAAGCCCTGGATCTTAGCTGGAAGCCCATCCGGTCCATCCACCTGAGGCCTT 1356
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Db ||||| 1357 CTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTGACACACTGCC 1416
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Qy 553 AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAA 612
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Qy 853 AGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC 912

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QY	1993	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCACCTCT	2052
Db	3097	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCACCTCT	3156
QY	2053	CTCCTGTGACCATCACCAACGGGTGCCTCTTGGCCCTGGCTTTCCCTTGGCCTTCCTCAGC	2112
Db	3157	CTCCTGTGACCATCACCAACGGGTGCCTCTTGGCCCTGGCTTTCCCTTGGCCTTCCTCAGC	3216
QY	2113	TTCACCTTGATACTGGGCCCTCTTCCTTGTCTCATGTCTGAAGCTGTGGACCAGAGACCTGGA	2172
Db	3217	TTCACCTTGATACTGGGCCCTCTTCCTTGTCTCATGTCTGAAGCTGTGGACCAGAGACCTGGA	3276
QY	2173	CTTTTGTCTGCTTAAGGGAAATGAGGGAAAGTAAAGACAGTGAAGGGTGGAGGGTTTGATC	2232
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QY	2233	AGGSCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCCTGGAAAGTGATTTCCCGTGTGA	2292
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QY	2293	CTCATGGATAGGATACAAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCAT	2352
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Qy	193	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTTGAGGCCTT	252		
Db	1081	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCGAGGCCTT	1140		
Qy	253	CTCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAAACAGCTGACCACTGCC	312		
Db	1141	CTCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAAACAGCTGACCACTGCC	1200		
Qy	313	CCTGGCTGGACTTGGGGCTTGATGTCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA	372		

Db	1201	CTGGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGTCTCTCTCCCA	1260
QY	373	GGCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCTTACCA	432
Db	1261	GGCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCTTACCA	1320
QY	433	GTGCTGTCCCTATAGGATGTGTGCCAGCTTCTTCAAGGCTCTGGGCAGTGGGAGCTGA	492
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QY	493	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCTCCTTTGCCAGACA	552
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QY	613	GCCACACCCAGTGTCCAGGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	672
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QY	673	CTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGGCCATCGTTGCTCTCCGTCTCTG	732
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QY	793	GTTTGTGTAGGTGCGATTGACGGCGCCAAACCTTGACTGGCATTTCTGTGGCCTTCT	852
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QY	973	GCTGCTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGCCCTATGG	1032
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QY	1033	GAAGTCCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCTAGGCTGCCCTGGCACTGGCAGG	1092
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QY	1093	GCTGGCCGCCGACTGCCCTGGCCTCAGTGGGAGAATACGGGGCTTCCCACCTCTGCCCT	1152
Db	1981	GCTGGCCGCCCGCTGCCCTGGCCTCAGTGGGAGAATACGGGGCTTCCCACCTCTGCCCT	2040
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QY	1273	GCCGGGGGGCAGTTTGAGGCCGTGTGGGACTGGCCCATGGTGAAGCTGGCCCTGGCT	1332
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QY	1333	CATCTTCGCAGACGGGCTCCTCTACTGTCCGTGGCCTTCTCAGCTTCGCTCCCATGCT	1392
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QY	1393	GGGCCTCTTCCCTGTACAGCCCGGAGGCCGTCAAGTCTGTCTGCTGGTGGTGTGCCCT	1452
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Db	2401	TCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCGGGGA	2460
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Db	2521	CATTCTGGAAGCTTCTGAAGCTGGCGGGCCCCCTGGGCTGGAGACCTATGSGCTTCCCCTC	2580
QY	1693	AGTGACCTCATCTCTCTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGGCAGCCATTGTGT	1752
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QY	1753	AGAGCCAGAGGGAAACCACTTTGGGAAACCCCAAACCTTCCATGGATGGAGAACTGCTGCT	1812
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QY	1813	GAGGCAGAGGGATCTAGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGGCTTTCAGCC	1872
Db	2701	GAGGCAGAGGGATCTAGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGGCTTTCAGCC	2760
QY	1873	CTCTGGCTTGGCCTTGTCTTACACCGTGTAAATATCCCTCCCCATTTCTTCTTCCCCTC	1932
Db	2761	CTCTGGCTTGGCCTTGTCTTACACCGTGTAAATATCCCTCCCCATTTCTTCTTCCCCTC	2820
QY	1933	TCTTCCCCTTCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAAACAATAACAACCA	1992
Db	2821	TCTTCCCCTTCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAAACAATAACAACCA	2880
QY	1993	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACCTGGCTCCAATGATCACCTCT	2052
Db	2881	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACCTGGCTCCAATGATCACCTCT	2940
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Novel gonadotropin receptor.			
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GI:18627553			
JP 2000125884-A/5.			
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PAT 31-JAN-2002			
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SOURCE	unidentified
ORGANISM	unidentified
REFERENCE	1 (bases 1 to 3041)
AUTHORS	Heikopu,Y.C. and Supekku,P.J.V.D.
TITLE	Novel gonadotropin receptor
JOURNAL	Patent: JP 2000125884-A 5 09-MAY-2000;
COMMENT	AKZO NOBEL NV
OS	Unidentified
PN	JP 2000125884-A/5
PD	09-MAY-2000
PF	05-FEB-1999 JP 1999029120
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24-SEP-1998 EP 98203213.8	
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Best Local Similarity	99.7%; Pred. No. 0;
Matches 2255; Conservative	0; Mismatches 4; Indels 3; Gaps 3;
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Db	777 CTCCTCTGAAGCCCTTGGATCTTAGCTGGAAAGCCCATCCGGTCCATCCACCCAGGCCTT 836
QY	253 CTCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACTGCC 312
Db	837 CTCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACTGCC 896
QY	313 CTTGGCTGGACTTGGGGGCTTGTATGTCATCTGAAGCTCAAGGGAACCTTGTCTCTCCCA 372
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Db	1257	CTTTGAAAGCTGGGCATCCGCTGGCCGTGGCCATCGTGTGCTCTCCGTGCTGTG 1316
QY	733	CAATGGACTGGTGTGCTGACCGGTTCGCTGGGGGCTTCCCCCTGCCCCCGGTCAA 792
Db	1317	CAATGGACTGGTGTGCTGACCGGTTCGCTGGGGGCTTCCCCCTGCCCCCGGTCAA 1376
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AX016191

LOCUS AX016191 3041 bp DNA linear PAT 07-SEP-2000

DEFINITION Sequence 9 from Patent EP0950711.

ACCESSION AX016191

VERSION AX016191.1 GI:10041796

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Heikoop,J.C. and Van Der Spek,P.J.

TITLE Gonadotropin receptor

JOURNAL Patent: EP 0950711-A 9 20-OCT-1999;

AKZO NOBEL NV (NL)

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Query Match 89.3%; Score 2219.6; DB 6; Length 3041;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2255; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

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VERSION	AX527920.1	GI:25172361	
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ORGANISM	Homo sapiens		
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AUTHORS	Herrmann, J.L., Rastelli, L. and Shimkets, R.A.		
TITLE	Novel proteins and nucleic acids encoding same and antibodies directed against these proteins		
JOURNAL	Patent: WO 0229038-A 5 11-APR-2002;		
	Curagen Corporation (US)		
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VERSION AX549295.1 GI:25813958
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Burmer,G.C., Roush,C.L. and Brown,J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 580 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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Qy 2233 A 2233
Db 3119 A 3119

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 10:59:27 ; Search time 877.045 Seconds
(without alignments)
16779.616 Million cell updates/sec

Title: US-10-664-667-4
Perfect score: 2486
Sequence: 1 taatacagactcactataggg.....agtgtaacctaaattcaatt 2486

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
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12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2485	100.0	2486	6 AAI67922	Aai67922 Human LGR
2	2485	100.0	2486	11 ADN02242	Adn02242 Human par
3	2485	100.0	2486	12 ADK19407	Adk19407 cDNA enco
4	2309.8	92.9	3451	12 ADQ76775	Adq76775 Human LGR
5	2309.4	92.9	2322	5 AAF98722	Aaf98722 Human lat
6	2257.4	90.8	2711	6 AAI67924	Aai67924 Partial c
7	2257.4	90.8	2711	11 ADN02245	Adn02245 Human par
8	2257.4	90.8	2711	12 ADK19410	Adk19410 Partial c
9	2255.8	90.7	2988	6 ABZ11841	Abz11841 Human pol
10	2255.8	90.7	2988	12 ADM44359	Adm44359 Novel hum
11	2247.8	90.4	3306	12 ADQ76773	Adq76773 Human LGR
12	2247.8	90.4	3349	6 ADH50807	Adh50807 Human G-p
13	2247.2	90.4	3325	10 ADD89048	Add89048 Encoding
14	2243	90.2	2964	10 ADI21981	Adi21981 Novel hum
15	2241	90.1	3429	6 AAD37674	Aad37674 Human G-p
16	2238	90.0	3443	10 ADD89090	Add89090 Encoding
17	2238	90.0	3492	6 AAI67926	Aai67926 Human LGR
18	2238	90.0	3492	11 ADN02248	Adn02248 Human ful
19	2238	90.0	3492	12 ADK19413	Adk19413 Full leng
20	2238	90.0	3492	12 ADQ15073	Adq15073 Human can

21	2231.4	89.8	3273	11 ADN39801	Adn39801 Cancer/an
22	2231.4	89.8	3273	13 ADR46630	Adr46630 Cancer-as
23	2219.6	89.3	3041	2 AAZ40461	Aaz40461 Human gon
24	2219.6	89.3	3381	10 ADG42572	Adg42572 Novel hum
25	2218	89.2	3381	6 ABK49424	Abk49424 DNA enco
26	2123.8	85.4	2168	10 ADI21492	Adi21492 Novel hum
27	2085.8	83.9	3119	8 ABZ42549	Abz42549 Human G p
28	1966.8	79.1	3000	6 AAS98067	Aas98067 Human DNA
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30	1898	76.3	1899	11 ADN02244	Adn02244 Human par
31	1898	76.3	1899	12 ADK19409	Adk19409 ORF of cD
32	1844.2	74.2	1987	2 AAZ40460	Aaz40460 Human gon
33	1754.4	70.6	2208	6 AAI67925	Aai67925 Human LGR
34	1754.4	70.6	2208	11 ADN02247	Adn02247 Human par
35	1754.4	70.6	2208	12 ADK19412	Adk19412 ORF of pa
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39	1754.4	70.6	2901	12 ADK19415	Adk19415 ORF of fu
40	1754.4	70.6	3042	10 ADC16698	Adc16698 cDNA enco
41	1754.4	70.6	3438	10 ABT31938	Abt31938 Human bre
42	1752.8	70.5	2786	10 ADC16710	Adc16710 Human G-p
43	1752.8	70.5	3042	10 ADC16700	Adc16700 cDNA enco
44	1752.6	70.5	2487	6 ADH50804	Adh50804 Human G-p
45	1749.6	70.4	2901	10 ADC16695	Adc16695 cDNA with

ALIGNMENTS

RESULT 1
AAI67922
ID AAI67922 standard; cDNA; 2486 BP.
XX

AC AAI67922;

DT 13-MAR-2002 (first entry)

XX Human LGR6 polypeptide encoding cDNA (clone fahr).

KW Large G-protein coupled receptor 6; LGR6; GPCR; immunomodulator;
anti-HIV; cytostatic; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; neuroleptic; antidepressant; tranquilizer; antimigraine;
osteopathic; antiarteriosclerotic; vasotropic; hypotensive; cardiant;
KW antiarrhythmic; anorectic; gene therapy; human; ss.
XX Homo sapiens.

OS Homo sapiens.

XX
FH Key Location/Qualifiers
CDS 2..1903

FT /*tag= a
FT /product= "LGR6 polypeptide"
FT /transl_except= (pos: 170..172, aa: Xaa)
FT /note= "Xaa = unknown"

FT WO200185768-A2.

XX
PD 15-NOV-2001.

XX
PF 08-MAY-2001; 2001WO-US015002.

XX
PR 08-MAY-2000; 2000US-00566588.

XX
PA (MILL-) MILLENNIUM PHARM INC.

XX
PI Gu W;

XX
DR WPI; 2002-055584/07.

XX
DR P-PSDB; AAG66139.

XX
PT Novel isolated large G-protein coupled receptor 6 polypeptide, useful for
diagnosing and treating weight disorder, metabolic disorder, central
nervous system disorder, endocrine disorder and cardiovascular disorder.

XX Example 1; Fig 4; 198pp; English.

CC The invention provides isolated large G-protein coupled receptor 6 (LGR6)

CC polypeptides and polynucleotides encoding them. The LGR6 polypeptides and

CC polynucleotides are useful as targets for developing modulating agents

CC that regulate a variety of cellular process, e.g. neural and endocrine

CC processes, as well as thermogenesis. They are useful for developing novel

CC diagnostic and therapeutic agents for LGR6 associated disorders such as

CC weight disorders (anorexia, obesity), eating disorders, acquired

CC immunodeficiency syndrome (AIDS)-related wasting, cancer-related wasting,

CC metabolic disorders, central nervous system disorders (e.g. Alzheimer's

CC disease, Parkinson's disease, Huntington's disease, Gilles de la

CC Tourette's syndrome, multiple sclerosis, amyotrophic lateral sclerosis,

CC epilepsy, Jakob-Creutzfeldt disease, depression, schizophrenia,

CC obsessive-compulsive disorder, anxiety, panic disorder, migraine),

CC endocrine disorders (hypo and hyperthyroidism, dwarfism, gigantism,

CC acromegaly), and cardiovascular disorders (atherosclerosis, restenosis,

CC hypertension, myocardial infarction, arrhythmia). The LGR6 polypeptides,

CC polynucleotides and antibodies are useful in screening assays, detection

CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),

CC predictive medicine (e.g. diagnostic assays, prognostic assays,

CC monitoring clinical trials and pharmacogenomics), and in methods of

CC treatment (e.g. therapeutic and prophylactic). The present sequence

CC represents a human LGR6 polypeptide encoding cDNA

XX

SQ Sequence 2486 BP; 455 A; 773 C; 692 G; 565 T; 0 U; 1 Other;

Query Match 100.0%; Score 2485; DB 6; Length 2486;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAATACGACTCACTATAGGGAAGCTGGTACGCCCTGCAGGTACCGGTCCGGAAFTCCCGG 60

DB 1 TAATACGACTCACTATAGGGAAGCTGGTACGCCCTGCAGGTACCGGTCCGGAAFTCCCGG 60

QY 61 GTCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTC 120

DB 61 GTCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTC 120

QY 121 TCTTGCTGCCCTAGCGGCCTCCAAACACACCGCATCTGGGAAATTGGAGCTNGACACCTT 180

DB 121 TCTTGCTGCCCTAGCGGCCTCCAAACACACCGCATCTGGGAAATTGGAGCTNGACACCTT 180

QY 181 CAGCCAGCTGAGCTCCCTGCAAGCCCCTGGATCTTAGTGGAAACGCCATCCGGTCCATCCA 240

DB 181 CAGCCAGCTGAGCTCCCTGCAAGCCCCTGGATCTTAGTGGAAACGCCATCCGGTCCATCCA 240

QY 241 CCCTGAGGCCTTCTCCACCGCTGCACTCCCTGGTCAAGCTGGACCTGACAGAACCCAGCT 300

DB 241 CCCTGAGGCCTTCTCCACCGCTGCACTCCCTGGTCAAGCTGGACCTGACAGAACCCAGCT 300

QY 301 GACCACACTGCCCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAGGGAAACCT 360

DB 301 GACCACACTGCCCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAGGGAAACCT 360

QY 361 TGCTCTCTCCAGGCCTTCTCCAAGGACAGTTTCCAAAAACTGAGGATCCTGGAGGTGCC 420

DB 361 TGCTCTCTCCAGGCCTTCTCCAAGGACAGTTTCCAAAAACTGAGGATCCTGGAGGTGCC 420

QY 421 TTATGCCTACCAGTGCTGTCCCTATGGGATGTGTGCGAGCTTCTTCAAGGCCCTCTGGGCA 480

DB 421 TTATGCCTACCAGTGCTGTCCCTATGGGATGTGTGCGAGCTTCTTCAAGGCCCTCTGGGCA 480

QY 481 GTGGGAGGCTGAAGACCTTCACTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCT 540

DB 481 GTGGGAGGCTGAAGACCTTCACTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCT 540

QY 541 CCTTGCCAGACAAGCAGAGAACCACCTATGACCAGGACCTGGATGAGCTCCAGTGGAGAT 600

DB 541 CCTTGCCAGACAAGCAGAGAACCACCTATGACCAGGACCTGGATGAGCTCCAGTGGAGAT 600

QY 601 GGAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCC 660

DB 601 GGAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCC 660

QY 661 CTGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCT 720

DB 661 CTGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCT 720

QY 721 CTCCGTGCTCTGCAATGGACTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780

DB 721 CTCCGTGCTCTGCAATGGACTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780

QY 781 GCCCCCGGTCAAAGTTTGTGGTAGGTGCGATTGCAAGCGGCCAAACACCTTGACTGGCATTT 840

DB 781 GCCCCCGGTCAAAGTTTGTGGTAGGTGCGATTGCAAGCGGCCAAACACCTTGACTGGCATTT 840

QY 841 CTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGC 900

DB 841 CTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGC 900

QY 901 CCGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTCCGA 960

DB 901 CCGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTCCGA 960

QY 961 GGCATCGGTGCTGCTCACTCTGGCCGCACTGTCAGTGCAGCGTCTCCGTCCTCTGTGT 1020

DB 961 GGCATCGGTGCTGCTCACTCTGGCCGCACTGTCAGTGCAGCGTCTCCGTCCTCTGTGT 1020

QY 1021 CCGGGCCTATGGGAAGTCCCCCTCCCTGGGACGCTTCGAGCAGGGGTCCCTAGGCTGCCT 1080

DB 1021 CCGGGCCTATGGGAAGTCCCCCTCCCTGGGACGCTTCGAGCAGGGGTCCCTAGGCTGCCT 1080

QY 1081 GGCACCTGGCAGGCTGGCCCGCCGCACTGCCCTGGCCCTCAGTGGGAGAAATACGGGGCCTC 1140

DB 1081 GGCACCTGGCAGGCTGGCCCGCCGCACTGCCCTGGCCCTCAGTGGGAGAAATACGGGGCCTC 1140

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DB 1141 CCCACTCTGCCCTGCCCCTACGGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTACCGT 1200

QY 1201 GGCCCTGGTGATGATGAACCTCCTTCTGTTTCTGGTCTGTGGCCGTGCCTACATCAAAC 1260

DB 1201 GGCCCTGGTGATGATGAACCTCCTTCTGTTTCTGGTCTGTGGCCGTGCCTACATCAAAC 1260

QY 1261 GTACTGTGACCTGCCCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCA 1320

DB 1261 GTACTGTGACCTGCCCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCA 1320

QY 1321 CGTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCTCAGCTT 1380

DB 1321 CGTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCTCAGCTT 1380

QY 1381 CGCCTCCATGCTGGGCCTCTTCCCTGTCAAGCCCGAGGCCGTCAAGTCTGTCTGTGTT 1440

DB 1381 CGCCTCCATGCTGGGCCTCTTCCCTGTCAAGCCCGAGGCCGTCAAGTCTGTCTGTGTT 1440

QY 1441 GGTGTGCCCTGCCCTGCCCTCAACCCACTGCTGTACCTGCTTCAACCCCCACTT 1500

DB 1441 GGTGTGCCCTGCCCTGCCCTCAACCCACTGCTGTACCTGCTTCAACCCCCACTT 1500

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DB 1501 CCGGATGACCTTCGGCGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGC 1560

QY 1561 TGCGCGCGGGGAGCTGGAGAAGAGCTCCTGTGATTTACCCAGGCCCTGGTGGCTTCTC 1620

DB 1561 TGCGCGCGGGGAGCTGGAGAAGAGCTCCTGTGATTTACCCAGGCCCTGGTGGCTTCTC 1620

QY 1621 TGATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGGGCGGCCCTGGGTGGAGACCTA 1680

DB 1621 TGATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGGGCGGCCCTGGGTGGAGACCTA 1680

QY 1681 TGGCTTCCCCCTCAGTGACCTCATCTCCTGTGTCAGCAGCCAGGGGCCCCCAGGCTGGAGG 1740

Db 1681 TGGCTTCCCCTCAGTGACCCCTCATCTCCTGTGTCAGCAGCCAGGGGGCCCCCAGGCTGGAGGG 1740

QY 1741 CAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGG 1800

Db 1741 CAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGG 1800

QY 1801 AGAACTGCTGTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGCTGG 1860

Db 1801 AGAACTGCTGTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGCTGG 1860

QY 1861 CGGCTTTCAGCCCTCTGGCTTGGCCCTTGTCTTCACACGCTGTAATAATCCCTCCCCATTCT 1920

Db 1861 CGGCTTTCAGCCCTCTGGCTTGGCCCTTGTCTTCACACGCTGTAATAATCCCTCCCCATTCT 1920

QY 1921 TCTCTTCCCCTCTCTTCCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAA 1980

Db 1921 TCTCTTCCCCTCTCTTCCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAA 1980

QY 1981 CAAATACAACCAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACCTGGCTCCA 2040

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QY 2041 CTGATCACCTCTCTCTGTGACCATCACCAACGGGTGCTCTTGGCCTGGCTTCCCTTG 2100

Db 2041 CTGATCACCTCTCTCTGTGACCATCACCAACGGGTGCTCTTGGCCTGGCTTCCCTTG 2100

QY 2101 GCCTTCCTCAGCTTACCTTGATCTACCTTGGCCCTCTTCCCTGTTCATGTCTGAAGCTGGAC 2160

Db 2101 GCCTTCCTCAGCTTACCTTGATCTACCTTGGCCCTCTTCCCTGTTCATGTCTGAAGCTGGAC 2160

QY 2161 CAGAGACCTGGACTTTTGTCTGTCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGT 2220

Db 2161 CAGAGACCTGGACTTTTGTCTGTCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGT 2220

QY 2221 GGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCTGGAAAGTGA 2280

Db 2221 GGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCTGGAAAGTGA 2280

QY 2281 TTTCCCGTGTGACTCATGTAGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACA 2340

Db 2281 TTTCCCGTGTGACTCATGTAGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACA 2340

QY 2341 TATGCCATGCATAAAGACTTCCTATTAAAAATAAGCTTTGGAAGAGATTAAAAAANA 2400

Db 2341 TATGCCATGCATAAAGACTTCCTATTAAAAATAAGCTTTGGAAGAGATTAAAAAANA 2400

QY 2401 AAAGGGCGCGCTCTAGAGGATCCAAGCTTACGTACGCTGCATGCGACGTCATAGCTC 2460

Db 2401 AAAGGGCGCGCTCTAGAGGATCCAAGCTTACGTACGCTGCATGCGACGTCATAGCTC 2460

QY 2461 TTCTATAGTGTACACCTAAATTCAATT 2486

Db 2461 TTCTATAGTGTACACCTAAATTCAATT 2486

RESULT 2

ADN02242 ID ADN02242 standard; cDNA; 2486 BP.

XX AC ADN02242;

DT 17-JUN-2004 (first entry)

XX Human partial large G protein-coupled receptor, LGR6, cDNA #1.

DE Human; ss; large G protein-coupled receptor 6; LGR6; heart failure;
XX ischaemic heart disease; myocardial infarction; hypertension;
KW pericarditis; atherosclerosis; hepatic failure; viral hepatitis; cancer;
KW intracerebral haemorrhage; brain abscess; Alzheimer's disease;
KW Pick disease; Parkinson's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; inflammatory bowel disease;
KW Crohn's disease; benign prostatic hypertrophy;
KW systemic lupus erythematosus.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 2..1903

FT /*tag= a

FT /partial

FT /note= "No start codon shown"

FT /product= "Partial LGR6"

XX US2003166047-A1.

PN 04-SEP-2003.

XX 08-MAY-2001; 2001US-00851595.

PF 06-MAY-1999; 99US-0132896P.

PR 08-MAY-2000; 2000US-00566588.

XX (MILL-) MILLENNIUM PHARM INC.

PA Gu W;

PI WPI; 2003-898067/82.

XX P-PSDB; ADN02243.

DR New isolated LGR6 nucleic acids and polypeptides, useful for diagnosing and treating LGR6-mediated disorders, such as myocardial infarction, hypertension, atherosclerosis, viral hepatitis, cancer and/or Alzheimer's disease.

XX Claim 1; SEQ ID NO 4; 145pp; English.

XX The invention relates to an isolated LGR6 (large G protein-coupled receptor) nucleic acid molecule comprising the mouse and human cDNA sequences appearing as ADN02239, ADN02241, ADN02242, ADN02244, ADN02245, ADN02247, ADN02248 and ADN02250. Also included are a host cell or a non-human mammalian host cell containing an LGR6 nucleic acid (and producing LGR6), an isolated LGR6 polypeptide appearing as ADN02240, ADN02243, ADN02246 and ADN02249, an antibody which selectively binds to LGR6, a method for detecting the presence of LGR6 in a sample, a kit (comprising a compound which selectively binds to LGR6, or hybridises to LGR6 nucleic acid, and instructions for use), a method for detecting LGR6 nucleic acid in a sample, a method for identifying a compound which binds to LGR6, a method for modulating the activity of LGR6 and a method for identifying a compound that modulates the activity of LGR6. The methods and compositions of the present invention are useful for diagnosing and treating large G-protein coupled receptor 6 (LGR6)-mediated or -related disorders, such as heart failure, ischaemic heart disease, myocardial infarction, hypertension, pericarditis, atherosclerosis, hepatic failure, viral hepatitis, cancer, intracerebral haemorrhage, brain abscess, Alzheimer's disease, Pick disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, inflammatory bowel disease, Crohn's disease, benign prostatic hypertrophy and systemic lupus erythematosus. The present sequence is a partial human cDNA for LGR6.

SQ Sequence 2486 BP; 455 A; 773 C; 692 G; 565 T; 0 U; 1 Other;

Query Match 100.0%; Score 2485; DB 11; Length 2486;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAATACGACTCACTATAGGAAAGCTGGTACGCTGCAGGTACCGTCCGGAATTCCCGG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 GTCGACCCACCGCTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCTC 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 TCTTGCTGCCCTAGCGGCTCCAACACACCGCATCTGGGAAATTGGAGCTNGACACCTT 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 TCTTGCTGCCCTAGCGGCTCCAACACACCGCATCTGGGAAATTGGAGCTNGACACCTT 180

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QY	301	GACACACACTGCCCCTGGCTGGACTTGGGGCTTGATGCAATCTGAAGCTCAAAGGGAACCT	360
Db	301		
QY	361	TGCTCTCTCCAGGCCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTTGAGGTGCC	420
Db	361		
QY	421	TTATGCCCTACCAGTGCTGCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCA	480
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QY	481	GTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCT	540
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QY	541	CCTTGCCAGACAAGCAGAGAACCACCTATGACCAGGACCTGGATGAGCTCCAGCTGGAGAT	600
Db	541		
QY	601	GGAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCC	660
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QY	661	CTGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGCCATCGTGTGCT	720
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QY	721	CTCCGTGCTCTGCAATGGAATGGAATGGTGGTGTGACCGCTGTTCGCTGGCGGCCTGCCCCCT	780
Db	721		
QY	781	GCCCCCGGTCAAAGTTTGTGGTAGGTGCGATTGAGSGCGCCAACACCTTGACTGGCATTT	840
Db	781		
QY	841	CTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGC	900
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QY	901	CCGTGGGAGACGSGGCTAGGCTGCCGGGCCACTGGCTTCCCTGGCAGTACTTGGGTGCGA	960
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QY	961	GGCATCGGTGCTGCTGCTCACTCTGGCCGCAAGTGCAGTGCAGCGTCTCCGTCTCCTGTGT	1020
Db	961		
QY	1021	CCGGGCCCTATGGGAAGTCCCCCTCCCTGGGCAAGGTTTCGAGCAGGGGTCCCTAGGCTGCCT	1080
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QY	1081	GGCACTGGCAGGGCTGCGCGCGCACTGCCCTTGCCCTCAGTGGGAGAAATACGGGGCCTC	1140
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QY	1141	CCCACTCTGCCTGCCCTACCGCCACCTTGAGGCTCAGCCAGAGCCCTGGGCTTCAACCGT	1200
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QY	1261	GTACTGTGACCTGCGCGGGCGACTTTAGGGCGTGTGGGACTGCGCCATGCTGAGGCA	1320
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QY	1981	CAAAATACAAACAAAACCTCAGCAGTGTGATCTATAGCAGGATGGCCCACTGCTGCTCCA	2040
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QY	2041	CTGATCACCTCTCTCCTGTGACCATCAACACGGGTGCCCTCTTGGCCTGGCTTCCCTTG	2100
Db	2041		
QY	2101	GCCTTCCCTCAGCTTCACTTGATACCTGGCCCTCTTCCCTTGTCATGTCTGAAGCTGTGGAC	2160
Db	2101		
QY	2161	CAGAGACCTGGACTTTTGTCTGCTTAAAGGAAATGAGGGAAGTAAAGACAGTGAAGGGGT	2220
Db	2161		
QY	2221	GGAGGTTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGCCCTGGAAAGGTGA	2280
Db	2221		
QY	2281	TTTCCCGTGTGACTCATGGATAGGATACAAAATGTGTTCCATGTACATTAATCTTGACA	2340
Db	2281		
QY	2341	TATGCCATGCATAAAGACTTCTTATTTAAAAATAAGCTTTTGGAAAGAGATTAATAAAAAA	2400

Db 2341 TATGCCATGCATAAAGACTTCCTATTAAATAAGCTTTGGAAAGAGATTATAAAAAAAAAA 2400
Qy 2401 AAAGGGCGCGCTCTAGAGGATCCAAGCTTACGTACGCGTGCATGCGACGTCAATAGCTC 2460
Db 2401 AAAGGGCGCGCTCTAGAGGATCCAAGCTTACGTACGCGTGCATGCGACGTCAATAGCTC 2460
Qy 2461 TTCTATAGTGTACACCTAAATTC AATT 2486
Db 2461 TTCTATAGTGTACACCTAAATTC AATT 2486

RESULT 3
ADK19407
ID ADK19407 standard; cDNA; 2486 BP.
XX
AC ADK19407;
XX
DT 17-JUN-2004 (first entry)
DE CDNA encoding human LGR6 polypeptide #1.
XX
KW G-protein coupled receptor; GPCR; large G-protein coupled receptor 6;
KW LGR6; weight disorder; neural disorder; endocrine disorder;
KW cardiovascular disorder; anorectic; anabolic; immunomodulator;
KW neuroprotective; nootropic; antiparkinsonian; anti-HIV; anticonvulsant;
KW antithyroid; osteopathic; cardiant; vasotropic; hypotensive;
KW antiarteriosclerotic; antiarrhythmic; human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 2..1903
FT /*tag= a
FT /partial
FT /product= "LGR6 polypeptide #1"
FT /note= "This sequence lacks a start codon"
FT /transl_except= (pos:170..172,aa:Xaa)
FT /note= "Xaa= Unknown"
XX
PN US2004058377-A1.
XX
PD 25-MAR-2004.
XX
PF 18-SEP-2003; 2003US-00664667.
XX
PR 06-MAY-1999; 99US-0132896P.
PR 08-MAY-2000; 2000US-00566588.
PR 08-MAY-2001; 2001US-00851595.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gu W;
XX
DR WPI; 2004-268789/25.
DR P-PSDB; ADK19408.
XX
PT New large G-protein coupled receptor 6 nucleic acid molecules and
PT polypeptides, useful for diagnosing, preventing or treating diseases
PT associated with aberrant nucleic acid or protein activity, e.g. obesity,
PT anorexia or cachexia.
XX
PS Claim 2; SEQ ID NO 4; 145pp; English.
XX
CC The present invention relates to the isolation of novel members of the G-
CC protein coupled receptor (GPCR) family designated as large G-protein
CC coupled receptor 6 (LGR6), and the polynucleotide sequences encoding
CC them. The invention also discloses LGR6 fusion proteins, antigenic
CC peptides, anti-LGR6 antibodies, recombinant expression vectors, host
CC cells, and non-human transgenic animals in which an LGR6 gene has been
CC introduced or disrupted. The LGR6 polynucleotide sequences, polypeptide
CC sequences, and antibodies are useful for diagnosing, treating or
CC preventing diseases associated with aberrant LGR6 expression or activity,

CC such as weight disorders (e.g. obesity, anorexia nervosa or cachexia),
CC neural disorders (e.g. central nervous system disorder, including
CC Alzheimer's disease, Parkinson's disease, AIDS-related dementia, multiple
CC sclerosis and Huntington's disease), endocrine disorders (e.g.
CC hypothyroidism, hyperthyroidism or acromegaly), or cardiovascular
CC disorders (e.g. ischaemia-reperfusion injury, coronary artery disease,
CC myocardial infarction, arrhythmia, atherosclerosis, hypertension or
CC congestive heart failure). The LGR6 polynucleotide and polypeptide
CC sequences are also useful as targets for developing modulating agents
CC that regulate a variety of cellular processes, e.g. neural and endocrine
CC processes and thermogenesis. They can be used in screening assays (e.g.
CC chromosome mapping, tissue typing or in forensic biology), or in
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials or pharmacogenomics). The present sequence
CC encodes a human LGR6 polypeptide.
XX
SQ Sequence 2486 BP; 455 A; 773 C; 692 G; 565 T; 0 U; 1 Other;

Query Match 100.0%; Score 2485; DB 12; Length 2486;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAATACGACTCACTATAGGGAAGCTGGTACGCTGCAGGTACCGTCCGGAATCCCGG 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 TAATACGACTCACTATAGGGAAGCTGGTACGCTGCAGGTACCGTCCGGAATCCCGG 60
Qy 61 GTCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGTCAATCCAGCCTC 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 GTCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGTCAATCCAGCCTC 120
Qy 121 TCTTGTGCTGCCCTAGCGGCCTCCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTT 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 TCTTGTGCTGCCCTAGCGGCCTCCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTT 180
Qy 181 CAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCCGTCCATCCA 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 CAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCCGTCCATCCA 240
Qy 241 CCCTGAGGCGCTTCTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGAACACAGCT 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CCCTGAGGCGCTTCTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGAACACAGCT 300
Qy 301 GACCACACTGCCCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGAACCT 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 GACCACACTGCCCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGAACCT 360
Qy 361 TGCTCTCTCCAGGCGCTTCTCCAAGGACAGTTCCTCAAAAACCTGAGGATCCTGGAGTGCC 420
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TGCTCTCTCCAGGCGCTTCTCCAAGGACAGTTCCTCAAAAACCTGAGGATCCTGGAGTGCC 420
Qy 421 TTATGCCTACCAGTGTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCGCTCTGGGCA 480
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 TTATGCCTACCAGTGTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCGCTCTGGGCA 480
Qy 481 GTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCGCGCTGGGCCT 540
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCGCGCTGGGCCT 540
Qy 541 CCTTGCCAGACAAGCAGAGAACCACTATGACCAAGGACCTGGATGAGCTCCAGCTGGAGAT 600
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 CCTTGCCAGACAAGCAGAGAACCACTATGACCAAGGACCTGGATGAGCTCCAGCTGGAGAT 600
Qy 601 GGAGGACTCAAAGCCACACCCCGCTGCTCCAGTGTAGCCCTACTCCAGGCGCGCTTCAAGCC 660
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 GGAGGACTCAAAGCCACACCCCGCTGCTCCAGTGTAGCCCTACTCCAGGCGCGCTTCAAGCC 660
Qy 661 CTGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCTGGCCCGTGTGGGCCCATCGTGTGCT 720
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 CTGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCTGGCCCGTGTGGGCCCATCGTGTGCT 720
Qy 721 CTCCGTGCTCTGCAATGGACTGGTGTGCTGCTGACCGTGTTCGTTGGGGGCGCTGCCCCCT 780
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 CTCCGTGCTCTGCAATGGACTGGTGTGCTGCTGACCGTGTTCGTTGGGGGCGCTGCCCCCT 780

QY	781	GCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCAAACACCTTGACTGGCATTTT	840	QY	1861	CGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACACGTCGTAATAATCCCTCCCATTTCT	1920
Db	781			Db	1861		
QY	841	CTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGC	900	QY	1921	TCTCTTCCCTCTCTTCCCTTTCCCTCTCTCCCCCTCGGTGAATGATGGCTTCTTCTATAAA	1980
Db	841			Db	1921		
QY	901	CCGCTGGGAGACGGGGCTAGGCTGCCGGCCACTGSCCTTCCCTGGCAGTACTTGGGTCGGA	960	QY	1981	CAAAATACAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCACTACCTGGCTCCA	2040
Db	901			Db	1981		
QY	961	GGCATCGGTGCTGCTCACTCTTGGCCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGT	1020	QY	2041	CTGATCACCTCTCTCTGTGACCATCACCAACGGGTGCCTCTTGGCCTGGCTTCCCTTG	2100
Db	961			Db	2041		
QY	1021	CCGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGTCCCTAGGCTGCCT	1080	QY	2101	GCCTTCCCTCAGCTTACCTTGATACCTGGGCTCTTCTTGTCTGTCATGTCGAACTGTGGAC	2160
Db	1021			Db	2101		
QY	1081	GGCACTGGCAGGGCTGGCCGCCGCACTGCCCTGGCTCAGTGGGAGAAATACGGGGCCTC	1140	QY	2161	CAGAGACCTGGACTTTGTCTGCTTAAAGGAAATGAGGGAAGTAAAGACAGTGAAGGGGT	2220
Db	1081			Db	2161		
QY	1141	CCCACCTGCTGCCCTACGCGCCACCTGAGGCTCAGCCAGCAGCCCTGGGCTTCAACCGT	1200	QY	2221	GGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCTTGGAAAGGTGA	2280
Db	1141			Db	2221		
QY	1201	GGCCCTGGTGATGAATACTCTTCTGTTTCCCTGCTGCTGGCCGCTGCCTACATCAAACT	1260	QY	2281	TTTCCCGTGTGACTCATGGATAGGATACAAAATGTGTTCCATGTACCAATTAATCTTGACA	2340
Db	1201			Db	2281		
QY	1261	GTA	1320	QY	2341	TATGCCATGCATAAAAGACTTCCTATTAAATAAAGCTTTGGAAGAGATTAATAAAAAA	2400
Db	1261			Db	2341		
QY	1321	CGTGGCCTGGCTCATCTTCGCAGACGGGCTCCTACTGTCCCCTGGCTTCCCTCAGCTT	1380	QY	2401	AAAGGCGGCGCTCTAGAGGATCCAAAGCTTACGTACGCGTCATGCGACGTATAGCTC	2460
Db	1321			Db	2401		
QY	1381	CGCTCCATGTGGGCTCTTCCCTGTACGCCAGGCGCGTCAAGTCTGTCTGCTGGT	1440	QY	2461	TTCTATAGTGTACCTAAATTCAATT	2486
Db	1381			Db	2461		
QY	1441	GGTGCTGCCCTGCTGCTCAACCCACTGCTGTACTGCTTCAACCCCTTCAACCTT	1500	QY	2461	TTCTATAGTGTACCTAAATTCAATT	2486
Db	1441			Db	2461		
QY	1501	CCGGGATGACCTTCGGGGCTTCGGCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGC	1560	QY	2461	TTCTATAGTGTACCTAAATTCAATT	2486
Db	1501			Db	2461		
QY	1561	TGCGGCGGGGAGCTGGAGAAGAGCTCCTGTGATTTACCCAGGCCCCTGGTAGCCTTCTC	1620	QY	2461	TTCTATAGTGTACCTAAATTCAATT	2486
Db	1561			Db	2461		
QY	1621	TGATGTGGATCTCAFTCTGGAAGCTTCTGAAGCTGGGCGCCCCCTGGCTGGAGACCTA	1680	QY	2461	TTCTATAGTGTACCTAAATTCAATT	2486
Db	1621			Db	2461		
QY	1681	TGGCTTCCCTCAGTGACCTCTATCTCCTGTACAGCCAGGGCCCCCAGGCTGGAGGG	1740	QY	2461	TTCTATAGTGTACCTAAATTCAATT	2486
Db	1681			Db	2461		
QY	1741	CAGCCATTGTGTAGACCCAGAGGGGAACCACTTTGGGAACCCCAACCTTCCATGGATGG	1800	QY	2461	TTCTATAGTGTACCTAAATTCAATT	2486
Db	1741			Db	2461		
QY	1801	AGAACTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGGTGG	1860	QY	2461	TTCTATAGTGTACCTAAATTCAATT	2486
Db	1801			Db	2461		
QY	1861	AGAACTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGGTGG	1920	QY	2461	TTCTATAGTGTACCTAAATTCAATT	2486
Db	1861			Db	2461		

RESULT 4
ADQ76775
ID ADQ76775 standard; DNA; 3451 BP.
XX
AC ADQ76775;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human LGR6 splice variant LGR6.2 nucleotide sequence.
XX
KW Human; leucine-rich repeat-containing G-protein coupled receptor;
KW receptor; LGR6.2; cytosolic; immunomodulator; muscular-gen.;
KW gynaecological; antiinfertility; endocrine-gen.; anabolic; hypertensive;
KW vulnary; dermatological; gene therapy; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 47..1093
FT /*tag= b
FT /product= "Human LGR6.2"
FT sig_peptide 47..103
FT /*tag= a
FT mat_peptide 104..1090
FT /*tag= c
PN WO2004058818-A2.
XX

15-JUL-2004.

23-DEC-2003; 2003WO-EP051091.

26-DEC-2002; 2002US-0436001P.

(ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

Muda M;

WPI; 2004-534126/51.

Novel isolated leucine-rich repeat-containing G-protein coupled receptor-6 splicing variant 1 and 2 polypeptides, useful for treating or preventing endometriosis, female or male infertility, Addison's disease, Cushing's disease, cancers.

Claim 1; SEQ ID NO 4; 85pp; English.

The present nucleotide sequence encodes human LGR6.2, a novel splice variant of leucine-rich repeat-containing G-protein coupled receptor 6 (LGR6-SV). It was initially identified as an expressed sequence tag clone. The LGR6.2 coding sequence consists of the same exons present in another splice variant, LGR6.1 ADQ76773, plus an extended exon that introduces a stop codon resulting in truncation of the coding sequence, removing the transmembrane domains and the cytoplasmic C-terminal domain of LGR6.1. Thus, LGR6.2 is a secreted, probably soluble, N-terminal extracellular domain version of LGR6.1 and probably functions as an antagonist of the LGR6.1 signalling pathway. Tissue distribution studies indicate a high level of expression in ovary and pituitary tissues. The N-terminal extracellular domain of LGR6.2 can be used as an antagonist of the LGR6 signalling pathway. The invention provides LGR6.1 and LGR6.2 polypeptides and nucleic acids, as well as selective binding agents, vectors, host cells and methods for producing LGR6-SV polypeptides. Also provided are pharmaceutical compositions and methods for the diagnosis, treatment, amelioration and/or prevention of diseases, disorders and conditions associated with LGR6-SV polypeptides. LGR6-SV polypeptides and nucleic acids can be used for diagnosing or treating: cancers such as hepatocellular carcinoma, adenomatous polyposis, malignant transformation of epithelial cells, colorectal cancer, breast cancer, ovarian cancer, etc.; cachexia and muscular dystrophy; miscarriage, endometriosis, uterine cancer, and female infertility; Cushing's disease and Addison's disease; male infertility and testicular cancer; leukaemia; and diseases and conditions affecting the kidney. They may also be useful for treating diseases and conditions involving cell proliferation and differentiation, such as tissue damage and degeneration, ageing, wound healing, cancer, hyperplasia and hypertrophy.

Sequence 3451 BP; 728 A; 1063 C; 920 G; 740 T; 0 U; 0 Other;

Query Match 92.9%; Score 2309.8; DB 12; Length 3451;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2325; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 71 GCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCTCTTGCTGCC 130
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1066 GGGGGCATGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCTCTTGCTGCC 1125

Qy 131 CTAGCGGCCTCCAACACAACCGCATCTGGGAATTTGGAGCTNGACACCTTCAGCCAGCTG 190
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1126 CTAGCGGCCTCCAACACAACCGCATCTGGGAATTTGGAGCT-GACACCTTCAGCCAGCTG 1184

Qy 191 AGTCCCCTGCAAGCCCTGGATCTTAGCTGGAAAGCCATCCGGTCCATCCACCCTGAGGCC 250
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1185 AGTCCCCTGCAAGCCCTGGATCTTAGCTGGAAAGCCATCCGGTCCATCCACCCTGAGGCC 1244

Qy 251 TTCTCCACCCTGCACTCCCTGGTCAAGCTGGACTGACAGACAACCAAGCTGACCACTG 310
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1245 TTCTCCACCCTGCACTCCCTGGTCAAGCTGGACTGACAGACAACCAAGCTGACCACTG 1304

Qy 311 CCCCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCC 370
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1305 CCCCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCC 1364


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Qy 1451 CTGCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCCACTTCCGGGATGAC 1510
    |||||||
Db 2445 CTGCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCCACTTCCGGGATGAC 2504
    |||||||
Qy 1511 CTTGCGCGGCTTCGGCCCCCGCAGGGGACTCAGGGCCCTAGCCTATGCTGCGCGCGG 1570
    |||||||
Db 2505 CTTGCGCGGCTTCGGCCCCCGCAGGGGACTCAGGGCCCTAGCCTATGCTGCGCGCGG 2564
    |||||||
Qy 1571 GAGCTGGAGAGAGCTCCTGTGATTCTACCCAGGCCCTGTAGCCTTCTCTGATGTGGAT 1630
    |||||||
Db 2565 GAGCTGGAGAGAGCTCCTGTGATTCTACCCAGGCCCTGTAGCCTTCTCTGATGTGGAT 2624
    |||||||
Qy 1631 CTCATTCTGGAAGCTTCTGAAGCTGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCC 1690
    |||||||
Db 2625 CTCATTCTGGAAGCTTCTGAAGCTGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCC 2684
    |||||||
Qy 1691 TCAGTGACCCCTCATCTCCTGTACGACGCCAGGGGCCCCAGGCTGGAGGCGAGCATTGT 1750
    |||||||
Db 2685 TCAGTGACCCCTCATCTCCTGTACGACGCCAGGGGCCCCAGGCTGGAGGCGAGCATTGT 2744
    |||||||
Qy 1751 GTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTG 1810
    |||||||
Db 2745 GTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTG 2804
    |||||||
Qy 1811 CTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGTGGCGGCTTTTCAG 1870
    |||||||
Db 2805 CTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGTGGCGGCTTTTCAG 2864
    |||||||
Qy 1871 CCCTCTGGCTTGGCCCTTGTCTCACACGCTGTAATAATATCCCTCCCCATTCCTTCTTCCCC 1930
    |||||||
Db 2865 CCCTCTGGCTTGGCCCTTGTCTCACACGCTGTAATAATATCCCTCCCCATTCCTTCTTCCCC 2924
    |||||||
Qy 1931 TCTCTTCCCTTTCCTCTCTCCCTCCCTCGGTGAATGATGGCTGCTTCTAAACAAATACAAC 1990
    |||||||
Db 2925 TCTCTTCCCTTTCCTCTCTCCCTCCCTCGGTGAATGATGGCTGCTTCTAAACAAATACAAC 2984
    |||||||
Qy 1991 CAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCAGTACCTGGCTCCACTGATCACCT 2050
    |||||||
Db 2985 CAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCAGTACCTGGCTCCACTGATCACCT 3044
    |||||||
Qy 2051 CTCTCCTGTGACCATCACCAACGGGTGCCCTCTTGGCCTGGCTTCCCTTGGCCTTCTCTCA 2110
    |||||||
Db 3045 CTCTCCTGTGACCATCACCAACGGGTGCCCTCTTGGCCTGGCTTCCCTTGGCCTTCTCTCA 3104
    |||||||
Qy 2111 GCTTCACCTTGATACTGGSCCTCTTCTCTGTCTCATGTCTGAAGCTGTGGACCCAGACCTG 2170
    |||||||
Db 3105 GCTTCACCTTGATACTGGSCCTCTTCTCTGTCTCATGTCTGAAGCTGTGGACCCAGACCTG 3164
    |||||||
Qy 2171 GACTTTTGTCTGCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGGTGAGGGTTGA 2230
    |||||||
Db 3165 GACTTTTGTCTGCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGGTGAGGGTTGA 3224
    |||||||
Qy 2231 TCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCTTGAAGGTTGATTTCCCGTGT 2290
    |||||||
Db 3225 TCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCTTGAAGGTTGATTTCCCGTGT 3284
    |||||||
Qy 2291 GACTCATGGATAGGATACAAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGC 2350
    |||||||
Db 3285 GACTCATGGATAGGATACAAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGC 3344
    |||||||
Qy 2351 ATAAAGACTTCCATTAAAAATAAGCTTTTGGAAAGAGATTAAAAA 2403
    |||||||
Db 3345 ATAAAGACTTCCATTAAAAATAAGCTTTTGGGAGAGAAAAA 3397
    |||||||
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RESULT 5
AAF98722
ID AAF98722 standard; DNA; 2322 BP.
XX
AC AAF98722;
XX
DT 02-JUL-2001 (first entry)
XX
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DE Human late stage ovarian tumour polynucleotide marker 37.
XX
KW Human; ovarian cancer; identification; detection; characterisation;
KW tumour; kinase; marker; cytostatic; antisense gene therapy; ds.
OS Homo sapiens.
XX
PN WO200118542-A2.
XX
PD 15-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-US024199.
XX
PR 03-SEP-1999; 99US-0152547P.
PR 16-MAR-2000; 2000US-0190347P.
PR 21-MAR-2000; 2000US-0191321P.
PR 31-MAY-2000; 2000US-0208382P.
PR 20-JUL-2000; 2000US-00220467.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lee J, Thompshe P, Lillie J;
XX
DR WPI; 2001-211428/21.
XX
PT Detection, assessment, prevention and therapy of ovarian cancer,
PT comprises detecting changes in the expression of a variety of markers.
XX
PS Claim 1; Page 1188-1189; 1198pp; English.
XX
CC The present invention describes a method for assessing whether a patient
CC is afflicted with ovarian cancer by comparing: (1) the expression of a
CC marker (I) (see AAF98594 to AAF98730), in a patient sample; and (2) the
CC normal level of expression of (I) in a control non-ovarian cancer sample,
CC where a significant difference between the level of expression in (a) and
CC (b) is an indication that the patient is afflicted with ovarian cancer.
CC (I) have cytostatic activities and can be used in antisense gene therapy.
CC The method, compositions and kits from the present invention can be used
CC for: (1) assessing and treating ovarian cancer; (2) making isolated
CC hybridoma, which produces an antibody useful for ovarian cancer
CC assessment; and (3) inhibiting ovarian cancer in a patient. AAF98573 to
CC AAF98593 represent human kinase marker primers and probes which are used
CC in the exemplification of the present invention
XX
SQ Sequence 2322 BP; 407 A; 733 C; 652 G; 530 T; 0 U; 0 Other;

Query Match 92.9%; Score 2309.4; DB 5; Length 2322;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2321; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 67 CCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCCTGCGGCTCATCCAGCCTCTCTTGC 126
    |||||||
Db 1 CCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCCTGCGGCTCATCCAGCCTCTCTTGC 60
    |||||||
Qy 127 TGCCCTAGCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCA 186
    |||||||
Db 61 TGCCCTAGCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCA 119
    |||||||
Qy 187 GCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTTGAACGCCCATCCGGTCCATCCACCCCTGA 246
    |||||||
Db 120 GCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTTGAACGCCCATCCGGTCCATCCACCCCTGA 179
    |||||||
Qy 247 GGCCTTCTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTGACCAC 306
    |||||||
Db 180 GGCCTTCTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTGACCAC 239
    |||||||
Qy 307 ACTGCCCTTGGCTGGACTTGGGGGCTTGATGTCATCTGAAGCTCAAAGGGAACCTTGCTCT 366
    |||||||
Db 240 ACTGCCCTTGGCTGGACTTGGGGGCTTGATGTCATCTGAAGCTCAAAGGGAACCTTGCTCT 299
    |||||||
Qy 367 CTCCCAGGCCTTCTCCAAGGACAGTTTCCAAAACTGAGGATCCTGGAGGTGCCTTATGC 426
    |||||||
Db 300 CTCCCAGGCCTTCTCCAAGGACAGTTTCCAAAACTGAGGATCCTGAAGGTGCCTTATGC 359
    |||||||
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QY	427	CTACAGTGTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTTGGCAGTGGA	486
Db	360	CTACAGTGTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTTGGCAGTGGA	419
QY	487	GGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGCCCTCCTTGC	546
Db	420	GGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGCCCTCCTTGC	479
QY	547	CAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGA	606
Db	480	CAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGA	539
QY	607	CTCAAGCCACACCCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGA	666
Db	540	CTCAAGCCACACCCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGA	599
QY	667	GTACCTCTTTGAAAGCTGGGGATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTTCGGT	726
Db	600	GTACCTCTTTGAAAGCTGGGGATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTTCGGT	659
QY	727	GCTCTGCAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGCCCTGCCCCCTGCCCCC	786
Db	660	GCTCTGCAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGCCCTGCCCCCTGCCCCC	719
QY	787	GGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCAAACACTTGACTGGCATTTCTCTGTGG	846
Db	720	GGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCAAACACTTGACTGGCATTTCTCTGTGG	779
QY	847	CCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTG	906
Db	780	CCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTG	839
QY	907	GGAGACGGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGGTCGGAGGCATC	966
Db	840	GGAGACGGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGGTCGGAGGCATC	899
QY	967	GGTGTGCTGTCACTGTGGCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGC	1026
Db	900	GGTGTGCTGTCACTGTGGCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGC	959
QY	1027	CTATGGGAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGSCACT	1086
Db	960	CTATGGGAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGSCACT	1019
QY	1087	GGCAGGGCTGGCCGCCGCACTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCCTTCCCCACT	1146
Db	1020	GGCAGGGCTGGCCGCCGCACTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCCTTCCCCACT	1079
QY	1147	CTGCCCTGCCCTACCGGCCACTGAGGGTTCAGCCAGAGCCCTGGGCTTCACCGTGGCCCT	1206
Db	1080	CTGCCCTGCCCTACCGGCCACTGAGGGTTCAGCCAGAGCCCTGGGCTTCACCGTGGCCCT	1139
QY	1207	GGTGATGATGAACCTCCTTCTGTCTTCTGGTCGTGGCCGCTTACATCAAACTGTACTG	1266
Db	1140	GGTGATGATGAACCTCCTTCTGTCTTCTGGTCGTGGCCGCTTACATCAAACTGTACTG	1199
QY	1267	TGACCTGCCCGGGCGACTTTTGAGGCCGTGTGGGACTCGGCCCATGGTGAGGCACGTGGC	1326
Db	1200	TGACCTGCCCGGGCGACTTTTGAGGCCGTGTGGGACTCGGCCCATGGTGAGGCACGTGGC	1259
QY	1327	CTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCTCTCAGCTTCGCCCTC	1386
Db	1260	CTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCTCTCAGCTTCGCCCTC	1319
QY	1387	CATGCTGGGCCCTCTTCCCTGTACGCCCGGAGCCCGTCAAGTCTGTCTCTGCTGGTGGTCT	1446
Db	1320	CATGCTGGGCCCTCTTCCCTGTACGCCCGGAGCCCGTCAAGTCTGTCTCTGCTGGTGGTCT	1379
QY	1447	GCCCCCTGCCCTGCCCTCAACCCCACTGTGTACCTGTCTTCAACCCCCCACTTCCGGGA	1506
Db	1380	GCCCCCTGCCCTGCCCTCAACCCCACTGTGTACCTGTCTTCAACCCCCCACTTCCGGGA	1439

QY	1507	TGACCTTCGGCGGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGCGGC	1566
Db	1440	TGACCTTCGGCGGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGCGGC	1499
QY	1567	CGGGGAGCTGGAGAAGAGCTCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGT	1626
Db	1500	CGGGGAGCTGGAGAAGAGCTCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGT	1559
QY	1627	GGATCTCATTTCTGGAAAGCTTCTGAAGCTGGCGGCCCTCTGGGCTGGAGACCTATGGCTT	1686
Db	1560	GGATCTCATTTCTGGAAAGCTTCTGAAGCTGGCGGCCCTCTGGGCTGGAGACCTATGGCTT	1619
QY	1687	CCCCTCAGTGACCCCTCATCTCTGTCAGCAGCCAGGSGCCCCCAGGCTGGAGSGCAGCCA	1746
Db	1620	CCCCTCAGTGACCCCTCATCTCTGTCAGCAGCCAGGSGCCCCCAGGCTGGAGSGCAGCCA	1679
QY	1747	TTGTGTAGAGCCAGAGGGGAACCACTTTTGGGAACCCCCCAACCTCCATGGATGGAGAACT	1806
Db	1680	TTGTGTAGAGCCAGAGGGGAACCACTTTTGGGAACCCCCCAACCTCCATGGATGGAGAACT	1739
QY	1807	GCTGTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGGCTT	1866
Db	1740	GCTGTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGGCTT	1799
QY	1867	TCAGCCCTCTGGCTTGGCCTTTCCTTTCACACAGTGTAAATATCCCTCCCCATTTCTCTCTT	1926
Db	1800	TCAGCCCTCTGGCTTGGCCTTTCCTTTCACACAGTGTAAATATCCCTCCCCATTTCTCTCTT	1859
QY	1927	CCCCCTCTTCCCCCTTCTCTCCCCCTCGGTGATGATGGCTGCTTCTTAAACAAATA	1986
Db	1860	CCCCCTCTTCCCCCTTCTCTCCCCCTCGGTGATGATGGCTGCTTCTTAAACAAATA	1919
QY	1987	CAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACCTGGCTCCACTGATC	2046
Db	1920	CAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACCTGGCTCCACTGATC	1979
QY	2047	ACCTCTCTCTGTGACCATCACCAACGGGTGCCTTCTGGCCCTGGCTTTCCCTTGGCCTTC	2106
Db	1980	ACCTCTCTCTGTGACCATCACCAACGGGTGCCTTCTGGCCCTGGCTTTCCCTTGGCCTTC	2039
QY	2107	CTCAGCTTCACCTTGATPACTGGGCCTCTTCTCTTGTCTATGTCTGAAGCTGTGGACAGAGA	2166
Db	2040	CTCAGCTTCACCTTGATPACTGGGCCTCTTCTCTTGTCTATGTCTGAAGCTGTGGACAGAGA	2099
QY	2167	CCTGGACTTTTGTCTGCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGG	2226
Db	2100	CCTGGACTTTTGTCTGCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGG	2159
QY	2227	TTGATCAGGGCAGTGTGACAGGGAGACCTCACAGAGAAAGCCCTGGAAGGTGATTTCCC	2286
Db	2160	TTGATCAGGGCAGTGTGACAGGGAGACCTCACAGAGAAAGCCCTGGAAGGTGATTTCCC	2219
QY	2287	GTGTGACTCATGGATAGGATACAAAATGTGTTCATGTACCATTAACTTTGACATATGCC	2346
Db	2220	GTGTGACTCATGGATAGGATACAAAATGTGTTCATGTACCATTAACTTTGACATATGCC	2279
QY	2347	ATGCATAAAGACTTCCTATTAAAAATAAGCTTTTGGAAAGAGATTA	2389
Db	2280	ATGCATAAAGACTTCCTATTAAAAATAAGCTTTTGGAAAGAGATTA	2322

RESULT 6

AAI67924

ID AAI67924 standard; cDNA; 2711 BP.

XX AAI67924;

AC AAI67924;

XX 13-MAR-2002 (first entry)

XX Partial cDNA of human LGR6 polypeptide (clone fahr).

DE Large G-protein coupled receptor 6; LGR6; GPCR; immunomodulator;

XX anti-HIV; cytostatic; nootropic; neuroprotective; antiparkinsonian;

KW

Matches 2269; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			
QY	133	AGGGCCTCCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG	192
Db	442	ATCGGCCTCCAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG	500
QY	193	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCCTT	252
Db	501	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCCTT	560
QY	253	CTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACACTGCC	312
Db	561	CTCCACCCCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACACTGCC	620
QY	313	CCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAGGGAACTTGTCTCTCTCCCA	372
Db	621	CCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAGGGAACTTGTCTCTCTCCCA	680
QY	373	GGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATAGCCTACCA	432
Db	681	GGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATAGCCTACCA	740
QY	433	GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCAGTGGGAGGCTGA	492
Db	741	GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCAGTGGGAGGCTGA	800
QY	493	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCCTCCTTGGCAGACA	552
Db	801	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCCTCCTTGGCAGACA	860
QY	553	AGCAGAGAACCACTATGACAGGACCTGGATGAGCTCCAGCTGGAGATGGAGACTCAAA	612
Db	861	AGCAGAGAACCACTATGACAGGACCTGGATGAGCTCCAGCTGGAGATGGAGACTCAAA	920
QY	613	GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	672
Db	921	GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	980
QY	673	CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTTGTCTCCCTGCTCTG	732
Db	981	CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTTGTCTCCCTGCTCTG	1040
QY	733	CAATGGACTGGTGTCTGTGACCGTGTTCGCTGGCGGGCCCTGCCCCCTGCCCCCGGTCAA	792
Db	1041	CAATGGACTGGTGTCTGTGACCGTGTTCGCTGGCGGGCCCTGCCCCCTGCCCCCGGTCAA	1100
QY	793	GTTTGTGGTAGGTGCGATTGCAGGGCCCAACACCTTGACTGGCATTTCCCTGAGCCCTTCT	852
Db	1101	GTTTGTGGTAGGTGCGATTGCAGGGCCCAACACCTTGACTGGCATTTCCCTGAGCCCTTCT	1160
QY	853	AGCCTCAGTTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	912
Db	1161	AGCCTCAGTTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	1220
QY	913	GGGGCTAGGCTGCCGGGCACCTGGCTTCCTGGCAGTACTTGGGTCCGAGGCATCGGTGCT	972
Db	1221	GGGGCTAGGCTGCCGGGCACCTGGCTTCCTGGCAGTACTTGGGTCCGAGGCATCGGTGCT	1280
QY	973	GCTGCTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGCCCTATGG	1032
Db	1281	GCTGCTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGCCCTATGG	1340
QY	1033	GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTAGGCTGCCTGGCACTGGCAGG	1092
Db	1341	GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTAGGCTGCCTGGCACTGGCAGG	1400
QY	1093	GCTGGCCCGCCTGCCCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCCT	1152
Db	1401	GCTGGCCCGCCTGCCCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCCT	1460
QY	1153	GCCCTACGCGCCACTGAGGGTACGCCAGCGCCTGGGCTTCACCGTGGCCCTGGGTGAT	1212
Db	1461	GCCCTACGCGCCACTGAGGGTACGCCAGCGCCTGGGCTTCACCGTGGCCCTGGGTGAT	1520

QY	1213	GATGAACTCCTTCTGTTTCTGGTCTGGCCCGTGCCTACATCAAACTGTACTGTGACCT	1272
Db	1521	GATGAACTCCTTCTGTTTCTGGTCTGGCCCGTGCCTACATCAAACTGTACTGTGACCT	1580
QY	1273	GCCGGGGGCGACTTTGAGGCCGTGTGGACTGCGCCCATGGTGAGGCACGTGGCCTGGCT	1332
Db	1581	GCCGGGGGCGACTTTGAGGCCGTGTGGACTGCGCCCATGGTGAGGCACGTGGCCTGGCT	1640
QY	1333	CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCTCAGCTTCGCCTCCATGCT	1392
Db	1641	CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCTCAGCTTCGCCTCCATGCT	1700
QY	1393	GGGCCTCTTCCCTGTCAACCCGAGGCCGTCAAGTCTGTCTGCTGCTGGTGGTGGCCTCCT	1452
Db	1701	GGGCCTCTTCCCTGTCAACCCGAGGCCGTCAAGTCTGTCTGCTGCTGGTGGTGGCCTCCT	1760
QY	1453	GCCTGCCTGCCTCAACCCACTGTCTACCTGCTCTTCAACCCCCACTTCCGGGATGACCT	1512
Db	1761	GCCTGCCTGCCTCAACCCACTGTCTACCTGCTCTTCAACCCCCACTTCCGGGATGACCT	1820
QY	1513	TCGGGGGCTTCGGCCCCCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGA	1572
Db	1821	TCGGGGGCTTCGGCCCCCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGA	1880
QY	1573	GCTGGAGAAAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT	1632
Db	1881	GCTGGAGAAAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT	1940
QY	1633	CATTCTGGAAGCTTCTGAAGCTGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCCTC	1692
Db	1941	CATTCTGGAAGCTTCTGAAGCTGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCCTC	2000
QY	1693	AGTGACCCTCATCTCTGTGTCAGCAGCCAGGGGCCCCCGAGGCTGGAGGGCAGCCATTGT	1752
Db	2001	AGTGACCCTCATCTCTGTGTCAGCAGCCAGGGGCCCCCGAGGCTGGAGGGCAGCCATTGT	2060
QY	1753	AGAGCCAGAGGGAAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTGCT	1812
Db	2061	AGAGCCAGAGGGAAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTGCT	2120
QY	1813	GAGGCAGAGGGATCTACGCCAGCAGGTGAGGCTTGTACAGGGGTGGCGCTTTCAGCC	1872
Db	2121	GAGGCAGAGGGATCTACGCCAGCAGGTGAGGCTTGTACAGGGGTGGCGCTTTCAGCC	2180
QY	1873	CTCTGGCTTGGCCTTGTCTTACACAGTGTAAATATCCCTCCCCATCTTCTCTTCCCCTC	1932
Db	2181	CTCTGGCTTGGCCTTGTCTTACACAGTGTAAATATCCCTCCCCATCTTCTCTTCCCCTC	2240
QY	1933	TCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAACAATAACAAACCA	1992
Db	2241	TCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAACAATAACAAACCA	2300
QY	1993	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACCTGGCTCCAATGATCACCTCT	2052
Db	2301	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACCTGGCTCCAATGATCACCTCT	2360
QY	2053	CTCCTGTGACCATCACCAACGGGTGCCTTCTTGGCCCTGGCTTTCCTTGGCCTTCCCTCAGC	2112
Db	2361	CTCCTGTGACCATCACCAACGGGTGCCTTCTTGGCCCTGGCTTTCCTTGGCCTTCCCTCAGC	2420
QY	2113	TTACACCTTGATACTGGGCCCTCTTCCCTTGTCTATGTCTGAAGCTGTGGACAGAGACCTGGA	2172
Db	2421	TTACACCTTGATACTGGGCCCTCTTCCCTTGTCTATGTCTGAAGCTGTGGACAGAGACCTGGA	2480
QY	2173	CTTTTGTCTGCTTAAGGGAAATGAGGGAACTAAAGACAGTGAAGGGGTGGAGGGTGTATC	2232
Db	2481	CTTTTGTCTGCTTAAGGGAAATGAGGGAACTAAAGACAGTGAAGGGGTGGAGGGTGTATC	2540
QY	2233	AGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGCCCTGGAAGGTGATTTCCCCTGTGA	2292
Db	2541	AGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGCCCTGGAAGGTGATTTCCCCTGTGA	2600

QY 973 GCTGCTCACTCTGGCCGACGTGCAGTGCAGCGTCTCGTCTCCTGTGTCCGGGCTATGG 1032
Db 1281 GCTGCTCACTCTGGCCGACGTGCAGTGCAGCGTCTCGTCTCCTGTGTCCGGGCTATGG 1340
QY 1033 GAAGTCCCCCTCCCTGGGACGCTTCGAGCAGGGGTCTTAGGCTGCCCTGGCACTGGCAGG 1092
Db 1341 GAAGTCCCCCTCCCTGGGACGCTTCGAGCAGGGGTCTTAGGCTGCCCTGGCACTGGCAGG 1400
QY 1093 GCTGGCCGCGCACTGCCCTGGCCCTCAGTGGGAGAAACAGGGGCTCCCACTCTGCCT 1152
Db 1401 GCTGGCCGCGCACTGCCCTGGCCCTCAGTGGGAGAAACAGGGGCTCCCACTCTGCCT 1460
QY 1153 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT 1212
Db 1461 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT 1520
QY 1213 GATGAACTCCTTCTGTTTCCTGGTCTGTGGCCGTGCTACATCAAACTGTACTGTGACCT 1272
Db 1521 GATGAACTCCTTCTGTTTCCTGGTCTGTGGCCGTGCTACATCAAACTGTACTGTGACCT 1580
QY 1273 GCCCGGGGCGACTTTGAGGCCGTGTGGGACTGCGGCATGGTGAGGCACGTGGCCTGGCT 1332
Db 1581 GCCCGGGGCGACTTTGAGGCCGTGTGGGACTGCGGCATGGTGAGGCACGTGGCCTGGCT 1640
QY 1333 CATCTTCGCAGACGGGCTCCTCTACTGTCCCCTGGCTTCCTCAGCTTCGCTCCATGCT 1392
Db 1641 CATCTTCGCAGACGGGCTCCTCTACTGTCCCCTGGCTTCCTCAGCTTCGCTCCATGCT 1700
QY 1393 GGGCCTCTTCCCTGTACGCCCCGAGGCCGTCAAGTCTGTCTCTGTGGTGGTGGCTGCCCT 1452
Db 1701 GGGCCTCTTCCCTGTACGCCCCGAGGCCGTCAAGTCTGTCTCTGTGGTGGTGGCTGCCCT 1760
QY 1453 GCCTGCCTGCCTCAACCCACTGCTGTACTGCTCTTCAACCCCCACTTCGSGGATGACCT 1512
Db 1761 GCCTGCCTGCCTCAACCCACTGCTGTACTGCTCTTCAACCCCCACTTCGSGGATGACCT 1820
QY 1513 TCGGGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGCTGCGGCCGGGA 1572
Db 1821 TCGGGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGCTGCGGCCGGGA 1880
QY 1573 GCTGGAGAAAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT 1632
Db 1881 GCTGGAGAAAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT 1940
QY 1633 CATTCGGAAGCTTCTGAAGCTGGCGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTC 1692
Db 1941 CATTCGGAAGCTTCTGAAGCTGGCGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTC 2000
QY 1693 AGTGACCTCATCTCCTGTTCAGCAGCCAGGGGCCCCAGGCTGGAGGCGAGCCATTGTGT 1752
Db 2001 AGTGACCTCATCTCCTGTTCAGCAGCCAGGGGCCCCAGGCTGGAGGCGAGCCATTGTGT 2060
QY 1753 AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAAGCTGCTGT 1812
Db 2061 AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAAGCTGCTGT 2120
QY 1813 GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTTCAGGGGTGGCGGCTTTCAGCC 1872
Db 2121 GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTTCAGGGGTGGCGGCTTTCAGCC 2180
QY 1873 CTCTGGCTTGGCCTTGTCTTCACACGTGTAATATCCCTCCCAATTCCTCTTCCCCCTC 1932
Db 2181 CTCTGGCTTGGCCTTGTCTTCACACGTGTAATATCCCTCCCAATTCCTCTTCCCCCTC 2240
QY 1933 TCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAACAAATACAACCA 1992
Db 2241 TCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAACAAATACAACCA 2300
QY 1993 AAACCTCAGCAGTGTGATCTATAGCAGGATGGCCAGTACCTGGCTCCACTGATCACCTCT 2052
Db 2301 AAACCTCAGCAGTGTGATCTATAGCAGGATGGCCAGTACCTGGCTCCACTGATCACCTCT 2360
QY 2053 CTCCTGTGACCATCACCAACGGGTGCCTCTTGGCCTGGCTTTCCTTGGCCTTCCTCAGC 2112

Db 2361 CTCCTGTGACCATCACCAACGGGTGCCTCTTGGCCTGGCTTCCCTTGGCCTTCCTCAGC 2420
QY 2113 TTCACCTTGATACTGGGCCCTCTTCCCTTGTCACTGTCTGAAGCTGTGGACCAAGACCTGGA 2172
Db 2421 TTCACCTTGATACTGGGCCCTCTTCCCTTGTCACTGTCTGAAGCTGTGGACCAAGACCTGGA 2480
QY 2173 CTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGTTGATC 2232
Db 2481 CTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGTTGATC 2540
QY 2233 AGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGCCCTGGAAGGTGATTTCCCCTGTGA 2292
Db 2541 AGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGCCCTGGAAGGTGATTTCCCCTGTGA 2600
QY 2293 CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAAATCTTGACATATGCCATGCAT 2352
Db 2601 CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAAATCTTGACATATGCCATGCAT 2660
QY 2353 AAAGACTTCTATTAAAATAAGCTTTGGAAGAGATTAAAAAAA 2403
Db 2661 AAAGACTTCTATTAAAATAAGCTTTGGAAGAGATTAAAAAAA 2711

RESULT 9

ABZ11841
ID ABZ11841 standard; cDNA; 2988 BP.
XX
AC ABZ11841;
XX
DT 20-JAN-2003 (first entry)
XX
Human polynucleotide SEQ ID NO 723.
DE
XX
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
cell-proliferative disorder; neurodegenerative disease; bacterial;
Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
DR P-PSDB; ABP69624.
XX
PT New polynucleotides comprising sequences assembled from expressed
sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
PS Claim 1; SEQ ID NO 723; 1012pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for

CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2988 BP; 585 A; 924 C; 825 G; 654 T; 0 U; 0 Other;

Query Match 90.7%; Score 2255.8; DB 6; Length 2988;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2268; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY	133	AGGGCTCCAACACAAACCGCATCTGGGAAATTGGAGTNGACACCTTCAGCCAGCTGAG	192
Db	718	ATCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG	776
QY	193	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCT	252
Db	777	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCT	836
QY	253	CTCCACCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAAACCAGCTGACCACACTGCC	312
Db	837	CTCCACCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAAACCAGCTGACCACACTGCC	896
QY	313	CTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGAAACCTTGCTCTCTCCCA	372
Db	897	CTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGAAACCTTGCTCTCTCCCA	956
QY	373	GGCTTCTCCAAGGACAGTTTCCAAAACCTGAGGATCTCGAGGTGCCCTTAGCCCTACCA	432
Db	957	GGCTTCTCCAAGGACAGTTTCCAAAACCTGAGGATCTCGAGGTGCCCTTAGCCCTACCA	1016
QY	433	GTGCTGTCCCTATGGGATGTGCGCAGCTTCTTCAAGGCCCTCGGGCAGTGGAGGCTGA	492
Db	1017	GTGCTGTCCCTATGGGATGTGCGCAGCTTCTTCAAGGCCCTCGGGCAGTGGAGGCTGA	1076
QY	493	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTCGGGCCTCCTTGCCAGACA	552
Db	1077	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTCGGGCCTCCTTGCCAGACA	1136
QY	553	AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAA	612
Db	1137	AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAA	1196
QY	613	GCCACACCCAGTGTCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT	672
Db	1197	GCCACACCCAGTGTCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT	1256
QY	673	CTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG	732
Db	1257	CTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG	1316
QY	733	CAATGGACTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	792
Db	1317	CAATGGACTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1376
QY	793	GTTTGGTAGGTGGATTGAGGGGCCCAACACCTTGACTGGCATTTCTGTGGCCTCTCT	852
Db	1377	GTTTGGTAGGTGGATTGAGGGGCCCAACACCTTGACTGGCATTTCTGTGGCCTCTCT	1436
QY	853	AGCCTCAGTCGATGCCCTGACCTTTGGTCAAGTCTCTGAGTACGAGCCCGCTGGGAGAC	912
Db	1437	AGCCTCAGTCGATGCCCTGACCTTTGGTCAAGTCTCTGAGTACGAGCCCGCTGGGAGAC	1496
QY	913	GGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTCCGAGGCATCGGTGCT	972

Db	1497	GGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTCCGAGGCATCGGTGCT	1556
QY	973	GCTGCTCACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGCCTATGG	1032
Db	1557	GCTGCTCACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGCCTATGG	1616
QY	1033	GAAGTCCCCCTCCCTGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGGCAGTGGCAGG	1092
Db	1617	GAAGTCCCCCTCCCTGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGGCAGTGGCAGG	1676
QY	1093	GCTGGCCGCGCAGTCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCCT	1152
Db	1677	GCTGGCCGCGCAGTCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCCT	1736
QY	1153	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT	1212
Db	1737	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT	1796
QY	1213	GATGAACCTCTTCTGTTTCTGGTCTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1272
Db	1797	GATGAACCTCTTCTGTTTCTGGTCTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1856
QY	1273	GCCCGGGGGCGACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT	1332
Db	1857	GCCCGGGGGCGACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT	1916
QY	1333	CATCTTCGAGACGGGCTCCTCTACTGTCCCGTGGCCTTCTCAGCTTCGCCCTCCATGCT	1392
Db	1917	CATCTTCGAGACGGGCTCCTCTACTGTCCCGTGGCCTTCTCAGCTTCGCCCTCCATGCT	1976
QY	1393	GGGCTCTTCCCTGTACGCCCGAGGCCGTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCT	1452
Db	1977	GGGCTCTTCCCTGTACGCCCGAGGCCGTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCT	2036
QY	1453	GCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCACTTCGGGGATGACCT	1512
Db	2037	GCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCACTTCGGGGATGACCT	2096
QY	1513	TCGGCGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGCTGCGGCCGGGA	1572
Db	2097	TCGGCGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGCTGCGGCCGGGA	2156
QY	1573	GCTGGAGAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT	1632
Db	2157	GCTGGAGAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT	2216
QY	1633	CATTCTGGAAGCTTCTGAAAGCTGGCGGCCCTGGCTGGAGACCTATGGCTTCCCTC	1692
Db	2217	CATTCTGGAAGCTTCTGAAAGCTGGCGGCCCTGGCTGGAGACCTATGGCTTCCCTC	2276
QY	1693	AGTGACCTCATCTCTCTGTCAGCAGCCAGGGGCCCTCCAGGCTGGAGGGCAGCCATGTGT	1752
Db	2277	AGTGACCTCATCTCTCTGTCAGCAGCCAGGGGCCCTCCAGGCTGGAGGGCAGCCATGTGT	2336
QY	1753	AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTCCATGGATGGAGAACTGTGCT	1812
Db	2337	AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTCCATGGATGGAGAACTGTGCT	2396
QY	1813	GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTGAGGGGTGGCGGCTTTCAGCC	1872
Db	2397	GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTGAGGGGTGGCGGCTTTCAGCC	2456
QY	1873	CTCTGGCTTGGCCCTTGTCTTACACGTGTAATATCCCTCCCATTTCTTCTTCCCTC	1932
Db	2457	CTCTGGCTTGGCCCTTGTCTTACACGTGTAATATCCCTCCCATTTCTTCTTCCCTC	2516
QY	1933	TCTTCCCTTCTCTTCCCTCCTGGTGAATGATGGCTGCTTCTTAAACAATAACCA	1992
Db	2517	TCTTCCCTTCTCTTCCCTCCTGGTGAATGATGGCTGCTTCTTAAACAATAACCA	2576
QY	1993	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCAGTACCTGGCTCCACTGATCACCTCT	2052
Db	2577	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCAGTACCTGGCTCCACTGATCACCTCT	2636

Db 1677 GCTGGCGCGCACCTGCCCCCTGGCCTCAGTGGGAGATAACGGGGCCTCCCCACTCTGCCT 1736

Qy 1153 GCCTACGCGCCACCTGAGGFTCAGCCAGAGCCCTGGGCTTCACCGTGGCCCTGGTGAT 1212

Db 1737 GCCCTACGCGCCACCTGAGGFTCAGCCAGAGCCCTGGGCTTCACCGTGGCCCTGGTGAT 1796

Qy 1213 GATGAACCTCCTTCTGTTTCCCTGCTGCTGGCCGCTGCCTACATCAAACTGTACTGTGACCT 1272

Db 1797 GATGAACCTCCTTCTGTTTCCCTGCTGCTGGCCGCTGCCTACATCAAACTGTACTGTGACCT 1856

Qy 1273 GCCCGGGGCGACTTTGAGGCCCTGTGGGACTGCGGCCATGGTGAGGCACGTGGCCTGGCT 1332

Db 1857 GCCCGGGGCGACTTTGAGGCCCTGTGGGACTGCGGCCATGGTGAGGCACGTGGCCTGGCT 1916

Qy 1333 CATCTTCGCAGACGGGCTCCTTACTGTCTCCGTGGCCCTTCTCAGCTTCGCCCTCCATGCT 1392

Db 1917 CATCTTCGCAGACGGGCTCCTTACTGTCTCCGTGGCCCTTCTCAGCTTCGCCCTCCATGCT 1976

Qy 1393 GGGCCTCTTCCCTGTACGCCCGAGGCCCGTCAAGTCTGTCTGCTGGTGGTGTGCCCT 1452

Db 1977 GGGCCTCTTCCCTGTACGCCCGAGGCCCGTCAAGTCTGTCTGCTGGTGGTGTGCCCT 2036

Qy 1453 GCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCACTTCCGGGATGACCT 1512

Db 2037 GCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCACTTCCGGGATGACCT 2096

Qy 1513 TCGCGGCTTCGGCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCCGGGGA 1572

Db 2097 TCGCGGCTTCGGCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCCGGGGA 2156

Qy 1573 GCTGGAGAAAGAGCTCCTGTGATTTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGATCT 1632

Db 2157 GCTGGAGAAAGAGCTCCTGTGATTTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGATCT 2216

Qy 1633 CATCTGGAAGCTTCTGAAGCTGGCGGCCCCCCCTGGGCTGGAGACCTATGGCTTCCCTC 1692

Db 2217 CATCTGGAAGCTTCTGAAGCTGGCGGCCCCCCCTGGGCTGGAGACCTATGGCTTCCCTC 2276

Qy 1693 AGTGACCCTCATCTCCTGTACAGCAGCCAGGGGCCCCCCAGGCTGGAGGCAGCCATTGTGT 1752

Db 2277 AGTGACCCTCATCTCCTGTACAGCAGCCAGGGGCCCCCCAGGCTGGAGGCAGCCATTGTGT 2336

Qy 1753 AGAGCCAGAGGGGAACCACTTTGGGAACCCCCCAACCTCCATGGATGGAGAACTGCTGCT 1812

Db 2337 AGAGCCAGAGGGGAACCACTTTGGGAACCCCCCAACCTCCATGGATGGAGAACTGCTGCT 2396

Qy 1813 GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGGTGGCGGCTTTCAGCC 1872

Db 2397 GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGGTGGCGGCTTTCAGCC 2456

Qy 1873 CTCTGGCTTGGCCTTTGCTTTCACACGTGTAATATCCCTCCCCCATTTCTTCTCTCCCTC 1932

Db 2457 CTCTGGCTTGGCCTTTGCTTTCACACGTGTAATATCCCTCCCCCATTTCTTCTCTCCCTC 2516

Qy 1933 TCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAACAAATACAAACCA 1992

Db 2517 TCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAACAAATACAAACCA 2576

Qy 1993 AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACTGGCTCCCACTGATCACTCT 2052

Db 2577 AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACTGGCTCCCACTGATCACTCT 2636

Qy 2053 CTCCTGTGACCATCACCAACGGGTGCCCTCTTGGCCCTGGCTTCCCTTGGCCTTCTCAGC 2112

Db 2637 CTCCTGTGACCATCACCAACGGGTGCCCTCTTGGCCCTGGCTTCCCTTGGCCTTCTCAGC 2696

Qy 2113 TTCACCTTGATCTGGGCCTCTTCTTGTGATGCTGAAGCTGTGGACCCAGAGACCTGGA 2172

Db 2697 TTCACCTTGATCTGGGCCTCTTCTTGTGATGCTGAAGCTGTGGACCCAGAGACCTGGA 2756

Qy 2173 CTTTTGTCTGCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGTTGATC 2232

Db 2757 CTTTTGTCTGCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGTGGAGGGTTGATC 2816

Qy 2233 AGGGCACAGTGGACAGGAGACCTCACAGAGAAAGCCTGGAAGGTGATTTCCCGTGTGA 2292

Db 2817 AGGGCACAGTGGACAGGAGACCTCACAGAGAAAGCCTGGAAGGTGATTTCCCGTGTGA 2876

Qy 2293 CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCAT 2352

Db 2877 CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCAT 2936

Qy 2353 AAAGACTTCTCTATTAAATAAAGCTTTTGGAAAGAGATTAAAAAAGGATTTAAAAA 2403

Db 2937 AAAGACTTCTCTATTAAATAAAGCTTTTGGAAAGAGATTAAAAAAGGATTTAAAAA 2987

RESULT 11

ADQ76773

ID ADQ76773 standard; DNA; 3306 BP.

XX

AC ADQ76773;

XX

DT 07-OCT-2004 (first entry)

XX

DE Human LGR6 splice variant LGR6.1 nucleotide sequence.

XX

KW Human; leucine-rich repeat-containing G-protein coupled receptor; receptor; LGR6.1; cytotstatic; immunomodulator; muscular-gen.; gynaeological; antiinfertility; endocrine-gen.; anabolic; hypertensive; vulnerary; dermatological; gene therapy; gene; ds.

OS Homo sapiens.

XX

FH Key

FT CDS Location/Qualifiers

FT 47. .2794

FT /*tag= b

FT /product= "LGR6.1"

FT 47. .103

FT /*tag= a

FT 104. .2791

FT /*tag= c

XX

PN WO2004058818-A2.

XX

PD 15-JUL-2004.

XX

PF 23-DEC-2003; 2003WO-EP051091.

XX

PR 26-DEC-2002; 2002US-0436001P.

XX

PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

XX

PI Muda M;

XX

DR WPI; 2004-534126/51.

DR P-PSDB; ADQ76774.

XX

XX Novel isolated leucine-rich repeat-containing G-protein coupled receptor-6 splicing variant 1 and 2 polypeptides, useful for treating or preventing endometriosis, female or male infertility, Addison's disease, Cushing's disease, cancers.

PS Claim 1; SEQ ID NO 1; 85pp; English.

XX

CC The present nucleotide sequence encodes human LGR6.1, a novel splice variant of leucine-rich repeat-containing G-protein coupled receptor 6 (LGR6-SV). It was identified from a search of the NCBI database using a human LGR6 nucleotide sequence as query sequence. The LGR6.1 coding sequence is identical to the LFR6 coding sequence with the exception of a novel exon encoding a leader peptide and 2 novel internal exons. It has 3 extra leucine-rich repeats and a distinct leader peptide as well as a novel C-terminus sequence compared with LGR6 ADQ76787. Tissue distribution studies indicate a high level of expression in ovary and pituitary tissues. The N-terminal extracellular domain of LGR6.1 can be

Db 2824 TCCTCCCTTTCTCTCTCCTCCCTCGGTGAATGATGGCTGCTTTCTAAACAAATACRACCA 2883

QY 1993 AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACCTAGCTGGCTCCACTGATCACCCTCT 2052

Db 2884 AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTCCCTGGCTCCACTGATCACCCTCT 2943

QY 2053 CTCCTGTGACCATCACCAACGGGTGCCTCTTTGGCCTGGCTTTCCCTTGGCCTTCCCTCAGC 2112

Db 2944 CTCCTGTGACCATCACCAACGGGTGCCTCTTTGGCCTGGCTTTCCCTTGGCCTTCCCTCAGC 3003

QY 2113 TTCACCTTGATACTGGGCCCTTTCCTTGTGCATGCTGAAAGTGTGGACCAGAGACCTTGGGA 2172

Db 3004 TTCACCTTGATACTGGGCCCTTTCCTTGTGCATGCTGAAAGTGTGGACCAGAGACCTTGGGA 3063

QY 2173 CTTTGTCTGCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGTTGATC 2232

Db 3064 CTTTGTCTGCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGTTGATC 3123

QY 2233 AGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCCTGGAAGGTGATTTCCCGTGTGA 2292

Db 3124 AGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCCTGGAAGGTGATTTCCCGTGTGA 3183

QY 2293 CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCCAT 2352

Db 3184 CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCCAT 3243

QY 2353 AAAGACTTCCTATTAAATAAGCTTTTGGAAAGAGATTAAAAAAGGAAAAA 2403

Db 3244 AAAGACTTCCTATTAAATAAGCTTTTGGAAAGAGATTAAAAAAGGAAAAA 3294

RESULT 12
ADH50807

ID ADH50807 standard; cDNA; 3349 BP.

XX AC ADH50807;

XX DT 25-MAR-2004 (first entry)

XX DE Human G-protein coupled receptor splice form 2 coding sequence.

XX KW Human; G-protein coupled receptor; receptor; gene; chromosome 1;

XX KW gene therapy; ss.

XX OS Homo sapiens.

XX XX Location/Qualifiers

FT CDS 82..2829

FT /*tag= a

FT /product= "G-protein coupled receptor splice form 2"

XX WO200268651-A2.

XX PN 06-SEP-2002.

XX XX 26-FEB-2002; 2002WO-US005518.

XX PR 26-FEB-2001; 2001US-0270873P.

XX PR 30-APR-2001; 2001US-00844362.

XX XX (PEKE) PE CORP NY.

XX PA Zhu S, Chaturvedi K, Ketchum K, Di Francesco V, Beasley EM;

XX PI WPI; 2002-707000/76.

XX DR P-PSDB; ADH50808.

XX XX New G-protein coupled receptor peptides and nucleic acids, useful as

PT models for developing human therapeutic targets, in identifying

PT therapeutic proteins, and as targets for the development of human

PT therapeutic agents.

XX XX Claim 4; SEQ ID NO 4; 173pp; English.

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SQ

Sequence 3349 BP; 684 A; 1041 C; 894 G; 730 T; 0 U; 0 Other;

Query Match 90.4%; Score 2247.8; DB 6; Length 3349;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 2263; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 133 AGCGGCTCCAAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG 192

Db 1060 ATCGGCTCCAAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG 1118

QY 193 CTCCTGTCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTTGAGGCCTT 252

Db 1119 CTCCTGTCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTTGAGGCCTT 1178

QY 253 CTCACACCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTGACCCACTGCC 312

Db 1179 CTCACACCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTGACCCACTGCC 1238

QY 313 CCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA 372

Db 1239 CCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA 1298

QY 373 GGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCCTTATGCCCTACCA 432

Db 1299 GGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCCTTATGCCCTACCA 1358

QY 433 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGAGCTGGAGGCTGA 492

Db 1359 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGAGCTGGAGGCTGA 1418

QY 493 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCCTCTTGGCCAGACA 552

Db 1419 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCCTCTTGGCCAGACA 1478

QY 553 AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAA 612

Db 1479 AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAA 1538

QY 613 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 672

Db 1539 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 1598

The present sequence is the transcript coding sequence for splice form 2 of a novel human G-protein coupled receptor (GPCR) related to the leucine -rich repeat-containing GPCR subfamily. The GPCR gene ADH50806 is located on chromosome 1. Two alternatively spliced variants were identified, splice form 1 and splice form 2 ADH50807. Splice forms 1 ADH50804 and are expressed in head/neck tissue, infant brain, and stomach. Splice form 2 is also expressed in colon tumours and leucocytes. The GPCR development of human therapeutic targets; to aid in the identification of therapeutic proteins; as targets for the development of human therapeutic agents; to raise antibodies or to elicit another immune response which may be used as reagents in assays designed to quantitatively determine levels of the protein in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed; to identify compounds that modulate receptor activity of the protein in its natural state; to screen compounds for the ability to stimulate or inhibit interaction between the receptor protein and a molecule that normally interacts with the receptor protein; and as targets for diagnosing a disease or predisposition to a disease mediated by the polypeptide. The nucleic acids are also useful: as probes, primers and chemical intermediates; for making vectors, host cells or transgenic animals; for monitoring the effectiveness of modulating compounds on the expression or activity of the GPCR gene in clinical trials or in a treatment regimen; in diagnostic assays for qualitative changes in GPCR nucleic acid; for testing individuals for a genotype which, while not necessarily causing disease, affects the treatment modality; in nucleic acid arrays and gene chips; for breeding transgenic animals; as antisense constructs to control GPCR gene expression in cells, tissues and organisms; and in gene therapy.

QY	673	CTTTGAAAGCTGGGGCATCCGCGCTGGCCGTTGGGCGCATCGTGTGCTCTCCGTGCTCTG	732	Db	2679	AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTCCATGGATGGAGAACTGCTGCT	2738
Db	1599	CTTTGAAAGCTGGGGCATCCGCGCTGGCCGTTGGGCGCATCGTGTGCTCTCCGTGCTCTG	1658	QY	1813	GAGGCCAGAGGGATCTAGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGCTTTCAGCC	1872
Db	1659	CAATGGACTGGTGTCTGCTGACCGTGTTCGCTGGCGGCGTGTCCCGCTGCCCGCGTCAA	1718	Db	2739	GAGGCCAGAGGGATCTAGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGCTTTCAGCC	2798
QY	793	GTTTGTGGTAGGTGCGATTGCAGGCGCCAAACACCTTGACTGGCATTTCCTGTGSGCTTCT	852	QY	1873	CTCTGGCTTGGCCTTGTCTTACACCGTGTAAATATCCCTCCCAATTCTTCTTCCCCCTC	1932
Db	1719	GTTTGTGGTAGGTGCGATTGCAGGCGCCAAACACCTTGACTGGCATTTCCTGTGSGCTTCT	1778	Db	2799	CTCTGGCTTGGCCTTGTCTTACACCGTGTAAATATCCCTCCCAATTCTTCTTCCCCCTC	2858
QY	853	AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	912	QY	1933	TCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAACAAATACAAACCA	1992
Db	1779	AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	1838	Db	2859	TCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAACAAATACAAACCA	2918
QY	913	GGGGCTAGGCTGCCGGGCACCTGGCTTCCTGGCAGTACTTGGGTGCGAGGCATCGGTGCT	972	QY	1993	AAACTCAGCAGTGTGATCTATAGCAGGATGSCCCAGTACCTGGCTCCACTGATCACCTCT	2052
Db	1839	GGGGCTAGGCTGCCGGGCACCTGGCTTCCTGGCAGTACTTGGGTGCGAGGCATCGGTGCT	1898	Db	2919	AAACTCAGCAGTGTGATCTATAGCAGGATGSCCCAGTCCCTGGCTCCAATGATCACCTCT	2978
QY	973	GCTGCTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGCCGCGCTATGG	1032	QY	2053	CTCCTGTGACCATCACCAACGGGTGCCTCTTGGCCCTGGCTTCCCTTGGCCTTCCCTCAGC	2112
Db	1899	GCTGCTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGCCGCGCTATGG	1958	Db	2979	CTCCTGTGACCATCACCAACGGGTGCCTCTTGGCCCTGGCTTCCCTTGGCCTTCCCTCAGC	3038
QY	1033	GAAGTCCCCCTCCCTGSSCAGCGTTCGAGCAGGGGTCCTAGGCTGCCCTGGCACTGGCAGG	1092	QY	2113	TTACCTTGTATACTGGGCCCTCTTCCCTTGTATGTCTGAAGCTGTGGACCAAGACCTTGA	2172
Db	1959	GAAGTCCCCCTCCCTGSSCAGCGTTCGAGCAGGGGTCCTAGGCTGCCCTGGCACTGGCAGG	2018	Db	3039	TTACCTTGTATACTGGGCCCTCTTCCCTTGTATGTCTGAAGCTGTGGACCAAGACCTTGA	3098
QY	1093	GCTGGCGCGCGCACTGCCCTGGCCCTCAGTGGGAGAAATACGGGGCCTCCCACTCTGCCT	1152	QY	2173	CTTTTGTCTGCTTAAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATC	2232
Db	2019	GCTGGCGCGCGCACTGCCCTGGCCCTCAGTGGGAGAAATACGGGGCCTCCCACTCTGCCT	2078	Db	3099	CTTTTGTCTGCTTAAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATC	3158
QY	1153	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT	1212	QY	2233	AGGGCACAGTGGACAGGGAGACCTCACAGAGAAAAGCCCTGGAAGGTGATTTCCCGTGTGA	2292
Db	2079	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT	2138	Db	3159	AGGGCACAGTGGACAGGGAGACCTCACAGAGAAAAGCCCTGGAAGGTGATTTCCCGTGTGA	3218
QY	1213	GATGAACTCCTTCTGTTTCTTGGTCTGTTGGCGGTGCTACATCAAACTGTACTGTGACCT	1272	QY	2293	CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAAATCTTGACATATGCCATGCAT	2352
Db	2139	GATGAACTCCTTCTGTTTCTTGGTCTGTTGGCGGTGCTACATCAAACTGTACTGTGACCT	2198	Db	3219	CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAAATCTTGACATATGCCATGCAT	3278
QY	1273	GCCGCGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCCTGGCT	1332	QY	2353	AAAGACTTCTCTATTAAATAAGCTTTGGAAGAGATTAAAAAATAAAAAA 2403	
Db	2199	GCCGCGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCCTGGCT	2258	Db	3279	AAAGACTTCTCTATTAAATAAGCTTTGGAAGAGATTAAAAAATAAAAAA 3329	
QY	1333	CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCTCCATGCT	1392	RESULT 13			
Db	2259	CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTTCGCTCCATGCT	2318	ADD89048			
QY	1393	GGGCTCTTCCCTGTACGCCCGAGGCCGTCAAGTCTGTCTGCTGGTGGTGTGCTGCCCT	1452	ID ADD89048 standard; cdNA; 3325 BP.			
Db	2319	GGGCTCTTCCCTGTACGCCCGAGGCCGTCAAGTCTGTCTGCTGGTGGTGTGCTGCCCT	2378	XX			
QY	1453	GCCTGCCCTCAACCCACTGCTGTACTGCTTCAACCCCCACTTCGCGGATGACCT	1512	AC ADD89048;			
Db	2379	GCCTGCCCTCAACCCACTGCTGTACTGCTTCAACCCCCACTTCGCGGATGACCT	2438	XX			
QY	1513	TCGGCGGCTTCGGCCCGCGCAGGGGACTCAGGSCCCCTAGCCCTATGCTGCGGCCGGGA	1572	DT 29-JAN-2004 (first entry)			
Db	2439	TCGGCGGCTTCGGCCCGCGCAGGGGACTCAGGSCCCCTAGCCCTATGCTGCGGCCGGGA	2498	XX			
QY	1573	GCTGGAGAAAGACTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGATCT	1632	DE Encoding sequence TAT251.			
Db	2499	GCTGGAGAAAGACTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGATCT	2558	XX			
QY	1633	CATTCTGGAAGCTTCTGAAGCTGGGCGGCCCTGGCTGGAGACCTATGGCTTCCCTC	1692	XX			
Db	2559	CATTCTGGAAGCTTCTGAAGCTGGGCGGCCCTGGCTGGAGACCTATGGCTTCCCTC	2618	KW tumour-associated antigenic target polypeptide; Cytostatic; tumour; cancer; ss.			
QY	1693	AGTGACCTCATCTCCTGTCAAGCCAGGGCCCCCAGGCTGGAGGCAGCCATTGTGT	1752	XX			
Db	2619	AGTGACCTCATCTCCTGTCAAGCCAGGGCCCCCAGGCTGGAGGCAGCCATTGTGT	2678	OS Homo sapiens.			
QY	1753	AGAGCCAGAGGGGAACCACTTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT	1812	XX			

PR	21-AUG-2002; 2002US-0405645P.	
XX	(GETH) GENENTECH INC.	
PA		
XX		
PI	Frantz G, Hillan KJ, Phillips H, Polakis P, Smith V, Spencer SD;	
PI	Williams PM, Wu TD, Zhang Z;	
XX		
DR	WPI; 2003-569537/53.	
DR	P-PSDB; ADD89064.	
XX		
PT	New antibodies against tumor-associated antigenic target polypeptide,	
PT	useful for treating or diagnosing tumors or cancers in mammals, e.g.	
PT	prostate cancer, lung cancer, prostate adenocarcinomas or renal cell	
PT	carcinomas.	
XX		
PS	Claim 1; SEQ ID NO 52; 252pp; English.	
XX		
CC	The present invention relates to antibodies against tumour-associated	
CC	antigenic target polypeptide. The antibody is useful for treating or	
CC	diagnosing tumours or cancers in mammals, e.g. prostate cancer, lung	
CC	cancer, breast caner, colon cancer, ovarian cancer, prostate	
CC	adenocarcinomas, renal cell carcinomas, or pleural mesothelioma. The	
CC	present sequence represents a TAT polypeptide encoding sequence.	
XX		
SQ	Sequence 3325 BP; 663 A; 1042 C; 893 G; 727 T; 0 U; 0 Other;	
	Query Match 90.4%; Score 2247.2; DB 10; Length 3325;	
	Best Local Similarity 99.8%; Pred. No. 0;	
	Matches 2260; Conservative 0; Mismatches 3; Indels 1; Gaps 1;	
QY	133 AGCGGCCTCCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACACTTCAGCCAGCTGAG	192
Db		
	1063 ATCGGCCTCCAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG	1121
QY	193 CTCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCCGTCCATCCACCCCTGAGSCCTT	252
Db		
	1122 CTCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCCGTCCATCCACCCCTGAGSCCTT	1181
QY	253 CTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTGACCACACTGCC	312
Db		
	1182 CTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTGACCACACTGCC	1241
QY	313 CTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAGGGAACTTGCTCTCTCCCA	372
Db		
	1242 CTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAGGGAACTTGCTCTCTCCCA	1301
QY	373 GGCCTTCTCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCCCTACCA	432
Db		
	1302 GGCCTTCTCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCCCTACCA	1361
QY	433 GTGCTGTCCCTATGSGATGTGTGCCAGCTTCTTCAAGSCCTCTGGCAGTGGAGGCTGA	492
Db		
	1362 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGSCCTCTGGCAGTGGAGGCTGA	1421
QY	493 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTCGGGCCTCCTTGCCAGACA	552
Db		
	1422 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTCGGGCCTCCTTGCCAGACA	1481
QY	553 AGCAGAGAAACCACTATGACAGGACCTGGATGAGCTCAGCTGGAGATGGAGGACTCAAA	612
Db		
	1482 AGCAGAGAAACCACTATGACAGGACCTGGATGAGCTCAGCTGGAGATGGAGGACTCAAA	1541
QY	613 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	672
Db		
	1542 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	1601
QY	673 CTTTGAAGCTGGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG	732
Db		
	1602 CTTTGAAGCTGGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG	1661
QY	733 CAATGGACTGGTGTGCTGCTGCTGCTGGCGGGCCTGCCCCCTGCCCCCGGTCAA	792
Db		
	1662 CAATGGACTGGTGTGCTGCTGCTGCTGGCGGGCCTGCCCCCTGCCCCCGGTCAA	1721

QY	793 GTTTGTGGTAGGTGCGATTGTCAGGCGCCAAACACCTTGACTGGCATTTCTGTGGCCTTCT	852
Db		
	1722 GTTTGTGGTAGGTGCGATTGTCAGGCGCCAAACACCTTGACTGGCATTTCTGTGGCCTTCT	1781
QY	853 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	912
Db		
	1782 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	1841
QY	913 GGGCTAGGCTCCCGGCCACTGGCTTCTTGGCAGTACTTGGGTCGGAGGCATCGGTGCT	972
Db		
	1842 GGGCTAGGCTCCCGGCCACTGGCTTCTTGGCAGTACTTGGGTCGGAGGCATCGGTGCT	1901
QY	973 GCTGCTCACTCTGGCCGCGCAGTGCAGTGCAGCGTCTCCGTCTCTCTGTGCCGGCCTATGG	1032
Db		
	1902 GCTGCTCACTCTGGCCGCGCAGTGCAGTGCAGCGTCTCCGTCTCTGTGCCGGCCTATGG	1961
QY	1033 GAAGTCCCCCTCCCTGGGAGCGTTTCGAGCAGGGGTCTTAGGCTGCCCTGGCAGG	1092
Db		
	1962 GAAGTCCCCCTCCCTGGGAGCGTTTCGAGCAGGGGTCTTAGGCTGCCCTGGCAGG	2021
QY	1093 GCTGGCCGCGCACTGCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCCCACTCTGCCT	1152
Db		
	2022 GCTGGCCGCGCACTGCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCCCACTCTGCCT	2081
QY	1153 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTTGGGCTTACCGTGGCCCTGGTGAT	1212
Db		
	2082 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTTGGGCTTACCGTGGCCCTGGTGAT	2141
QY	1213 GATGAACTCCTTCTGTTCCTGGTCTGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCT	1272
Db		
	2142 GATGAACTCCTTCTGTTCCTGGTCTGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCT	2201
QY	1273 GCCCGGGGCGACTTTGAGGCCGTGTGGGACTGCGGCATGGTGAGGCACGTGGCCTGGCT	1332
Db		
	2202 GCCCGGGGCGACTTTGAGGCCGTGTGGGACTGCGGCATGGTGAGGCACGTGGCCTGGCT	2261
QY	1333 CATCTTCGAGACGGGCTCTCTACTGTCCCCTGGGCTTCTCAGCTTCGCCCTCCATGCT	1392
Db		
	2262 CATCTTCGAGACGGGCTCTCTACTGTCCCCTGGGCTTCTCAGCTTCGCCCTCCATGCT	2321
QY	1393 GGGCCTCTTCCCTGTCAAGCCCGCAGGCCGTCAAGTCTGTCTGTGGTGGTGTGCCCT	1452
Db		
	2322 GGGCCTCTTCCCTGTCAAGCCCGCAGGCCGTCAAGTCTGTCTGTGGTGGTGTGCCCT	2381
QY	1453 GCCTGCCTGCCTCAACCCACTGCTGTACCTGTCTTCAACCCCCCACTTCCGGGATGACCT	1512
Db		
	2382 GCCTGCCTGCCTCAACCCACTGCTGTACCTGTCTTCAACCCCCCACTTCCGGGATGACCT	2441
QY	1513 TCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTCGGCCGGGA	1572
Db		
	2442 TCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTCGGCCGGGA	2501
QY	1573 GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGATCT	1632
Db		
	2502 GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGATCT	2561
QY	1633 CATCTGGAAGCTTCTGAAGCTGGGCGGCCCTGGGCTGGAGACCTATGSCCTTCCCTC	1692
Db		
	2562 CATCTGGAAGCTTCTGAAGCTGGGCGGCCCTGGGCTGGAGACCTATGSCCTTCCCTC	2621
QY	1693 AGTGACCTCATCTCCTGTACGACCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGT	1752
Db		
	2622 AGTGACCTCATCTCCTGTACGACCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGT	2681
QY	1753 AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTCCATGGATGGAGAACTGCTGCT	1812
Db		
	2682 AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTCCATGGATGGAGAACTGCTGCT	2741
QY	1813 GAGGCGAGAGGGATCTACGCCAGCAGGTGGAGGCTGTGAGGGGTGGCGCTTTCAGCC	1872
Db		
	2742 GAGGCGAGAGGGATCTACGCCAGCAGGTGGAGGCTGTGAGGGGTGGCGCTTTCAGCC	2801

QY 1873 CTCTGGCTTGGCCTTTGCTTCACACGTTGTAATAATATCCCTCCCCATTCTTCTCTTCCCCTC 1932
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Db 2802 CTCTGGCTTGGCCTTTGCTTCACACGTTGTAATAATATCCCTCCCCATTCTTCTTCCCCTC 2861
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QY 1933 TCTTCCCTTTCTCTCTCCCTCGGTGAATGATGGCTGCTTCTAAACAATAACAACCA 1992
|||||
Db 2862 TCTTCCCTTTCTCTCTCCCTCGGTGAATGATGGCTGCTTCTAAACAATAACAACCA 2921
|||||
QY 1993 AAACTCAGCAGTGTGATCTATAGCAGGATGGCCACGTACCTGGCTCCACTGATCACCTCT 2052
|||||
Db 2922 AAACTCAGCAGTGTGATCTATAGCAGGATGGCCACGTACCTGGCTCCACTGATCACCTCT 2981
|||||
QY 2053 CTCCTGTGACCATCACCAACGGGTGCCTCTTGGCCCTGGCTTCCCTTGGCCTTCCCTCAGC 2112
|||||
Db 2982 CTCCTGTGACCATCACCAACGGGTGCCTCTTGGCCCTGGCTTCCCTTGGCCTTCCCTCAGC 3041
|||||
QY 2113 TTCACCTTGATACTGGCCTCTTCTTGTCTGATGCTGAAGCTGTGGACCAGACCTTGA 2172
|||||
Db 3042 TTCACCTTGATACTGGCCTCTTCTTGTCTGATGCTGAAGCTGTGGACCAGACCTTGA 3101
|||||
QY 2173 CTTTGTCTGTCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGTGGAGGTTGATC 2232
|||||
Db 3102 CTTTGTCTGTCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGTGGAGGTTGATC 3161
|||||
QY 2233 AGGCACAGTGGACAGGGACCTCACAGAGAAAGSCCTGGAAGTGATTTCCCGTGTGA 2292
|||||
Db 3162 AGGCACAGTGGACAGGGAGACCTCACAGAGAAAGSCCTGGAAGTGATTTCCCGTGTGA 3221
|||||
QY 2293 CTCATGGATAGGATACAAAATGTGTTCCATGTACCAATTAATCTTGACATATGCCATGCAT 2352
|||||
Db 3222 CTCATGGATAGGATACAAAATGTGTTCCATGTACCAATTAATCTTGACATATGCCATGCAT 3281
|||||
QY 2353 AAAGACTTCCTATTAAATAAGCTTTTGGAAAGAGATTAAAAAAA 2396
|||||
Db 3282 AAAGACTTCCTATTAAATAAGCTTTTGGAAAGAGAAAAA 3325
|||||

RESULT 14

ADI21981
ID ADI21981 standard; cDNA; 2964 BP.
XX
AC ADI21981;
XX
DT 15-APR-2004 (first entry)
XX
DE Novel human protein cDNA #240.
XX
KW forensic; nutritional source; damaged tissue; diseased tissue;
KW myeloid cell disorder; lymphoid cell disorder;
KW bone cartilage tissue growth; tendon tissue growth;
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human;
KW ss; gene.
XX
OS Homo sapiens.
XX
PN WO2003025148-A2.
XX
PD 27-MAR-2003.
XX
PF 19-SEP-2002; 2002WO-US029964.
XX
PR 19-SEP-2001; 2001US-0323739P.
PR 13-SEP-2002; 2002US-00323739.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac R, wang D;
PI Haley-Vicente D;
XX
DR WPI; 2003-354603/33.
DR P-PSDB; ADI21265.

XX
PT New polynucleotides and secreted proteins, useful for treating myeloid or
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve
PT tissue growth or regeneration, in wound healing, and in tissue repair and
PT replacement.
XX
PS Claim 1; SEQ ID NO 240; 156pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding a
CC polypeptide with biological activity. The polynucleotides and
CC polypeptides are useful in diagnostics, forensics, gene mapping,
CC identification of mutations responsible for genetic disorders and other
CC traits, to assess biodiversity, as nutritional sources or supplements.
CC The polynucleotides may also be used as molecular weight markers,
CC chromosome markers or map related gene positions, or as an antigen to
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are
CC useful for raising antibodies, as markers for tissues in which the
CC corresponding polypeptide is expressed, for re-engineering damaged or
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in
CC bone cartilage, tendon, ligament and/or nerve tissue growth or
CC regeneration, in wound healing, in tissue repair and replacement, in
CC healing of burns, incisions and ulcers, and in treating cancer. The
CC present sequence represents cDNA encoding a novel human protein.
XX
SQ Sequence 2964 BP; 563 A; 936 C; 825 G; 640 T; 0 U; 0 Other;

Query Match 90.2%; Score 2243; DB 10; Length 2964;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2257; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 133 AGCGGCCTCCAAACAAACCGCATCTGGGAATTGGAGCTNGACACCTTCAGCCAGCTGAG 192
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Db 703 ATCGGCCTCCAAACAAACCGCATCTGGGAATTGGAGCT-GACACCTTCAGCCAGCTGAG 761
|||||
QY 193 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCTT 252
|||||
Db 762 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCTT 821
|||||
QY 253 CTCCACCCCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTGACCACTGCC 312
|||||
Db 822 CTCCACCCCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTGACCACTGCC 881
|||||
QY 313 CCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA 372
|||||
Db 882 CCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA 941
|||||
QY 373 GGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGTGCCCTATGCCTACCA 432
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Db 942 GGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGTGCCCTATGCCTACCA 1001
|||||
QY 433 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGAGTGGGAGGCTGA 492
|||||
Db 1002 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGAGTGGGAGGCTGA 1061
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QY 493 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCTCCTTGCCAGACA 552
|||||
Db 1062 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCTCCTTGCCAGACA 1121
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QY 553 AGCAGAGAACCACTATGACCAGGACCTTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 612
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Db 1122 AGCAGAGAACCACTATGACCAGGACCTTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 1181
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QY 613 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCCTGTGAGTACCT 672
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Db 1182 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCCTGTGAGTACCT 1241
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QY 673 CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG 732
|||||
Db 1242 CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG 1301
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QY 733 CAATGGACTGGTGTGCTGACCCGTGTTGGTGGGGCCCTGCCCCCTGCCCGGTCAA 792
|||||
Db 1302 CAATGGACTGGTGTGCTGACCCGTGTTGGTGGGGCCCTGTCCCCCTGCCCGGTCAA 1361
|||||

Qy	793	GTTTGTGGTAGGTGCGATTGCAGGCGCCAAACACCTTGACTGGCATTTCTGTGGCCTTCT	852
Db	1362	GTTTGTGGTAGGTGCGATTGCAGGCGCCAAACACCTTGACTGGCATTTCTGTGGCCTTCT	1421
Qy	853	AGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	912
Db	1422	AGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	1481
Qy	913	GSGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGGTGGAGGCATCGGTGCT	972
Db	1482	GGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGGTGGAGGCATCGGTGCT	1541
Qy	973	GCTGCTCACTCTGGCCGCGAGTCGAGTGCAGCGTCTCCGTCTCCTGTGTCGGGCCCTATGG	1032
Db	1542	GCTGCTCACTCTGGCCGCGAGTCGAGTGCAGCGTCTCCGTCTCCTGTGTCGGGCCCTATGG	1601
Qy	1033	GAAGTCCCCCTCCCTGGGCGAGCGTTCGAGCAGGGGTCCTAGGCTGCCCTGGCACCTGGCAGG	1092
Db	1602	GAAGTCCCCCTCCCTGGGCGAGCGTTCGAGCAGGGGTCCTAGGCTGCCCTGGCACCTGGCAGG	1661
Qy	1093	GCTGSCCGCGCACTGCCCTGGCTCAGTGGGAGAAATACGGGGCTTCCCCACTCTGCCT	1152
Db	1662	GCTGSCCGCGCACTGCCCTGGCTCAGTGGGAGAAATACGGGGCTTCCCCACTCTGCCT	1721
Qy	1153	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT	1212
Db	1722	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT	1781
Qy	1213	GATGAACTCCTTCTGTTTCCGTGGTGGCCGGTGCCATACAAACTGTACTGTGACCT	1272
Db	1782	GATGAACTCCTTCTGTTTCCGTGGTGGCCGGTGCCATACAAACTGTACTGTGACCT	1841
Qy	1273	GCCGGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGTFAGGCACGTGGCCTGGCT	1332
Db	1842	GCCGGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGTFAGGCACGTGGCCTGGCT	1901
Qy	1333	CATCTTCGCAGACGGGCTCCTACTGTGTCCCGTGGCCTTCCTCAGCTTCGCCCTCCATGCT	1392
Db	1902	CATCTTCGCAGACGGGCTCCTACTGTGTCCCGTGGCCTTCCTCAGCTTCGCCCTCCATGCT	1961
Qy	1393	GSGCCTCTTCCCTGTCAAGCCCGAGGCCCGTCAAGTCTGTCTGCTGGTGGTGCCTGCCCT	1452
Db	1962	GSGCCTCTTCCCTGTCAAGCCCGAGGCCCGTCAAGTCTGTCTGCTGGTGGTGCCTGCCCT	2021
Qy	1453	GCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCACTTCGGGGATGACCT	1512
Db	2022	GCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCACTTCGGGGATGACCT	2081
Qy	1513	TCGGCGGCTTCGGCCCCCGCGAGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGA	1572
Db	2082	TCGGCGGCTTCGGCCCCCGCGAGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGA	2141
Qy	1573	GCTGAGAAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT	1632
Db	2142	GCTGAGAAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT	2201
Qy	1633	CATTCTGGAAGCTTCTGAAGCTGGGCGGCCCTCCCTGGGCTGGAGACCTATGGCTTCCCCTC	1692
Db	2202	CATTCTGGAAGCTTCTGAAGCTGGGCGGCCCTCCCTGGGCTGGAGACCTATGGCTTCCCCTC	2261
Qy	1693	AGTGACCTCATCTCCTGTCAAGCAGCCAGGGCCCCCAGGCTGGAGGGCAGCCATTGTGT	1752
Db	2262	AGTGACCTCATCTCCTGTCAAGCAGCCAGGGCCCCCAGGCTGGAGGGCAGCCATTGTGT	2321
Qy	1753	AGAGCAGAGGGGAACCACTTTTGGAAACCCCAACCCCTCCATGGATGGAGAACTGCTGCT	1812
Db	2322	AGAGCAGAGGGGAACCACTTTTGGAAACCCCAACCCCTCCATGGATGGAGAACTGCTGCT	2381
Qy	1813	GAGGCGAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGTGGCGGCTTTCAGCC	1872
Db	2382	GAGGCGAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGTGGCGGCTTTCAGCC	2441

Qy	1873	CTCTGGCTTGGCCTTTGCTTCACACGTGTAAATATCCCTCECCATTCTTCTCTTCCCTC	1932
Db	2442	CTCTGGCTTGGCCTTTGCTTCACACGTGTAAATATCCCTCCCCATTCTTCTTCCCTC	2501
Qy	1933	TCTTCCCTTTCTCTTCCCTCTGGTGAATGATGGTGTCTTCTAAACAATAACACCA	1992
Db	2502	TCTTCCCTTTCTCTTCCCTCTGGTGAATGATGGTGTCTTCTAAACAATAACACCA	2561
Qy	1993	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCACTGACCTGGCTCCAATGATCACCTCT	2052
Db	2562	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCACTGACCTGGCTCCAATGATCACCTCT	2621
Qy	2053	CTCCTGTGACCATCACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCCTCAGC	2112
Db	2622	CTCCTGTGACCATCACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCCTCAGC	2681
Qy	2113	TTACCTTGATACTGGGCTCTTCCCTTGTTCATGTCGAAAGCTGTGGACCAGAGACCTGGA	2172
Db	2682	TTACCTTGATACTGGGCTCTTCCCTTGTTCATGTCGAAAGCTGTGGACCAGAGACCTGGA	2741
Qy	2173	CTTTTGTCTGCTTAAGGAAATGAGGGAAGTAAAGACAGTGAAGGGTGGAGGGTTGATC	2232
Db	2742	CTTTTGTCTGCTTAAGGAAATGAGGGAAGTAAAGACAGTGAAGGGTGGAGGGTTGATC	2801
Qy	2233	AGGCACAGTGGACAGGAGACCTCACAGAGAAAGCCTGGAAGGTGATTTCCCGTGTGA	2292
Db	2802	AGGCACAGTGGACAGGAGACCTCACAGAGAAAGCCTGGAAGGTGATTTCCCGTGTGA	2861
Qy	2293	CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCAT	2352
Db	2862	CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCAT	2921
Qy	2353	AAAGACTTCCATTAAATAAAGCTTTGGAAGAGATTAAAAAAA	2395
Db	2922	AAAGACTTCCATTAAATAAAGCTTTGGAAGAGAAAAAAA	2964

RESULT 15

AAD37674

ID AAD37674 standard; cDNA; 3429 BP.

XX

AC AAD37674;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human G-protein coupled receptor-10 (GCREC-10) cDNA.

XX

KW Human; G-protein coupled receptor-10; GCREC-10; atherosclerosis; cancer; cell proliferative disorder; gastrointestinal; autoimmune; metabolic; neurological; inflammatory; cardiovascular; viral infection; anorexia; cirrhosis; multiple sclerosis; Huntington's disease; gene therapy; Alzheimer's disease; heart failure; hepatitis; cholecystitis; obesity; rheumatoid arthritis; Hashimoto's thyroiditis; angina pectoris; osteoporosis; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .2847

FT /*tag= a /product= "Human GCREC-10 protein"

FT sig_peptide 1. .75

FT /*tag= b

FT mat_peptide 76. .2844

FT /*tag= c

FT /product= "Mature GCREC-10 protein"

XX WO200226825-A2.

XX

PD 04-APR-2002.

XX

PF 28-SEP-2001; 2001WO-US030661.

XX

Db 2577 CATTCGGAAGCTTCTGAAGCTGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCCTC 2636

QY 1693 AGTGACCCCTCATCTCCTGTCTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGT 1752

Db 2637 AGTGACCCCTCATCTCCTGTCTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGT 2696

QY 1753 AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT 1812

Db 2697 AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT 2756

QY 1813 GAGGGCAGAGGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGTGGCGGCTTTCAGCC 1872

Db 2757 GAGGGCAGAGGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGTGGCGGCTTTCAGCC 2816

QY 1873 CTCTGGCTTGGCCCTTGTCTTACACGCTGTAATAATATCCCTCCCCATTTCTCTTCCCCCTC 1932

Db 2817 CTCTGGCTTGGCCCTTGTCTTACACGCTGTAATAATATCCCTCCCCATTTCTCTTCCCCCTC 2876

QY 1933 TCTTCCCTTTCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAACAAATACAAACCA 1992

Db 2877 TCTTCCCTTTCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAACAAATACAAACCA 2936

QY 1993 AAACCTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACCTGGCTCCACTGATCACCTCT 2052

Db 2937 AAACCTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACCTGGCTCCACTGATCACCTCT 2996

QY 2053 CTCCTGTGACCATCACCAACGGGTGCTCTTGGCCTGGCTTTCCTTGGCCTTCCCTCAGC 2112

Db 2997 CTCCTGTGACCATCACCAACGGGTGCTCTTGGCCTGGCTTTCCTTGGCCTTCCCTCAGC 3056

QY 2113 TTCACCTTGATACCTGGCCCTCTTCCCTGTCTCATGTCTGAAGCTGTGGACCCAGAGACCTGGA 2172

Db 3057 TTCACCTTGATACCTGGCCCTCTTCCCTGTCTCATGTCTGAAGCTGTGGACCCAGAGACCTGGA 3116

QY 2173 CTTTGTCTGCTTAAGGGAATAGGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATC 2232

Db 3117 CTTTGTCTGCTTAAGGGAATAGGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATC 3176

QY 2233 AGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCCTGGAAGGTGATTTCCCGTGTGA 2292

Db 3177 AGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCCTGGAAGGTGATTTCCCGTGTGA 3236

QY 2293 CTCATGGATAGGATACAAAATGTGTTCATGTACCATTAATCTTGACATATGCCATGCAT 2352

Db 3237 CTCATGGATAGGATACAAAATGTGTTCATGTACCATTAATCTTGACATATGCCATGCAT 3296

QY 2353 AAAGACTTCCCTATTAAATAAGCTTTGGAAGAGATTAAAA 2393

Db 3297 AAAGACTTCCCTATTAAATAAGCTTTGGAAGAGATTACACA 3337

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 12:03:58 ; Search time 943.376 Seconds
(without alignments)
15987.096 Million cell updates/sec

Title: US-10-664-667-4
Perfect score: 2486
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Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 303355566 residues

Total number of hits satisfying chosen parameters: 11245082

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2485	100.0	2486	10	US-09-851-595-4 Sequence 4, Appli
2	2485	100.0	2486	17	US-10-664-667-4 Sequence 4, Appli
3	2257.4	90.8	2711	10	US-09-851-595-7 Sequence 7, Appli
4	2257.4	90.8	2711	17	US-10-664-667-7 Sequence 7, Appli
5	2255.8	90.7	2988	17	US-10-302-172-723 Sequence 723, App
6	2247.8	90.4	3349	14	US-10-270-336-4 Sequence 4, Appli
7	2247.2	90.4	3325	17	US-10-331-496A-52 Sequence 52, Appl
8	2241	90.1	3429	18	US-10-398-036-26 Sequence 26, Appl
9	2238	90.0	3443	17	US-10-331-496A-94 Sequence 94, Appl
10	2238	90.0	3492	10	US-09-851-595-10 Sequence 10, Appl
11	2238	90.0	3492	17	US-10-664-667-10 Sequence 10, Appl

12	2238	90.0	3492	18	US-10-737-450-31	Sequence 31, Appl
13	2231.4	89.8	3273	17	US-10-295-027-1119	Sequence 1119, Ap
14	2231.4	89.8	3273	18	US-10-783-528-43	Sequence 43, Appl
15	2219.6	89.3	3381	10	US-09-970-944-5	Sequence 5, Appli
16	2085.8	83.9	3119	15	US-10-225-567A-580	Sequence 580, App
17	1898	76.3	1899	10	US-09-851-595-6	Sequence 6, Appli
18	1898	76.3	1899	17	US-10-664-667-6	Sequence 6, Appli
19	1754.4	70.6	2208	10	US-09-851-595-9	Sequence 9, Appli
20	1754.4	70.6	2208	17	US-10-664-667-9	Sequence 9, Appli
21	1754.4	70.6	2901	10	US-09-851-595-12	Sequence 12, Appl
22	1754.4	70.6	2901	17	US-10-664-667-12	Sequence 12, Appl
23	1754.4	70.6	3438	14	US-10-176-847-89	Sequence 89, Appl
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25	1743	70.1	119596	14	US-10-270-336-3	Sequence 3, Appli
26	1383.4	55.6	3637	10	US-09-851-595-1	Sequence 1, Appli
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30	983.4	39.6	1078	17	US-10-264-049-395	Sequence 395, App
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34	439.4	17.7	453	9	US-09-876-889-240	Sequence 240, App
35	416.2	16.7	422	10	US-09-918-995-34626	Sequence 34626, A
36	356.2	14.3	2082	19	US-10-851-470-3	Sequence 3, Appli
37	355.6	14.3	2651	17	US-10-295-027-483	Sequence 483, App
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ALIGNMENTS

RESULT 1
US-09-851-595-4
; Sequence 4, Application US/09851595
; Publication No. US20030166047A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/09/851,595
; CURRENT FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2486
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1900)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (172)
; OTHER INFORMATION: n = any nucleotide
US-09-851-595-4

Query Match 100.0%; Score 2485; DB 10; Length 2486;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 4, Application US/10664667
; Publication No. US20040058377A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/10/664,667
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/851,595
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
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; NAME/KEY: CDS
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (172)
; OTHER INFORMATION: n = any nucleotide
US-10-664-667-4

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	613	GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTTGAGTACCT	672
Db	921	GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTTGAGTACCT	980
QY	673	CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG	732
Db	981	CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG	1040
QY	733	CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGGCTGCCCCCTGCCCGGTCAA	792
Db	1041	CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGGCTGCCCCCTGCCCGGTCAA	1100
QY	793	GTGTGTTAGGTGCGATTGCAGGCGCCAAACACCTTGACTGGCATTTCTCTGTGGCCTTCT	852
Db	1101	GTGTGTTAGGTGCGATTGCAGGCGCCAAACACCTTGACTGGCATTTCTCTGTGGCCTTCT	1160
QY	853	AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTTGAGTACGGAGCCCGCTGGGAGAC	912
Db	1161	AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTTGAGTACGGAGCCCGCTGGGAGAC	1220
QY	913	GGGGCTAGGCTGCCGGCCACTGGCTTCCTGGCAGTACTTGGGTGGAGGCATCGGTGCT	972
Db	1221	GGGGCTAGGCTGCCGGCCACTGGCTTCCTGGCAGTACTTGGGTGGAGGCATCGGTGCT	1280
QY	973	GCTGCTCACTGTGGCGCAGTGCAGTGCAGCTCTCCGTCTCCTGTCTCGTGGGCCCTATGG	1032
Db	1281	GCTGCTCACTGTGGCGCAGTGCAGTGCAGCTCTCCGTCTCCTGTCTCGTGGGCCCTATGG	1340
QY	1033	GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCCTGGCAGCTGGCAGG	1092
Db	1341	GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCCTGGCAGCTGGCAGG	1400
QY	1093	GCTGGCCCGCCGCACTGCCCTTGCCCTCAGTGGAGAAATACGGGGCTTCCCCACTCTGCCT	1152
Db	1401	GCTGGCCCGCCGCACTGCCCTTGCCCTCAGTGGAGAAATACGGGGCTTCCCCACTCTGCCT	1460
QY	1153	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCCGTGGCCCTGGTGAT	1212
Db	1461	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCCGTGGCCCTGGTGAT	1520
QY	1213	GATGAACCTCCTTCTGTTCCTGGTCGTGGCGGTGCCCTACATCAAACTGTACTGTGACCT	1272
Db	1521	GATGAACCTCCTTCTGTTCCTGGTCGTGGCGGTGCCCTACATCAAACTGTACTGTGACCT	1580
QY	1273	GCCGCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT	1332
Db	1581	GCCGCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT	1640
QY	1333	CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCCTTCCTCAGCTTCGCCTCCATGCT	1392
Db	1641	CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCCTTCCTCAGCTTCGCCTCCATGCT	1700
QY	1393	GGGCCTCTTCCCTGTCAAGCCGAGGCCGTCAAGTCTGTCTGTGTGGTGTGCTGCCCT	1452
Db	1701	GGGCCTCTTCCCTGTCAAGCCGAGGCCGTCAAGTCTGTCTGTGTGGTGTGCTGCCCT	1760
QY	1453	GCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCACTTCCGGGATGACCT	1512
Db	1761	GCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCACTTCCGGGATGACCT	1820
QY	1513	TCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTCGGCCGGGA	1572
Db	1821	TCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTCGGCCGGGA	1880
QY	1573	GCTGGAGAAAGACTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTCTCTGATGTGGATCT	1632
Db	1881	GCTGGAGAAAGACTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTCTCTGATGTGGATCT	1940
QY	1633	CATTCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGCGCTTCCCCTC	1692
Db	1941	CATTCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGCGCTTCCCCTC	2000
QY	1693	AGTGACCCCTCATCTCCTGTCAAGCAGCCAGGGGCCCCCAGGCTGGAGGCAGCCATGTGT	1752
Db	2001	AGTGACCCCTCATCTCCTGTCAAGCAGCCAGGGGCCCCCAGGCTGGAGGCAGCCATGTGT	2060
QY	1753	AGAGCCAGAGGGGAACCACTTTGGGAAACCCCAACCTCCATGGATGGAGAACTGTGCT	1812
Db	2061	AGAGCCAGAGGGGAACCACTTTGGGAAACCCCAACCTCCATGGATGGAGAACTGTGCT	2120
QY	1813	GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGGCTTTCAGCC	1872
Db	2121	GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGGCTTTCAGCC	2180
QY	1873	CTCTGGCTTGGCCTTTGCTTCACACGTGTAAATAFCCCTCCCCATTTCTTCTTCCCCTC	1932
Db	2181	CTCTGGCTTGGCCTTTGCTTCACACGTGTAAATAFCCCTCCCCATTTCTTCTTCCCCTC	2240
QY	1933	TCCTCCCTTCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTTAAACAAATACAACCA	1992
Db	2241	TCCTCCCTTCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTTAAACAAATACAACCA	2300
QY	1993	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCAGTACCTGGCTCCACTGATCACCTCT	2052
Db	2301	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCAGTACCTGGCTCCACTGATCACCTCT	2360
QY	2053	CTCCTGTGACCATCACCAACGGGTGCTCTTGGCCCTGGCTTTCCCTTGGCCCTTCTCAGC	2112
Db	2361	CTCCTGTGACCATCACCAACGGGTGCTCTTGGCCCTGGCTTTCCCTTGGCCCTTCTCAGC	2420
QY	2113	TTACCTTGTGATACCTGGCCCTCTTCTTGTCTGTCATGTCTGAAGCTGTGGACAGACCTGGA	2172
Db	2421	TTACCTTGTGATACCTGGCCCTCTTCTTGTCTGTCATGTCTGAAGCTGTGGACAGACCTGGA	2480
QY	2173	CTTTTGTCTGCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAAGGGGTGGAGGGTTGATC	2232
Db	2481	CTTTTGTCTGCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAAGGGGTGGAGGGTTGATC	2540
QY	2233	AGGGCAGAGTGGACAGGGAGACCTCACAGAGAAAGGCCCTGGAAAGTGAATTTCCCGTGTGA	2292
Db	2541	AGGGCAGAGTGGACAGGGAGACCTCACAGAGAAAGGCCCTGGAAAGTGAATTTCCCGTGTGA	2600
QY	2293	CTCATGGATAGGATACAAAATGTGTTCATGTACCATTAATCTTGACATATGCCATGCAT	2352

Qy 1693 AGTGACCTCATCTCTGTGTCAGCAGCCAGGGCCCCCAGGCTGGAGGGCAGCCATTGTGT 1752
Db |||||
Qy 1753 AGAGCCAGAGGGGAACCACTTTTGGGAACCCCAACCTCCATGGATGGAGAACTGCTGCT 1812
Db |||||
Qy 1813 GAGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTTCAGGGGGTGGCGGCTTTCAGCC 1872
Db |||||
Qy 1873 CTCTGGCTTGGCCTTGTTCACACGTGTAATATCCCTCCCCATTCTTCTCTTCCCTC 1932
Db |||||
Qy 1933 TCTTCCCTTCTCTCCCTCGGTGAATGATGGCTGCTTCTAAACAAATACAACCA 1992
Db |||||
Qy 1993 AAACCTCAGCAGTGTATCTATAGCAGGATGGCCAGTACCTGGCTCCACTGATCACCTCT 2052
Db |||||
Qy 2053 CTCCTGTGACCATCACCAACGGGTGCCTCTTGGCCCTGGCTTCCCTTGGCCCTTCTCAGC 2112
Db |||||
Qy 2113 TTCACCTTGATACTGGGCCCTTCCCTTGTCTGTCATGTCTGAAGCTGTGGACCAGACCTGGA 2172
Db |||||
Qy 2173 CTTTGTCTCTTAAGGGAATAGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGTTGATC 2232
Db |||||
Qy 2233 AGGCACAGTGGACAGGAGACCTCACAGAGAAAGCGCTGGAAGGTGATTTCCCGTGTGA 2292
Db |||||
Qy 2293 CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCAT 2352
Db |||||
Qy 2353 AAAGACTTCCTATTAAATAAGCTTTTGGGAAGAGATTAAAAA 2403
Db |||||
Qy 2403 AAAGACTTCCTATTAAATAAGCTTTTGGGAAGAGATTAAAAA 2497
Db |||||

RESULT 6

US-10-270-336-4
; Sequence 4, Application US/10270336
; Publication No. US20030074678A1
; GENERAL INFORMATION:
; APPLICANT: ZHU, Shiaooping et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001146CON
; CURRENT APPLICATION NUMBER: US/10/270,336
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/270,873
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3349
; TYPE: DNA
; ORGANISM: Human
US-10-270-336-4

Query Match 90.4%; Score 2247.8; DB 14; Length 3349;
Best Local Similarity 99.6%; Pred. No. 0;

Matches 2263; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
Qy 133 AGGGCCTCCAAACAACCGCATCTGGGAAATTGGAGCTNGACACCTTACGCCAGCTGAG 192
Db |||||
Qy 1060 ATCGGCCTCCAAACAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG 1118
Qy 193 CTCCCTGCAAGCCCTGGATCTTAGCTGGAAACGCCCATCCGGTCCATCCACCCCTGAGGCCCTT 252
Db |||||
Qy 1119 CTCCCTGCAAGCCCTGGATCTTAGCTGGAAACGCCCATCCGGTCCATCCACCCGAGGCCCTT 1178
Qy 253 CTCCACCCCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAAACAGCTGACACACTGCC 312
Db |||||
Qy 1179 CTCCACCCCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAAACAGCTGACACACTGCC 1238
Qy 313 CCTGGCTGGACTTGGGGCTTGTATGCACTGAAAGCTCAAAGGAAACCTTGTCTCTCCCA 372
Db |||||
Qy 1239 CCTGGCTGGACTTGGGGCTTGTATGCACTGAAAGCTCAAAGGAAACCTTGTCTCTCCCA 1298
Qy 373 GGCCTTCTCCAAAGGACAGTTTCCCAAAACCTGAGGATCCTGGAGGTGCCCTTATGCCATACCA 432
Db |||||
Qy 1299 GGCCTTCTCCAAAGGACAGTTTCCCAAAACCTGAGGATCCTGGAGGTGCCCTTATGCCATACCA 1358
Qy 433 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAAGGCCCTCTGGGCAGTGGGAGGCTGA 492
Db |||||
Qy 1359 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAAGGCCCTCTGGGCAGTGGGAGGCTGA 1418
Qy 493 AGACCTTCACCTTGATGAGGAGTCTTCAAAAAGGCCCCCTGGGCCCTCTTGGCCAGACA 552
Db |||||
Qy 1419 AGACCTTCACCTTGATGAGGAGTCTTCAAAAAGGCCCCCTGGGCCCTCTTGGCCAGACA 1478
Qy 553 AGCAGAGAAACCACTATGACCAGGACCTGATGAGCTCCAGCTGGAGATGGAGGACTCAAA 612
Db |||||
Qy 1479 AGCAGAGAAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAA 1538
Qy 613 GCCACACCCCACTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAAGCCCTGTGAGTACCT 672
Db |||||
Qy 1539 GCCACACCCCACTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAAGCCCTGTGAGTACCT 1598
Qy 673 CTTTGAAGCTGGGGCATCCGCCCTGGCCGTGGGCCCATCGTGTGCTCTCCGTGCTCTG 732
Db |||||
Qy 1599 CTTTGAAGCTGGGGCATCCGCCCTGGCCGTGGGCCCATCGTGTGCTCTCCGTGCTCTG 1658
Qy 733 CAATGGACTGGTGTGCTGACCCGTGTCGTGGCGGGCCCTGCCCCCTGCCCCCGGTCAA 792
Db |||||
Qy 1659 CAATGGACTGGTGTGCTGACCCGTGTCGTGGCGGGCCCTGTCCCCCTGCCCCCGGTCAA 1718
Qy 793 GTTTGTGGTACGTGCGATTGACGGCGCCAAACACTTGAATTCCTGTGGCCCTTCT 852
Db |||||
Qy 1719 GTTTGTGGTACGTGCGATTGACGGCGCCAAACACTTGAATTCCTGTGGCCCTTCT 1778
Qy 853 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGATACGGAGCCGCTGGGAGAC 912
Db |||||
Qy 1779 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGATACGGAGCCGCTGGGAGAC 1838
Qy 913 GGGCTAGGCTGCCGGCCACTGGCTTCTCTGGCAGTACTTGGGTGCGAGGCGATCGGTGCT 972
Db |||||
Qy 1839 GGGCTAGGCTGCCGGCCACTGGCTTCTCTGGCAGTACTTGGGTGCGAGGCGATCGGTGCT 1898
Qy 973 GCTGCTCACTTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCTCTGTGTCGGGCCCTATGG 1032
Db |||||
Qy 1899 GCTGCTCACTTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCTCTGTGTCGGGCCCTATGG 1958
Qy 1033 GAAGTCCCCCTCCCTGGGCAGCGTTTCAGCAGGGGTCTTAGGCTGCTTGGCCGCTATGG 1092
Db |||||
Qy 1959 GAAGTCCCCCTCCCTGGGCAGCGTTTCAGCAGGGGTCTTAGGCTGCTTGGCAGTGGCAGG 2018
Qy 1093 GCTGGCCGCGCACTGCCCTTGGCTCAGTGGGAGAAATACGGGGCTTCCCCACTCTGCCT 1152
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Qy 2019 GCTGGCCGCGCGCTGCCCTTGGCTCAGTGGGAGAAATACGGGGCTTCCCCACTCTGCCT 2078
Qy 1153 GCCCTACGGCCACCTGAGGGTACGCCAGCAGCCCTGGGCTTCAACGTTGGCCCTGGTGAT 1212
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Qy 2079 GCCCTACGGCCACCTGAGGGTACGCCAGCAGCCCTGGGCTTCAACGTTGGCCCTGGTGAT 2138
Db |||||

Qy 1213 GATGAACCTCCTTCTGTTCCTGGTCGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCT 1272
Db |||||
Qy 2139 GATGAACCTCCTTCTGTTCCTGGTCGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCT 2198
Db |||||
Qy 1273 GCCGGGGCGACATTGTAGGCCGTGTGGGACTGCGCCATGCTGAGGCACGTGGCCTGGCT 1332
Db |||||
Qy 2199 GCCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGCTGAGGCACGTGGCCTGGCT 2258
Db |||||
Qy 1333 CATCTTCGCAGACGGGCTCCTCTACTGTGCCGTGGCCCTTCCTCAGCTTCGCCCTCCATGCT 1392
Db |||||
Qy 2259 CATCTTCGCAGACGGGCTCCTCTACTGTGCCGTGGCCCTTCCTCAGCTTTGCCCTCCATGCT 2318
Db |||||
Qy 1393 GGGCCTCTTCCCTGTCAAGCCCGAGGCCCGTCAAGTCTGTCTGCTGGTGGTGGTGGCCCT 1452
Db |||||
Qy 2319 GGGCCTCTTCCCTGTCAAGCCCGAGGCCCGTCAAGTCTGTCTGCTGGTGGTGGTGGCCGT 2378
Db |||||
Qy 1453 GCCTGCCTGCCTCAACCCACTGTGTACTGTCTCTTCAAGCCCCACTTCCGGGATGACCT 1512
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Qy 2379 GCCTGCCTGCCTCAACCCACTGTGTACTGTCTTCAAGCCCCACTTCCGGGATGACCT 2438
Db |||||
Qy 1513 TCGCGGCTTCGGCCCCGCGAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGA 1572
Db |||||
Qy 2439 TCGCGGCTTCGGCCCCGCGAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGA 2498
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Qy 1573 GCTGGAGAAAGACTCCTCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT 1632
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Qy 1633 CATCTGGAAGCTTCTGAAGCTGGGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCTC 1692
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Qy 2559 CATCTGGAAGCTTCTGAAGCTGGGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCTC 2618
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Qy 1693 AGTGACCTCATCTCTGTACAGCAGCCAGGGCCCCCAGGTGGAGGGCAGCCATTGTGT 1752
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Qy 2619 AGTGACCTCATCTCTGTACAGCAGCCAGGGCCCCCAGGTGGAGGGCAGCCATTGTGT 2678
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Qy 1753 AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT 1812
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Qy 2679 AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT 2738
Db |||||
Qy 1813 GAGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGTGGCGGCTTTCAGCC 1872
Db |||||
Qy 2739 GAGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGTGGCGGCTTTCAGCC 2798
Db |||||
Qy 1873 CTCTGGCTTGGCCTTTGCTTACACAGTGTAATAATATCCCTCCCCATTTCTTCTTCCCTC 1932
Db |||||
Qy 2799 CTCTGGCTTGGCCTTTGCTTACACAGTGTAATAATATCCCTCCCCATTTCTTCTTCCCTC 2858
Db |||||
Qy 1933 TCTTCCCTTCTCTCTCCTCCCTCGGTGAATGATGGCTGCTTCTAAACAAATACAACCA 1992
Db |||||
Qy 2859 TCTTCCCTTCTCTCTCCTCCCTCGGTGAATGATGGCTGCTTCTAAACAAATACAACCA 2918
Db |||||
Qy 1993 AAATCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACCTGGCTCCACTGATCACCTCT 2052
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Qy 2919 AAATCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTCCCTGGCTCCACTGATCACCTCT 2978
Db |||||
Qy 2053 CTCTGTGACCATCACCAACGGGTGCCTCTTGGCCCTGGCTTCCCTTGGCCTTCCCTCAGC 2112
Db |||||
Qy 2979 CTCTGTGACCATCACCAACGGGTGCCTCTTGGCCCTGGCTTCCCTTGGCCTTCCCTCAGC 3038
Db |||||
Qy 2113 TTCACCTTGATACTGGGCCTCTTCCCTTGTATGTCTGAAGTGTGGACCAGAGACCTGGA 2172
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Qy 3039 TTCACCTTGATACTGGGCCTCTTCCCTTGTATGTCTGAAGTGTGGACCAGAGACCTGGA 3098
Db |||||
Qy 2173 CTTTGTCTGCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGTTGATC 2232
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Qy 3099 CTTTGTCTGCTTAAGGGAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGTTGATC 3158
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Qy 2233 AGGSCACAGTGGACAGGGAGACCTCACAGAGAAAGCCCTGGAAGGTGATTTCCCGTGA 2292
Db |||||
Qy 3159 AGGSCACAGTGGACAGGGAGACCTCACAGAGAAAGCCCTGGAAGGTGATTTCCCGTGA 3218
Db |||||

Qy 2293 CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCAT 2352
Db |||||
Qy 3219 CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCAT 3278
Db |||||
Qy 2353 AAAGACTTCCTATTAAATAAGCTTTGGGAAGAGATTAAAAA 2403
Db |||||
Qy 3279 AAAGACTTCCTATTAAATAAGCTTTGGGAAGAGATTAAAAA 3329
Db |||||
RESULT 7
US-10-331-496A-52
; Sequence 52, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 52
; LENGTH: 3325
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-331-496A-52
Query Match 90.4%; Score 2247.2; DB 17; Length 3325;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2260; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 133 AGCGGCTCCAACACACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG 192
Db |||||
Qy 1063 ATCGGCTCCAACACACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG 1121
Db |||||
Qy 193 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCTT 252
Db |||||
Qy 1122 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCTT 1181
Db |||||
Qy 253 CTCCACCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACTGCC 312
Db |||||
Qy 1182 CTCCACCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACTGCC 1241
Db |||||
Qy 313 CTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA 372
Db |||||
Qy 1242 CTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA 1301
Db |||||

QY 373 GGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCA 432
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Dbb 1302 GGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCA 1361
QY 433 GTGCTGTCCCTATAGGATGTGTGCCAGCTTCTTCAAGGCTCTGGGCAGTGGAGGCTGA 492
Dbb|||||
Dbb 1362 GTGCTGTCCCTATAGGATGTGTGCCAGCTTCTTCAAGGCTCTGGGCAGTGGAGGCTGA 1421
QY 493 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCTCCTTGGCCAGACA 552
Dbb|||||
Dbb 1422 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCTCCTTGGCCAGACA 1481
QY 553 AGCAGAGAAACCACTATGACAGGACCTGGATGAGCTCAGCTGGAGATGGAGGACTCAAA 612
Dbb|||||
Dbb 1482 AGCAGAGAAACCACTATGACAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAA 1541
QY 613 GGCACACCCAGTGTCCAGTGTAGCCCTTACTCCAGGCCCTTCAAGCCCCTGTGAGTACCT 672
Dbb|||||
Dbb 1542 GGCACACCCAGTGTCCAGTGTAGCCCTTACTCCAGGCCCTTCAAGCCCCTGTGAGTACCT 1601
QY 673 CTTTGAAGCTGGGGCATCCGCCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG 732
Dbb|||||
Dbb 1602 CTTTGAAGCTGGGGCATCCGCCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG 1661
QY 733 CAATGGACTGGTGTGCTGCTACCGTGTTCGCTGGCGGGCCTGCCCCCCTGCCCGGTCAA 792
Dbb|||||
Dbb 1662 CAATGGACTGGTGTGCTGCTGACCGTGTTCGCTGGCGGGCTGCCCCCCTGCCCGGTCAA 1721
QY 793 GTTTGTGGTAGGTGCGATTGACGGCGCCAAACCTTGACTGGCATTTCTGTGGCCTTCT 852
Dbb|||||
Dbb 1722 GTTTGTGGTAGGTGCGATTGACGGCGCCAAACCTTGACTGGCATTTCTGTGGCCTTCT 1781
QY 853 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTGTAGTACGGAGCCCGCTGGGAGAC 912
Dbb|||||
Dbb 1782 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTGTAGTACGGAGCCCGCTGGGAGAC 1841
QY 913 GGGGCTAGGCTGCCGGCCACTGGCTTCTTGGCAGTACTTGGGTGGGATCGGTGCT 972
Dbb|||||
Dbb 1842 GGGGCTAGGCTGCCGGCCACTGGCTTCTTGGCAGTACTTGGGTGGGATCGGTGCT 1901
QY 973 GCTGCTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCTCCGGSCCTATGG 1032
Dbb|||||
Dbb 1902 GCTGCTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCTATGG 1961
QY 1033 GAAATCCCCCTCCCTGGGAGCGTTTCGAGCAGGGGTCTTAGGCTGCCCTGGCACTGGCAGG 1092
Dbb|||||
Dbb 1962 GAAATCCCCCTCCCTGGGAGCGTTTCGAGCAGGGGTCTAGGCTGCCCTGGCACTGGCAGG 2021
QY 1093 GCTGGCCGCGCACTGCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCCT 1152
Dbb|||||
Dbb 2022 GCTGGCCGCGCACTGCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCCT 2081
QY 1153 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCAACGCTGGCCTGGTGAT 1212
Dbb|||||
Dbb 2082 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCAACGCTGGCCTGGTGAT 2141
QY 1213 GATGAACCTCCTTCTGTTTCTGGTCGTGGCCGGTGCTTACATCAAACTGTACTGTGACCT 1272
Dbb|||||
Dbb 2142 GATGAACCTCCTTCTGTTTCTGGTCGTGGCCGGTGCTTACATCAAACTGTACTGTGACCT 2201
QY 1273 GCCCGGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT 1332
Dbb|||||
Dbb 2202 GCCCGGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT 2261
QY 1333 CATCTTCGACACGGGCTCCTCTACTGTCCCGTGGCCTTCTCAGCTTCGCCTCCATGCT 1392
Dbb|||||
Dbb 2262 CATCTTCGACACGGGCTCCTCTACTGTCCCGTGGCCTTCTCAGCTTCGCCTCCATGCT 2321
QY 1393 GGGCCTCTTCCCTGTACAGCCCGAGGCCCGTCAAGTGTCTCCTGTGGTGGTGTGCCCT 1452
Dbb|||||
Dbb 2322 GGGCCTCTTCCCTGTACAGCCCGAGGCCCGTCAAGTGTCTCCTGTGTGGTGTGCCCT 2381
QY 1453 GCCTGCCTGCCTCAACCCACTGCTGTACCTGTCTTCAACCCCCACCTTCGGGGATGACCT 1512

Dbb|||||
Dbb 2382 GCCTGCCTGCCTCAACCCACTGTCTGATACCTGTCTTCAACCCCACTTCCGGGATGACCT 2441
QY 1513 TCGCGGGCTTCGGCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGA 1572
Dbb|||||
Dbb 2442 TCGCGGGCTTCGGCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGA 2501
QY 1573 GCTGGAGAAGAGCTCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT 1632
Dbb|||||
Dbb 2502 GCTGGAGAAGAGCTCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT 2561
QY 1633 CATCTCGAAAGCTTCTGAAGCTGGCGGCCCTTGGGCTGGAGACCTATGCGCTTCCCCTC 1692
Dbb|||||
Dbb 2562 CATCTCGAAAGCTTCTGAAGCTGGCGGCCCTTGGGCTGGAGACCTATGCGCTTCCCCTC 2621
QY 1693 AGTGACCCCTCATCTCTGTCTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTTGT 1752
Dbb|||||
Dbb 2622 AGTGACCCCTCATCTCTGTCTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTTGT 2681
QY 1753 AGAGCCAGAGGGAAACCACTTTGGGAAACCCCAACCTCCATGGATGGAGAACTGCTGCT 1812
Dbb|||||
Dbb 2682 AGAGCCAGAGGGAAACCACTTTGGGAAACCCCAACCTCCATGGATGGAGAACTGCTGCT 2741
QY 1813 GAGGCGAGAGGATCTACGCCAGCAGGTGAGGCTTGTACAGGGGTGGCGGCTTTCAGCC 1872
Dbb|||||
Dbb 2742 GAGGCGAGAGGATCTACGCCAGCAGGTGAGGCTTGTACAGGGGTGGCGGCTTTCAGCC 2801
QY 1873 CTCTGGCTTGGCCTTGTCTTACACCGTGTAAATATCCCTCCCCATTTCTTCTCTTCCCCTC 1932
Dbb|||||
Dbb 2802 CTCTGGCTTGGCCTTGTCTTACACCGTGTAAATATCCCTCCCCATTTCTTCTTCCCCTC 2861
QY 1933 TCTTCCCCTTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTTAAACAAATACAACCA 1992
Dbb|||||
Dbb 2862 TCTTCCCCTTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTTAAACAAATACAACCA 2921
QY 1993 AAACCTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACCTGGCTCCAATGATCACCTCT 2052
Dbb|||||
Dbb 2922 AAACCTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACCTGGCTCCAATGATCACCTCT 2981
QY 2053 CTCTGTGACCATCACCAACGGGTGCCTCTTGGCCTGGCTTTCCTTGGCCTTCCCTCAGC 2112
Dbb|||||
Dbb 2982 CTCTGTGACCATCACCAACGGGTGCCTCTTGGCCTGGCTTTCCTTGGCCTTCCCTCAGC 3041
QY 2113 TTCACCTTGATACTGGGCCTCTTCTTGTTCATGTCTGAAGCTGTGGACAGAGACCTTGA 2172
Dbb|||||
Dbb 3042 TTCACCTTGATACTGGGCCTCTTCTTGTTCATGTCTGAAGCTGTGGACAGAGACCTTGA 3101
QY 2173 CTTTGTCTGCTTAAAGGAAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATC 2232
Dbb|||||
Dbb 3102 CTTTGTCTGCTTAAAGGAAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATC 3161
QY 2233 AGGGCACAGTGGACAGGGAGACCTCACAGAGAAAAGCCCTGGAAGGTGATTTCCCCTGTGA 2292
Dbb|||||
Dbb 3162 AGGGCACAGTGGACAGGGAGACCTCACAGAGAAAAGCCCTGGAAGGTGATTTCCCCTGTGA 3221
QY 2293 CTCATGGATAGGATACAAAATGTGTTCATGTACCAATTAATCTTGACATATGCCATGCAT 2352
Dbb|||||
Dbb 3222 CTCATGGATAGGATACAAAATGTGTTCATGTACCAATTAATCTTGACATATGCCATGCAT 3281
QY 2353 AAAGACTTCCCTATTAAAAATAAGCTTTGGAAGAGATTAAAAAAA 2396
Dbb|||||
Dbb 3282 AAAGACTTCCCTATTAAAAATAAGCTTTGGAAGAGAAAAAANAAAA 3325

RESULT 8
US-10-398-036-26
; Sequence 26, Application US/10398036
; Publication No. US20040137564A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS INC.; BAUGHN, Mariah R.;
; APPLICANT: GRAUL Richard C.; CHAWLA, Narinder K.;
; APPLICANT: GANDHI, Aameena R.; HAFALIA, April J.A.;
; APPLICANT: RAMKUMAR, Jayalaxmi; TRIBOULEY, Catherine M.;

Db 2577 CATTTGGAAGCTTCTGAAGCTGGGCGGCCCCCTTGGGCTGGAGACCTATGGCTTCCCTC 2636
QY 1693 AGTGACCTCATCTCCTGTGACGAGCCAGGGGCCCCCAGGCTGGAGGCGAGCCATTGTGT 1752
Db 2637 AGTGACCTCATCTCCTGTGACGAGCCAGGGGCCCCCAGGCTGGAGGCGAGCCATTGTGT 2696
QY 1753 AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCTCCATGGATGGAGAATGCTGCT 1812
Db 2697 AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCTCCATGGATGGAGAATGCTGCT 2756
QY 1813 GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTGAGGGGTGGCGGCTTCAGCC 1872
Db 2757 GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTGAGGGGTGGCGGCTTCAGCC 2816
QY 1873 CTCCTGGCTTGGCCTTGTTCACACAGTGAATAATCCTCCCTCCCATTTCTTCTTCCCTC 1932
Db 2817 CTCCTGGCTTGGCCTTGTTCACACAGTGAATAATCCTCCCTCCCATTTCTTCTTCCCTC 2876
QY 1933 TCTTCCCTTTCTCTCCTCCCTCGGTGAATGATGGTGTCTTCTAAACAATAACAACCA 1992
Db 2877 TCTTCCCTTTCTCTCCTCCCTCGGTGAATGATGGTGTCTTCTAAACAATAACAACCA 2936
QY 1993 AAACCTCAGCAGTGTATCTATAGCAGGATGGCCCGAGTACCTGGCTCCACTGATCACCTCT 2052
Db 2937 AAACCTCAGCAGTGTATCTATAGCAGGATGGCCCGAGTACCTGGCTCCACTGATCACCTCT 2996
QY 2053 CTCCTGTGACCATCACCAAGGGGTGCCTCTTGGCCTGGCTTCCCTTGGCCTTCCCTCAGC 2112
Db 2997 CTCCTGTGACCATCACCAAGGGGTGCCTCTTGGCCTGGCTTCCCTTGGCCTTCCCTCAGC 3056
QY 2113 TTCACCTTGATACCTGGGCTCTTCTTGTGATGTCTGAAGCTGTGGACCAGAGACCTGGA 2172
Db 3057 TTCACCTTGATACCTGGGCTCTTCTTGTGATGTCTGAAGCTGTGGACCAGAGACCTGGA 3116
QY 2173 CTTTTGTCTGCTTAAGGGAATGAGGGAAGTAAGACAGTGAAGGGGTGGAGGTTGATC 2232
Db 3117 CTTTTGTCTGCTTAAGGGAATGAGGGAAGTAAGACAGTGAAGGGGTGGAGGTTGATC 3176
QY 2233 AGGGCACAGTGGACAGGAGACCTCACAGAGAAAGGCCTGGAAGGTGATTTCCCGTGTGA 2292
Db 3177 AGGGCACAGTGGACAGGAGACCTCACAGAGAAAGGCCTGGAAGGTGATTTCCCGTGTGA 3236
QY 2293 CTCATGGATAGGATACAAATGTGTTCCATGTACCAATTAATCTTGACATATGCCATGCAT 2352
Db 3237 CTCATGGATAGGATACAAATGTGTTCCATGTACCAATTAATCTTGACATATGCCATGCAT 3296
QY 2353 AAAGACTTCCTATTAAATAAAGCTTTTGGAAAGAGATTAAAA 2393
Db 3297 AAAGACTTCCTATTAAATAAAGCTTTTGGAAAGAGATTACACA 3337

RESULT 9
US-10-331-496A-94
; Sequence 94, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02

; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 94
; LENGTH: 3443
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-331-496A-94

Query Match 90.0%; Score 2238; DB 17; Length 3443;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2246; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

QY 133 AGCGGCTCCAAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG 192
Db 1189 ATCGGCTCCAAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG 1247

QY 193 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCCATCCGGTCCATCCACCTGAGGCCTT 252
Db 1248 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCCATCCGGTCCATCCACCTGAGGCCTT 1307

QY 253 CTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTGACCACTGCC 312
Db 1308 CTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTGACCACTGCC 1367

QY 313 CCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGTCTCTCCCA 372
Db 1368 CCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGTCTCTCCCA 1427

QY 373 GGCCTTCTCAAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCA 432
Db 1428 GGCCTTCTCAAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCA 1487

QY 433 GTGCTGTCCTATGGGATGTGTGCCAGCTTCTCAAAGGCCTCTGGGCAAGTGGAGGCTGA 492
Db 1488 GTGCTGTCCTATGGGATGTGTGCCAGCTTCTCAAAGGCCTCTGGGCAAGTGGAGGCTGA 1547

QY 493 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCTCCTTGCCAGACA 552
Db 1548 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCTCCTTGCCAGACA 1607

QY 553 AGCAGAGAACCACACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 612
Db 1608 AGCAGAGAACCACACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 1667

QY 613 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 672
Db 1668 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 1727

QY 673 CTTTGAAGCTGGGGCATCCGCCCTGGCGTGTGGGCCATCGTGTGCTCTCCGTGCTGTG 732
Db 1728 CTTTGAAGCTGGGGCATCCGCCCTGGCGTGTGGGCCATCGTGTGCTCTCCGTGCTGTG 1787

QY 733 CAATGGACTGGTGTGCTGACCCGTGTTGCTGGCGGCCCTGCCCTTCCCTTCCCTTCCCTCAA 792
Db 1788 CAATGGACTGGTGTGCTGACCCGTGTTGCTGGCGGCCCTGCCCTTCCCTTCCCTTCCCTCAA 1847

QY 793 GTTTGTGGTAGGTGCGATTGTCAGGCGGCCAACACCTTGACTGGCATTTCTGTGGCCTTCT 852

Db 1848 GTTTGTGGTAGGTGCGATTGCAGSGCCCAACACCTTGACTGGCATTTCTGTGGCCCTTCT 1907

Qy 853 AGCCTCAGTCGATGCCCTGACCTTTGGTCAAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC 912

Db 1908 AGCCTCAGTCGATGCCCTGACCTTTGGTCAAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC 1967

Qy 913 GGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGGTGGAGGCATCGGTGCT 972

Db 1968 GGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGGTGGAGGCATCGGTGCT 2027

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Qy 1033 GAAGTCCCCCTCCCTGGCGAGCGTTGCGAGCAGGGGTCCTAGGCTGCCCTGGCACGTGGCAGG 1092

Db 2088 GAAGTCCCCCTCCCTGGCGAGCGTTCGAGCAGGGGTCCTAGGCTGCCCTGGCACGTGGCAGG 2147

Qy 1093 GCTGSCGCGCGCACTGCCCTGSCCTCAGTGGGAGAATACGGGGCCCTCCCCACTCTGCCT 1152

Db 2148 GCTGSCGCGCGCACTGCCCTGSCCTCAGTGGGAGAATACGGGGCCCTCCCCACTCTGCCT 2207

Qy 1153 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCAACGTGGCCCTGGTGAT 1212

Db 2208 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCAACGTGGCCCTGGTGAT 2267

Qy 1213 GATGAACCTCTTCTGTTTCCGTGCTGGGCGGTGCGCTACATCAAACTGTACTGTGACCT 1272

Db 2268 GATGAACCTCTTCTGTTTCCGTGCTGGGCGGTGCGCTACATCAAACTGTACTGTGACCT 2327

Qy 1273 GCCGCGGGCGGACTTTGAGGCCGTGTGGGACTGCGCCATGFGAGGCACGTGGCCTGGCT 1332

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Qy 1393 GGGCTCTTCCCTGFTCACGGCCGAGGCCGTCAAGTCTGTCTGCTGGTGGTGCTGCCCT 1452

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Qy 1453 GCCTGCCTGCCCTCAACCCACTGTGTACTGTCTTCAACCCCACTTCGGGGATGACCT 1512

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Db 2568 TCGGCGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGCTGCGGCCGGGA 2627

Qy 1573 GCTGGAGAAGAGCTCCTGTGATTTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT 1632

Db 2628 GCTGGAGAAGAGCTCCTGTGATTTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT 2687

Qy 1633 CATCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCCCTC 1692

Db 2688 CATCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCCCTC 2747

Qy 1693 AGTGACCTCATCTCCTGTGACGAGCCAGGGGCCCCCAAGCTGGAGGGCAGCCATTGTGT 1752

Db 2748 AGTGACCTCATCTCCTGTGACGAGCCAGGGGCCCCCAAGCTGGAGGGCAGCCATTGTGT 2807

Qy 1753 AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTCCATGGATGGAACTGCTGCT 1812

Db 2808 AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTCCATGGATGGAACTGCTGCT 2867

Qy 1813 GAGGSCAGAGGGATCTACGCCAGAGGTGGAGGCTTGTACGGGGGTGGCGCTTTCAGCC 1872

Db 2868 GAGGSCAGAGGGATCTACGCCAGAGGTGGAGGCTTGTACGGGGGTGGCGCTTTCAGCC 2927

Qy 1873 CTCTGGCTTGGCCTTGTCTTACAGCTGTAATAATCCCTCCCATTTCTTCTTCCCTC 1932

Db 2928 CTCTGGCTTGGCCTTGTCTTACAGCTGTAATAATCCCTCCCATTTCTTCTTCCCTC 2987

Qy 1933 TCTTCCCTTTCCCTCTCTCCOCTCGGTGAATGATGGCTGCTTCTAAAAACAATAACAACCA 1992

Db 2988 TCTTCCCTTTCCCTCTCTCCOCTCGGTGAATGATGGCTGCTTCTAAAAACAATAACAACCA 3047

Qy 1993 AAACCTCAGCAGTGTGATCTATAGCAGGATGGCCCACTGCTGGCTCCACTGATCACCTCT 2052

Db 3048 AAACCTCAGCAGTGTGATCTATAGCAGGATGGCCCACTGCTGGCTCCACTGATCACCTCT 3107

Qy 2053 CTCCTGTGACCATCACCAACGGGTGCCTCTTGGCCCTGGCTTTCCCTTGGCCCTTCCCTCAGC 2112

Db 3108 CTCCTGTGACCATCACCAACGGGTGCCTCTTGGCCCTGGCTTTCCCTTGGCCCTTCCCTCAGC 3167

Qy 2113 TTCACCTTGATACTGGGCCCTCTTCCCTTGTCTCATGTCTGAAGCTGTGGACCAGAGACCTGGA 2172

Db 3168 TTCACCTTGATACTGGGCCCTCTTCCCTTGTCTCATGTCTGAAGCTGTGGACCARAGACCTGGA 3227

Qy 2173 CTTTGTCTGCTTAAAGGGAATAGGGAAAGTAAAGACAGTGAAGGGGTGGAGGTTGATC 2232

Db 3228 CTTTGTCTGCTTAAAGGGAATAGGGAAAGTAAAGACAGTGAAGGGGTGGAGGTTGATC 3287

Qy 2233 AGGSCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCCTGGAAGGTGATTTCCCGTGTGA 2292

Db 3288 AGGSCACAGTGGACAGGGAGACCTCACARAAAAGSCCTGGAAGGKGATTTCCCGTGTGA 3347

Qy 2293 CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAAATCTTGACATATGCCATGCAT 2352

Db 3348 CTCATGGRTAGGAWACAAAATGTGTTCCATGTACCATTAAATCTTGACATATGCCATGCAT 3407

Qy 2353 AAAGACTTCCTATTAAAAATAAGCTTTTGAAGAGATT 2388

Db 3408 AAARACTTCCTATTAAAAATAAGCTTTTGRAGAGATT 3443

RESULT 10

US-09-851-595-10

; Sequence 10, Application US/09851595

; Publication No. US20030166047A1

; GENERAL INFORMATION:

; APPLICANT: Gu, Wei

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR

; FILE REFERENCE: MNI-080CP

; CURRENT APPLICATION NUMBER: US/09/851,595

; CURRENT FILING DATE: 2000-05-08

; PRIOR APPLICATION NUMBER: 09/556,588

; PRIOR FILING DATE: 2000-05-08

; PRIOR APPLICATION NUMBER: 60/132,896

; PRIOR FILING DATE: 1999-05-06

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 3492

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (104)...(3004)

US-09-851-595-10

Query Match 90.0%; Score 2238; DB 10; Length 3492;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 2246; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

Qy 133 AGCGGCCTCCAACACACACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG 192

Db 1238 ATCGGCCTCCAACACACACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG 1296

Qy 193 CTCCTGTCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTTGAGSCCTT 252

Db 1297 CTCCTGTCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTTGAGSCCTT 1356

Qy 253 CTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTGACCACACTGCC 312


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; Publication No. US20040058377A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/10/664,667
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/851,595
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 3492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)...(3004)
US-10-664-667-10

Query Match      90.0%; Score 2238; DB 17; Length 3492;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2246; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

QY 133 AGCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACACTTCAGCCAGCTGAG 192
DB 1238 ATCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG 1296

QY 193 CTCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCTT 252
DB 1297 CTCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCTT 1356

QY 253 CTCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTGACCACACTGCC 312
DB 1357 CTCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTGACCACACTGCC 1416

QY 313 CTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAAGGGAACCTTGCTCTCTCCCA 372
DB 1417 CTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAAGGGAACCTTGCTCTCTCCCA 1476

QY 373 GGCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCCCTACCA 432
DB 1477 GGCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCCCTACCA 1536

QY 433 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCTCTTGGGCAGTGGGAGGCTGA 492
DB 1537 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCTCTTGGGCAGTGGGAGGCTGA 1596

QY 493 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCTCCTTGCCAGACA 552
DB 1597 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCTCCTTGCCAGACA 1656

QY 553 AGCAGAGAAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAA 612
DB 1657 AGCAGAGAAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 1716

QY 613 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 672
DB 1717 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 1776

QY 673 CTTTGAAGCTGGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG 732
DB 1777 CTTTGAAGCTGGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG 1836

QY 733 CAATGGACTGGTGTGCTGCTGACCGTTCGCTGGCGGCGCTGCCCCCTGCCCCCGGTCAA 792
DB 1837 CAATGGACTGGTGTGCTGCTGACCGTTCGCTGGCGGCGCTGCCCCCTGCCCCCGGTCAA 1896

QY 793 GTTGTGGTAGGTGCGATTGACGGCGCCAACACCTTGACTGGCATTTTCTGTGGCCTTCT 852
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DB 1897 GTTGTGGTAGGTGCGATTGACGGCGCCAACACCTTGACTGGCATTTCTGTGGCCTTCT 1956
QY 853 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCCGCTGGGAGAC 912
DB 1957 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCCGCTGGGAGAC 2016
QY 913 GGGCTAGGCTGCCGGGCCACTGGCTTCTCTGGCAGTACTTGGGTCGGAGGCATCGGTGCT 972
DB 2017 GGGCTAGGCTGCCGGGCCACTGGCTTCTCTGGCAGTACTTGGGTCGGAGGCATCGGTGCT 2076
QY 973 GCTGCTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCTGTGTCCGGGCCCTATGG 1032
DB 2077 GCTGCTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCTGTGTCCGGGCCCTATGG 2136
QY 1033 GAAGTCCCCCTCCCTGGGAGCGTTTCGAGCAGGGGTCTTAGGCTGCCCTGGCAGTGGCAGG 1092
DB 2137 GAAGTCCCCCTCCCTGGGAGCGTTTCGAGCAGGGGTCTTAGGCTGCCCTGGCAGTGGCAGG 2196
QY 1093 GCTGGCCGCGCACTGCCCTGGCCCTCAGTGGGAGAAATACGGGGCCCTCCCCACTCTGCCT 1152
DB 2197 GCTGGCCGCGCACTGCCCTGGCCCTCAGTGGGAGAAATACGGGGCCCTCCCCACTCTGCCT 2256
QY 1153 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTTCACCGTGGCCCTGGTGAT 1212
DB 2257 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTTCACCGTGGCCCTGGTGAT 2316
QY 1213 GATGAACTCCTTCTGTTCCTGTGTCGTGGCCGGTGCTACATAAACTGTACTGTGACCT 1272
DB 2317 GATGAACTCCTTCTGTTCCTGTGTCGTGGCCGGTGCTACATAAACTGTACTGTGACCT 2376
QY 1273 GCCGGGGCGACTTTGAGGCCGTGTGGACTGGGCATGGTGAGGCACGTGGCCTGGCT 1332
DB 2377 GCCGGGGCGACTTTGAGGCCGTGTGGACTGGGCATGGTGAGGCACGTGGCCTGGCT 2436
QY 1333 CATCTTCGACAGCGGCTCCTCTACTGTCCCGTGGCTTCTCAGCTTCGCCCTCCATGCT 1392
DB 2437 CATCTTCGACAGCGGCTCCTCTACTGTCCCGTGGCTTCTCAGCTTCGCCCTCCATGCT 2496
QY 1393 GGGCCTCTTCCCTGTACGCCCGAGGCCGTCAAGTCTGTCTGTGGTGGTGTGCCCT 1452
DB 2497 GGGCCTCTTCCCTGTACGCCCGAGGCCGTCAAGTCTGTCTGTGGTGGTGTGCCCT 2556
QY 1453 GCCTGCCTGCCCTCAACCCACTGTGTACTGTCTTCAACCCCACTTCCGGGATGACCT 1512
DB 2557 GCCTGCCTGCCCTCAACCCACTGTGTACTGTCTTCAACCCCACTTCCGGGATGACCT 2616
QY 1513 TCGGGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTTAGCCCTATGCTCGGGCGGGGA 1572
DB 2617 TCGGGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTTAGCCCTATGCTCGGGCGGGGA 2676
QY 1573 GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGATCT 1632
DB 2677 GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGATCT 2736
QY 1633 CATCTTGGAAAGCTTCTGAAGCTGGGGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTC 1692
DB 2737 CATCTTGGAAAGCTTCTGAAGCTGGGGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTC 2796
QY 1693 AGTGACCCCTCATCTCCTGTACAGCAGCCAGGGGCCCCAGGCTGGAGGGCAGCATGTGT 1752
DB 2797 AGTGACCCCTCATCTCCTGTACAGCAGCCAGGGGCCCCAGGCTGGAGGGCAGCATGTGT 2856
QY 1753 AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTGTGCT 1812
DB 2857 AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCA TGGATGGAGAACTGTGCT 2916
QY 1813 GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGCTTGTCAAGGGGTGGCGGCTTTCAGCC 1872
DB 2917 GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGCTTGTCAAGGGGTGGCGGCTTTCAGCC 2976
QY 1873 CTCTGGCTTGGCCTTGTCTTACACGTGTAAATATCCCTCCCCATTTCTTCTTCCCCTC 1932
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Db 2977 CTCTGGCTTGGCCTTTGCTTCACACGTTGTAATAATATCCCTCCCATTCTTCTCTTCCCTC 3036

QY 1933 TCTTCCCTTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAACAATAACAACCA 1992

Db 3037 TCTTCCCTTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAACAATAACAACCA 3096

QY 1993 AAACTCAGCAGTGTGATCTATAGCAGGATGCCCCAGTACCTGGCTCCACTGATCACCTCT 2052

Db 3097 AAACTCAGCAGTGTGATCTATAGCAGGATGCCCCAGTACCTGGCTCCACTGATCACCTCT 3156

QY 2053 CTCCTGTGACCATCACCAACGGGTGCCTCTTTGGCCTGGCTTTCCCTTGGCCCTCCTCAGC 2112

Db 3157 CTCCTGTGACCATCACCAACGGGTGCCTCTTTGGCCTGGCTTTCCCTTGGCCCTCCTCAGC 3216

QY 2113 TTCACCTTGATCTGGGCTCTTCTCTTGTCATGTCTGAAGCTGTGGACGACGACCTGGA 2172

Db 3217 TTCACCTTGATCTGGGCTCTTCTCTTGTCATGTCTGAAGCTGTGGACCARAGACCTGGA 3276

QY 2173 CTTTGTCTGCTTAAAGGAAATGAGGAAAGTAAAGACAGTGAAGGGTGGAGGTTGATC 2232

Db 3277 CTTTGTCTGCTTAAAGGAAATGAGGAAAGTAAAGACAGTGAAGGGTGGAGGTTGATC 3336

QY 2233 AGGCACAGTGGACAGGAGACCTCACAGAGAAAGCCTTGAAGGTGATTTCCCGTGTGA 2292

Db 3337 AGGCACAGTGGACAGGAGACCTCACARAAAAGCCTTGAAGKGATTTCCCGTGTGA 3396

QY 2293 CTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCAT 2352

Db 3397 CTCATGGRTAGGAWACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCAT 3456

QY 2353 AAAGACTTCCTATTAAAAAAGCTTTTGGAAAGAGATT 2388

Db 3457 AAARACTTCCTATTAAAAAAGCTTTTGGRAGAGATT 3492

RESULT 12

US-10-737-450-31

; Sequence 31, Application US/10737450

; Publication No. US20040235071A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals, Inc

; APPLICANT: Lightcap, Eric S.

; APPLICANT: Ecsedy, Jeffrey A.

; APPLICANT: Hunter, John Joseph

; APPLICANT: MacBeth, Kyle J.

; APPLICANT: Tighe Nestor, Michelle

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

; TITLE OF INVENTION: CANCER USING 15986, 2188, 20743, 9148, 9151, 9791, 44252,

; TITLE OF INVENTION: 14184, 42461, 8204, 7970, 25552, 21657, 26492, 2411, 15088,

; TITLE OF INVENTION: 1905, 28899, 63380, 33935, 10480, 12686, 25501, 17694,

; TITLE OF INVENTION: 15701, 53062, 49908, 21612, 38949, 6216, 46863, 9235, 2201,

; TITLE OF INVENTION: 6985, 9883, 12238, 18057, 21617, 39228, 49928, 54476, 62113,

; TITLE OF INVENTION: 64316, 12264, 32362, 58198, 2887, 3205, 8557, 9600, 9693,

; TITLE OF INVENTION: 44867, 53058, 55556, 57658, 2208, 10252, 10302, 14218,

; TITLE OF INVENTION: 33877, 10317, 10485, 25964, 14815, 1363, 1397, 14827, 21708,

; FILE REFERENCE: MPI02-207PIRNOVMNIM

; CURRENT APPLICATION NUMBER: US/10737,450

; CURRENT FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: US 60/435,108

; PRIOR FILING DATE: 2002-12-20

; PRIOR APPLICATION NUMBER: US 60/436,443

; PRIOR FILING DATE: 2002-12-23

; PRIOR APPLICATION NUMBER: US 60/438,498

; PRIOR FILING DATE: 2003-01-07

; PRIOR APPLICATION NUMBER: US 60/444,370

; PRIOR FILING DATE: 2003-01-31

; PRIOR APPLICATION NUMBER: US 60/446,031

; PRIOR FILING DATE: 2003-02-06

; PRIOR APPLICATION NUMBER: US 60/453,635

; PRIOR FILING DATE: 2003-03-11

; PRIOR APPLICATION NUMBER: US 60/457,199

; PRIOR FILING DATE: 2003-03-25

; PRIOR APPLICATION NUMBER: US 60/462,458

; PRIOR FILING DATE: 2003-04-10

; PRIOR APPLICATION NUMBER: US 60/466,732

; PRIOR FILING DATE: 2003-04-30

; PRIOR APPLICATION NUMBER: US 60/469,184

; PRIOR FILING DATE: 2003-05-08

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 144

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 31

; LENGTH: 3492

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (104)...(3007)

US-10-737-450-31

Query Match 90.0%; Score 2238; DB 18; Length 3492;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 2246; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

QY 133 AGCGGCCTCCAAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTTCAGCCAGCTGAG 192

Db 1238 ATCGGCCTCCAAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTTCAGCCAGCTGAG 1296

QY 193 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCTT 252

Db 1297 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCTT 1356

QY 253 CTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACGCTGACCACTGCC 312

Db 1357 CTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACGCTGACCACTGCC 1416

QY 313 CCTGGCTGGAATTGGGGCTTGATGCACTCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA 372

Db 1417 CCTGGCTGGAATTGGGGCTTGATGCACTCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA 1476

QY 373 GGCCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGTGCCTTATGCCTACCA 432

Db 1477 GGCCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGTGCCTTATGCCTACCA 1536

QY 433 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGSCAGTGGGAGGCTGA 492

Db 1537 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGSCAGTGGGAGGCTGA 1596

QY 493 AGACCTTCACTTGTATGATGAGGAGTCTTCAAAAAGGCCCTCGGGCCCTCTTGCCAGACA 552

Db 1597 AGACCTTCACTTGTATGATGAGGAGTCTTCAAAAAGGCCCTCGGGCCCTCTTGCCAGACA 1656

QY 553 AGCAGAGAACACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 612

Db 1657 AGCAGAGAACACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 1716

QY 613 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 672

Db 1717 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 1776

QY 673 CTTTGAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCCATCGTGTGCTCTCCGTGCTCTG 732

Db 1777 CTTTGAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCCATCGTGTGCTCTCCGTGCTCTG 1836

QY 733 CAATGGACTGGTGTCTGCTGACCCGTGTTGCTGGCGGGCCCTGCCCCCTGCCCCCGGTCAA 792

Db 1837 CAATGGACTGGTGTCTGCTGACCCGTGTTGCTGGCGGGCCCTGCCCCCTGCCCCCGGTCAA 1896

QY 793 GTTTGTGTAGTGCATTGACGGCGCCAAACACTTGACTGGCATTTCTGTGGCCTTCT 852

Db 1897 GTTTGTGTAGTGCATTGACGGCGCCAAACACTTGACTGGCATTTCTGTGGCCTTCT 1956

QY 853 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC 912

Db 1957 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC 2016

QY	913	GGGGCTAGGCTGCCGGGCCACATGGCTTCCTGGCAGTACTTGGGTCGGAGGCATCGGTGCT	972
Db	2017	GGGGCTAGGCTGCCGGGCCACATGGCTTCCTGGCAGTACTTGGGTCGGAGGCATCGGTGCT	2076
QY	973	GCTGCTCACTCTGGCGCAGTGCAGTGCAGCGTCTCCGTCTCTCTGTCTCCGGSCCTATGG	1032
Db	2077	GCTGCTCACTCTGGCGCAGTGCAGTGCAGCGTCTCCGTCTCTCTGTCTCCGGSCCTATGG	2136
QY	1033	GAAGTCCCCCTCCCTTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCCTGGCACTGGCAGG	1092
Db	2137	GAAGTCCCCCTCCCTTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCCTGGCACTGGCAGG	2196
QY	1093	GCTGGCGCGCGCACTGCCCTTGGCCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCGCT	1152
Db	2197	GCTGGCGCGCGCACTGCCCTTGGCCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCGCT	2256
QY	1153	GCCCTACGGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGAT	1212
Db	2257	GCCCTACGGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGAT	2316
QY	1213	GATGAACCTCCTTCTGTTCCTGGTCGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCT	1272
Db	2317	GATGAACCTCCTTCTGTTCCTGGTCGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCT	2376
QY	1273	GCCGGGGCGCACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGSCCTGGCT	1332
Db	2377	GCCGGGGCGCACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGSCCTGGCT	2436
QY	1333	CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCCTCCATGCT	1392
Db	2437	CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCCTCCATGCT	2496
QY	1393	GGGCCTCTTCCCTGTACGCCCGAGGCCGTCAAAGTCTGTCTCTGCTGGTGGTGTGCCCCCT	1452
Db	2497	GGGCCTCTTCCCTGTACGCCCGAGGCCGTCAAAGTCTGTCTCTGCTGGTGGTGTGCCCCCT	2556
QY	1453	GCCTGCCCTCAACCCCACTGCTGTACCTGCTCTTCAACCCCCACTTCGGGATGACCT	1512
Db	2557	GCCTGCCCTCAACCCCACTGCTGTACCTGCTCTTCAACCCCCACTTCGGGATGACCT	2616
QY	1513	TCGGCGGCTTCGGCCCGCGCAGGGGACTCAGSGCCCTAGCCTATGCTGCGSCGGGA	1572
Db	2617	TCGGCGGCTTCGGCCCGCGCAGGGGACTCAGSGCCCTAGCCTATGCTGCGSCGGGA	2676
QY	1573	GCTGGAGAAAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT	1632
Db	2677	GCTGGAGAAAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT	2736
QY	1633	CATTCTGGAAGCTTCTGAAGCTGGGGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCCTC	1692
Db	2737	CATTCTGGAAGCTTCTGAAGCTGGGGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCCTC	2796
QY	1693	AGTGACCTCATCTCCTGTTCAGCAGCCAGGGGCCCCAGGCTGGAGGCAGCATGTGT	1752
Db	2797	AGTGACCTCATCTCCTGTTCAGCAGCCAGGGGCCCCAGGCTGGAGGCAGCATGTGT	2856
QY	1753	AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT	1812
Db	2857	AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT	2916
QY	1813	GAGGGCAGAGGGATCTACGCCAGCAGGTTGGAGGCTTGTTCAGGGGGTGGCGGCTTTCAGCC	1872
Db	2917	GAGGGCAGAGGGATCTACGCCAGCAGGTTGGAGGCTTGTTCAGGGGGTGGCGGCTTTCAGCC	2976
QY	1873	CTCTGGCTTGGCCTTTGCTTCACACGTGTAATATCCCTCCCCATTCCTTCTTTCCTCCCTC	1932
Db	2977	CTCTGGCTTGGCCTTTGCTTCACACGTGTAATATCCCTCCCCATTCCTTCTTTCCTCCCTC	3036
QY	1933	TCCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAAACAAATACAACCA	1992
Db	3037	TCCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAAACAAATACAACCA	3096

RESULT 13

US-10-295-027-1119

US 10 253 027 1112
: Sequence 1119, Application US/10295027

Sequence ID: US20030232350A1

: GENERAL INFORMATION:

APPLICANT: Afar. Daniel

APPLICANT: ALAI, DANIEL
APPLICANT: AZIZ, NATASHA

APPLICANT: AZIZ, Nafisaa
APPLICANT: Ginsberg, Wendy M.

APPLICANT: Gish Kurt C

APPLICANT: GISH, KYLE C.
APPLICANT: Glimme, Richard

APPLICANT: Glynn, Richard
APPLICANT: Herro; Peter A

APPLICANT: Hevezi, Peter

APPLICANT: Mack, David H.

APPLICANT: Murray, Richard

APPLICANT: Watson, Susan R.

APPLICANT: EOS Biotechnology, Inc.

; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

; TITLE OF INVENTION: Methods of

; FILE REFERENCE: 018501-012500US

; CURRENT APPLICATION NUMBER: US/1

; CURRENT FILING DATE: 2002-11-13

10; PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2000-09-15

; PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-11-15

: PRIOR APPLICATION NUMBER: US

EXPIRATION DATE: 2001-11-21

; PRIOR FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: US

; PRIOR APPLICATION NUMBER: US 60/334,333
 : PRIOR FILING DATE: 2001-11-29

; PRIOR FILING DATE: 2001-11-29
: PRIOR APPLICATION NUMBER: US

; PRIOR APPLICATION NUMBER: US 60/340,376
 : PRIOR FILING DATE: 2001-12-14

;; PRIOR FILING DATE: 2001-12-14
: PRIOR APPLICATION NUMBER: IIS

;; PRIOR APPLICATION NUMBER: US 60/347,211
: PRIOR FILING DATE: 2002-01-08

; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US

;; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2003-01-10

;
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US

; PRIOR APPLICATION NUMBER: US 60/355,250

PRIOR FILING DATE: 2002-02-08

; PRIOR APPLICATION NUMBER: US 60/356,714

; PRIOR FILING DATE: 2002-02-

; Remaining Prior Application

; NUMBER OF SEQ

; LENGTH: 3273									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-295-027-1119									
Query Match 89.8%; Score 2231.4; DB 17; Length 3273;									
Best Local Similarity 99.7%; Pred. No. 0;									
Matches 2246; Conservative 0; Mismatches 6; Indels 1; Gaps 1;									
Qy	133	AGCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG	192						
Db	1022	ATCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG	1080						
Qy	193	CTCCCTGCAAGCCCTGGATCTTAGCTGGAAACGCCATCCGCTCCATCCACCCCTGAGSCCTT	252						
Db	1081	CTCCCTGCAAGCCCTGGATCTTAGCTGGAAACGCCATCCGCTCCATCCACCCCGAGGCCTT	1140						
Qy	253	CTCCACCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCAACACTGCC	312						
Db	1141	CTCCACCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCAACACTGCC	1200						
Qy	313	CCTGGCTGGACCTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACTTGCTCTCTCCTCCA	372						
Db	1201	CCTGGCTGGACCTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACTTGCTCTCTCCTCCA	1260						
Qy	373	GGCCTTCTCAAGGACAGTFTCCAAAACTGAGGATCCTGGAGGTGCCTTAATGCTACCA	432						
Db	1261	GGCCTTCTCAAGGACAGTFTTCCCAAACTGAGGATCCTGGAGGTGCCTTAATGCTACCA	1320						
Qy	433	GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCTCTGGCAGTGGGAGGCTGA	492						
Db	1321	GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCTCTGGCAGTGGGAGGCTGA	1380						
Qy	493	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGSCCCCTGGGCCCTCCTTGGCAGACA	552						
Db	1381	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGSCCCCTGGGCCCTCCTTGGCAGACA	1440						
Qy	553	AGCAGAGAAACCACTATGACAGGACCTGGATGAGCTCCAGCTGGAGATGGAGACTCAA	612						
Db	1441	AGCAGAGAAACCACTATGACAGGACCTGGATGAGCTCCAGCTGGAGATGGAGACTCAA	1500						
Qy	613	GCCACACCCAGTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	672						
Db	1501	GCCACACCCAGTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	1560						
Qy	673	CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCATCGTGTGCTCCTCGCTCTG	732						
Db	1561	CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCATCGTGTGCTCCTCGCTCTG	1620						
Qy	733	CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGSGCTGCCCCCTGCCCCCGGTCAA	792						
Db	1621	CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGSGCTGCCCCCTGCCCCCGGTCAA	1680						
Qy	793	GTTTGTGGTAGGTGCGATGTCAGGCGCCAAACCTTGACTGGCATTTCCCTGTGGCCTTCT	852						
Db	1681	GTTTGTGGTAGGTGCGATGTCAGGCGCCAAACCTTGACTGGCATTTCCCTGTGGCCTTCT	1740						
Qy	853	AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	912						
Db	1741	AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	1800						
Qy	913	GGGGCTAGGCTGCCGGGCACCTGGCTTCTTGGCAGTACTGGGTGCGAGGCATCGGTGCT	972						
Db	1801	GGGGCTAGGCTGCCGGGCACCTGGCTTCTTGGCAGTACTGGGTGCGAGGCATCGGTGCT	1860						
Qy	973	GCTGCTCACTGTGGCCGAGTGCAGTGCAGCCTCCGCTCTCCGTCTCCGTGTCGGGCTATGG	1032						
Db	1861	GCTGCTCACTGTGGCCGAGTGCAGTGCAGCCTCTCCGTCTCCGTGTCGGGCTATGG	1920						
Qy	1033	GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGG	1092						
Db	1921	GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGG	1980						
Qy	1093	GCTGGCCGCGCATGTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTGTGCCT	1152						
Db	1981	GCTGGCCGCGCGCTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTGTGCCT	2040						
Qy	1153	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGAT	1212						
Db	2041	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGAT	2100						
Qy	1213	GATGAACTCCTTCTGTTTCTTGGTCTGGCCCGTGCCCTACATCAAACTGTACTGTGACCT	1272						
Db	2101	GATGAACTCCTTCTGTTTCTTGGTCTGGCCCGTGCTACATCAAACTGTACTGTGACCT	2160						
Qy	1273	GCCGCGGGGCGACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT	1332						
Db	2161	GCCGCGGGGCGACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT	2220						
Qy	1333	CATCTTCGACAGCGGCTCCTCTACTGTCCGTTGGCCTTCTCAGCTTCGCTCCATGCT	1392						
Db	2221	CATCTTCGACAGCGGCTCCTCTACTGTCCGTTGGCCTTCTCAGCTTTGCCTCCATGCT	2280						
Qy	1393	GGGCTCTTCCCTGTCAACCCGAGGCCGTCAAAGTCTGTCTGCTGGTGGTGGTCCCT	1452						
Db	2281	GGGCTCTTCCCTGTCAACCCGAGGCCGTCAAAGTCTGTCTGCTGGTGGTGGTCCCT	2340						
Qy	1453	GCCTGCCCTGCCTCAAACCCACTGCTGTACCTCTTCAACCCCCACTTCCGGGATGACCT	1512						
Db	2341	GCCTGCCCTGCCTCAAACCCACTGCTGTACCTCTTCAACCCCCACTTCCGGGATGACCT	2400						
Qy	1513	TCGGCGGCTTCGGCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGGGCCGGGA	1572						
Db	2401	TCGGCGGCTTCGGCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGGGCCGGGA	2460						
Qy	1573	GCTGGAGAAAGTCTCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT	1632						
Db	2461	GCTGGAGAAAGTCTCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT	2520						
Qy	1633	CATTCTGGAAGCTTCTGAAGCTGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCCTC	1692						
Db	2521	CATTCTGGAAGCTTCTGAAGCTGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCCTC	2580						
Qy	1693	AGTGACCCCTCATCTCTGTGAGCAGCCAGGGGCCCCCAGGCTGGAGGCGCATTTGTGT	1752						
Db	2581	AGTGACCCCTCATCTCTGTGAGCAGCCAGGGGCCCCCAGGCTGGAGGCGCATTTGTGT	2640						
Qy	1753	AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT	1812						
Db	2641	AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT	2700						
Qy	1813	GAGGCGAGAGGATCTACGCCAGAGTGGAGGCTTGTACGGGGGTGGCGGCTTTCAGCC	1872						
Db	2701	GAGGCGAGAGGATCTACGCCAGAGTGGAGGCTTGTACGGGGGTGGCGGCTTTCAGCC	2760						
Qy	1873	CTCTGGCTTGGCCTTGTCTTACACAGTGTAAATATCCCTCCCCATTTCTTCTTCCCCTC	1932						
Db	2761	CTCTGGCTTGGCCTTGTCTTACACAGTGTAAATATCCCTCCCCATTTCTTCTTCCCCTC	2820						
Qy	1933	TCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGTGTCTTAAACAAATACAAACCA	1992						
Db	2821	TCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGTGTCTTAAACAAATACAAACCA	2880						
Qy	1993	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTACCTGGCTCCACTGATCACCTCT	2052						
Db	2881	AAACTCAGCAGTGTGATCTATAGCAGGATGGCCCCAGTCCCTGGCTCCACTGATCACCTCT	2940						
Qy	2053	CTCCTGTGACCATCACCAACGGGTGCCTTGGCCCTGGCTTTCCCTTGGCCTTCCCTCAGC	2112						
Db	2941	CTCCTGTGACCATCACCAACGGGTGCCTTGGCCCTGGCTTTCCCTTGGCCTTCCCTCAGC	3000						
Qy	2113	TTACACCTTGATFACCTGGGCTCTTCTCTTGTGATGTCTGAAGCTGTGGACAGAGACCTGGA	2172						
Db	3001	TTACACCTTGATFACCTGGGCTCTTCTCTTGTGATGTCTGAAGCTGTGGACAGAGACCTGGA	3060						
Qy	2173	CTTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATC	2232						

Db 3061 ||||| CTTTGTCTGCTTAAGGGAATAGGGAAGTAAAGACAGTGAAGGGTGGAGGTTGATC 3120
Qy 2233 AGGCACAGTGGACAGGAGACCTCACAGAGAAAGCCCTGGAAGTGATTCCCGTGTGA 2292
Db 3121 AGGGCAGTGGACAGGAGACCTCACAGAGAAAGCCCTGGAAGTGATTCCCGTGTGA 3180
Qy 2293 CTCATGGATAGGATACAAAATGTGTCCATGTACCATTTAATCTTGACATATGCCATGCAT 2352
Db 3181 CTCATGGATAGGATACAAAATGTGTCCATGTACCATTTAATCTTGACATATGCCATGCAT 3240
Qy 2353 AAAGACTTCCTATTAAATAAGCTTTGGAAGAG 2385
Db 3241 AAAGACTTCCTATTAAATAAGCTTTGGAAGAG 3273

RESULT 14
US-10-783-528-43
; Sequence 43, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05882.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10/783,528
; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 3273
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-783-528-43

Query Match 89.8%; Score 2231.4; DB 18; Length 3273;
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Matches 2246; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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SUMMARIES

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4	3140	95.0	3451	6	CQ840814	CQ840814 Sequence

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6	3045.5	92.1	2711	6	AX301828	AX301828 Sequence
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8	3045.5	92.1	3119	6	AX549295	AX549295 Sequence
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KEYWORDS .
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Muda,M.
AUTHORS Spliced variants of lgr6
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JOURNAL Applied Research Systems ARS Holding N.V. (AN)
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ACCESSION AX301830
VERSION AX301830.1 GI:17382889
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ORGANISM Homo sapiens
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REFERENCE 1
AUTHORS Gu,W.
TITLE Novel g-protein coupled receptors and uses therefor
JOURNAL Patent: WO 0185768-A 9 15-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)
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DEFINITION Sequence 7 from Patent WO0185768.
ACCESSION AX301828
VERSION AX301828.1 GI:17382887
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,W.
TITLE Novel g-protein coupled receptors and uses therefor
JOURNAL Patent: WO 0185768-A 7 15-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)
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Qy      631 rHisVal 633
Db      2202 ACACGTG 2208

RESULT 7
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DEFINITION Sequence 12 from Patent WO0185768.
ACCESSION  AX301833
VERSION     AX301833.1  GI:17382893
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Gu.W.
TITLE       Novel g-protein coupled receptors and uses therefor
JOURNAL     Patent: WO 0185768-A 12 15-NOV-2001;
            Millennium Pharmaceuticals, Inc. (US)
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US-10-664-667-5 (1-633) x AX301833 (1-2901)

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Db      1275 CAAGCTGGACCTGACAGACAAACCACTGACCACTGCCCCCTGGCTGGACTTGGGGGCTT 1334
Qy      111 uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh 131
Db      1335 GATGCATCTGAAGCTCAAAGGAACCTTGCTCTCTCCAGGCCTTCTCCAAGGACAGTTT 1394
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Qy      191 nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy 211
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Db      1635 TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCG 1694
Qy      231 gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh 251
Db      1695 CCTGGCCGTGTGGGCCATCGTGTGTCTCCGTGCTCTGCAATGGACTGGTGTGCTGAC 1754
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Db      1815 AGGCGCCAACACCTTGACTGGCATTTCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGAC 1874
Qy      291 rPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaTh 311
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Qy      311 rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa 331
Db      1935 TGGCTTCTTGGCAGTACTTGGGTGCGAGGCATCGGTGCTGCTGCTCACTCTGCGCCGAGT 1994
Qy      331 lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe 351
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QY	391	yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe	411
Db	2175	TCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACCTCCTTCTGTTCCT	2234
QY	411	uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluA1	431
Db	2235	GGTGTGGCCGTTGCCTACATCAAACTGTACTGTGACCTGCCGGGGCGACTTGGAGGC	2294
QY	431	aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe	451
Db	2295	CGTGTGGGACTGCGCCATGCTGAGGCACGTGGCCCTGGCTCATCTTCGACAGCGGCTCCT	2354
QY	451	uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr	471
Db	2355	CTACTGTCCCGTGGCCTTCTCAGCTTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCC	2414
QY	471	oGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe	491
Db	2415	CGAGGCCGTCAAGTCTGTCTGTGGTGTGCTGCCCTGCCTGCCTGCCTCAACCCACT	2474
QY	491	uLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgArgLeuArgProArgAl	511
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QY	531	pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluA1	551
Db	2595	TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGGATCTCATTTCTGGAAGCTTCTGAAGC	2654
QY	551	aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysG1	571
Db	2655	TGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCTCAGTGACCCCTCATCTCTGTCA	2714
QY	571	nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisPh	591
Db	2715	GCAGCCAGGGCCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTT	2774
QY	591	eGlyAsnProGlnProSerMetAspGlyGluLeuLeuArgAlaGluGlySerThrPr	611
Db	2775	TGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGTGAGGGCAGAGGGATCTACGCC	2834
QY	611	oAlaGlyGlyLeuSerGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlase	631
Db	2835	AGCAGGTGAGGCTTGTAGGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTGTCTTC	2894
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ACCESSION	AX549295		
VERSION	AX549295.1	GI:25813958	
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Burmer,G.C., Roush,C.L. and Brown,J.P.		
TITLE	Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides		
JOURNAL	Patent: WO 02061087-A 580 08-AUG-2002;		

Lifespan Biosciences, Inc. (US)	
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Score:	3045.50
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DB:	6
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Db	982 AGCTGCCCAGCCTGCACAGGTGTCAGAAATTGGAGGAAA-TCGGCCTCCAACACACCCGC 1040
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Db	1160 CAAGCTGGACCTGACAGACAACCAGCTGACCACACTGCCCTGGCTGGACTTGGGGGCTT 1219
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Db 2060 TCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACCTCCTTCTGTTTCT 2119

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Db 2180 CGTGTGGACTGCGCCATGTTGAGGCACGTGGCCTGGCTCATCTTCGCAGACGGGCTCCT 2239

QY 451 uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr 471
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Db 2300 CGAGCCGTCAAGTCTGTCTGTGGTGGTGTGCCCTTGCTGCCTGCCTCAACCCACT 2359

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Db 2480 TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTTCTGGAAGCTTCTGAAGC 2539

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Db 2540 TGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCCTCAGTGACCCCTCATCTCTGTCA 2599

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QY 591 eGlyAsnProGlnProSerMetAspGlyGluLeuLeuArgAlaGluGlySerThrPr 611
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QY 611 oAlaGlyGlyLeuSerGlyGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSe 631
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AB049405
LOCUS Homo sapiens VTS20631 mRNA, g-protein coupled receptor family, 3119 bp mRNA linear PRI 11-OCT-2002
DEFINITION partial cds.
ACCESSION AB049405
VERSION AB049405.1 GI:13447609
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Metazoa; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Okaze,H., Hayashi,A., Kozuma,S. and Saito,T.
AUTHORS a member of g-protein coupled receptor family
TITLE Published Only in Database (2001)
JOURNAL
REFERENCE 2 (bases 1 to 3119)
AUTHORS Okaze,H., Hayashi,A., Kozuma,S. and Saito,T.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-2000) Toshiyuki Saito, National Institute of Radiological Sciences, Genome Research Group; Anagawa 4-9-1, Chiba,Inage-ku, Chiba 263-8555, Japan (E-mail:t_saito@nirs.go.jp, Tel:81-43-206-3135, Fax:81-43-251-9818)

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ORIGIN

Alignment Scores:
Pred. No.: 9.96e-208 Length: 3119
Score: 3045.50 Matches: 602
Percent Similarity: 92.61% Conservative: 12
Best Local Similarity: 90.80% Mismatches: 19
Query Match: 92.09% Indels: 32
DB: 9 Gaps: 4

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Db	1340 TGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGTGAAGACCTTACCTTGATGATGA	1399
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REFERENCE 1 (bases 1 to 3325)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 3325)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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    Baughn,M.R., Graul,R.C., Wallia,N.K., Gandhi,A.R., Hafalia,A.J.,
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Elliott,V.S., Burford,N., Khan,F.A., Yue,H., Lu,Y., Arvizu,C.,
Roopa,R., Nguyen,D.B., Lee,E.A., Lu,D.A., Ison,C.H., Walsh,R.T. and
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Db 2658 GCAGCCAGGGGGCCCCCAGGCTGGAGGGGCAGCCATTGTGTAGAGCCAGAGGGAACCACTT 2717

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Qy 611 oAlaGlyGlyLeuSerGlyGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSe 631

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Qy 631 rHisVal 633

Db 2838 ACACGTG 2844

RESULT 12

AX301831

LOCUS AX301831 3492 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 10 from Patent WO0185768.

ACCESSION AX301831

VERSION AX301831.1 GI:17382891

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Gu,W.

TITLE Novel g-protein coupled receptors and uses therefor

JOURNAL Patent: WO 0185768-A 10 15-NOV-2001; Millennium Pharmaceuticals, Inc. (US)

FEATURES

Location/Qualifiers

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LSSLRHLWLDNALTEIPVRALNNLPALQAMTLALNRISHIPDYAFQNLTSLVVLHLH

NNRIQHLGTHSFEGLHNLETLDLNVNKLQEPFVAIRTLGRLOELGFHNNNIKAIPKA

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ORIGIN

Alignment Scores:

Pred. No.: 1.14e-207 Length: 3492

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Best Local Similarity: 90.80% Mismatches: 19

Query Match: 92.09% Indels: 32

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US-10-664-667-5 (1-633) x AX301831 (1-3492)

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Db	1378	CAAGCTGGACCTGACAGACAACACAGCTGACCACACTGCCCTGGCTGGACTTGGGGGCTT 1437
QY	111	uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh 131
Db	1438	GATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCCCTTCTCCAAGGACAGTTT 1497
QY	131	eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy 151
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QY	291	rPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaTh 311
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QY	331	lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe 351
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QY	351	rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe 371

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QY	431	aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe 451
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ORGANISM		Homo sapiens
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AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE		1 Aziz,N., Gish,K.C., Wilson,K.E. and Zlotnik,A. Methods of diagnosis of cancer, composition and methods of

screening for modulators of cancer
Patent: WO 2004073657-A 43 02-SEP-2004;
PROTEIN DESIGN LABS, INC. (US)
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Score: 3041.50 Matches: 601
Percent Similarity: 92.46% Conservative: 12
Best Local Similarity: 90.65% Mismatches: 20
Query Match: 91.97% Indels: 32
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QY 471 oGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe 491
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Muda,M.
TITLE Spliced variants of lgr6
JOURNAL Patent: WO 2004058818-A 1 15-JUL-2004;
Applied Research Systems ARS Holding N.V. (AN)
FEATURES
source Location/Qualifiers
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V"

ORIGIN

Alignment Scores:

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Score: 3041.50 Matches: 601
Percent Similarity: 92.46% Conservative: 12
Best Local Similarity: 90.65% Mismatches: 20
Query Match: 91.97% Indels: 32
DB: 6 Gaps: 4

US-10-664-667-5 (1-633) x CQ840811 (1-3306)

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QY	211	sSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGlyIleAr	231	
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QY	591	eGlyAsnProGlnProSerMetAspGlyGluLeuLeuLeuArgAlaGluGlySerThrPr	611	

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Qy	631	rHisVal	633
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Search completed: April 14, 2005, 20:48:36
Job time : 5075 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 14, 2005, 12:30:08 ; Search time 613 seconds
(without alignments)
6112.881 Million cell updates/sec

Title: US-10-664-667-5
Perfect score: 3307
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2	3305	99.9	1899	11	ADN02244
3	3305	99.9	1899	12	ADK19409
4	3305	99.9	2486	6	AAI67922
5	3305	99.9	2486	11	ADN02242

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length DB	ID	Description
1	3305	99.9	1899	6	AAI67923 Human LGR
2	3305	99.9	1899	11	ADN02244 Human par
3	3305	99.9	1899	12	ADK19409 ORF of CD
4	3305	99.9	2486	6	AAI67922 Human LGR
5	3305	99.9	2486	11	ADN02242 Human par

6	3305	99.9	2486	12	ADK19407	Adk19407 cDNA enco
7	3150	95.3	2322	5	AAF98722	Aaf98722 Human lat
8	3140	95.0	3451	12	ADQ76775	Adq76775 Human LGR
9	3045.5	92.1	2208	6	AAI67925	Aai67925 Human LGR
10	3045.5	92.1	2208	11	ADN02247	Adn02247 Human par
11	3045.5	92.1	2208	12	ADK19412	Adk19412 ORF of pa
12	3045.5	92.1	2711	6	AAI67924	Aai67924 Human par
13	3045.5	92.1	2711	11	ADN02245	Adn02245 Human par
14	3045.5	92.1	2711	12	ADK19410	Adk19410 Partial c
15	3045.5	92.1	2786	10	ADC16710	Adc16710 Human G-p
16	3045.5	92.1	2901	6	AAI67927	Aai67927 Human LGR
17	3045.5	92.1	2901	10	ADC16695	Adc16695 cDNA with
18	3045.5	92.1	2901	10	ADC16692	Adc16692 cDNA enco
19	3045.5	92.1	2901	11	ADN02250	Adn02250 Human ful
20	3045.5	92.1	2901	12	ADK19415	Adk19415 ORF of fu
21	3045.5	92.1	3000	6	AAS98067	Aas98067 Human DNA
22	3045.5	92.1	3042	10	ADC16701	Adc16701 cDNA with
23	3045.5	92.1	3042	10	ADC16698	Adc16698 cDNA enco
24	3045.5	92.1	3119	8	ABZ42549	Abz42549 Human G p
25	3045.5	92.1	3325	10	ADD89048	Add89048 Encoding
26	3045.5	92.1	3429	6	AAD37674	Aad37674 Human G-p
27	3045.5	92.1	3438	10	ABT31938	Abt31938 Human bre
28	3045.5	92.1	3443	10	ADD89090	Add89090 Encoding
29	3045.5	92.1	3492	6	AAI67926	Aai67926 Human LGR
30	3045.5	92.1	3492	11	ADN02248	Adn02248 Human ful
31	3045.5	92.1	3492	12	ADK19413	Adk19413 Full leng
32	3045.5	92.1	3492	12	ADQ15073	Adq15073 Human can
33	3041.5	92.0	2901	10	ADC16694	Adc16694 cDNA enco
34	3041.5	92.0	2901	10	ADC16696	Adc16696 cDNA enco
35	3041.5	92.0	2964	10	ADI21981	Adi21981 Novel hum
36	3041.5	92.0	3042	10	ADC16702	Adc16702 cDNA with
37	3041.5	92.0	3042	10	ADC16700	Adc16700 cDNA enco
38	3041.5	92.0	3273	11	ADN39801	Adn39801 Cancer/an
39	3041.5	92.0	3273	13	ADR46630	Adr46630 Cancer-as
40	3041.5	92.0	3306	12	ADQ76773	Adq76773 Human LGR
41	3041.5	92.0	3618	10	ADF70543	Adf70543 Orphan re
42	3040.5	91.9	2487	6	ADH50804	Adh50804 Human G-p
43	3040	91.9	2988	6	ABZ11841	Abz11841 Human pol
44	3040	91.9	2988	12	ADM44359	Adm44359 Novel hum
45	3038.5	91.9	3349	6	ADH50807	Adh50807 Human G-p

ALIGNMENTS

RESULT 1
AAI67923
ID AAI67923 standard; cDNA; 1899 BP.
XX
AC AAI67923;
XX
DT 13-MAR-2002 (first entry)
XX
DE Human LGR6 polypeptide coding sequence (clone fahr).
XX
KW Large G-protein coupled receptor 6; LGR6; GPCR; immunomodulator;
KW anti-HIV; cytostatic; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; neuroleptic; antidepressant; tranquilizer; antimagaine;
KW osteopathic; antiarteriosclerotic; vasotropic; hypotensive; cardiant;
KW antiarrhythmic; anorectic; gene therapy; human; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT
FT Location/Qualifiers
FT 1..1899
FT /*tag= a
FT /product= "LGR6 polypeptide"
FT /transl_except= (pos: 169..171, aa: Xaa)
FT /note= "Xaa = unknown"

WO200185768-A2.

15-NOV-2001.

Db 1381 GCCTCCATGCTGGGCCCTCTTCCCTGTCTACGCCCGAGGCCGTCAAGTCTGTCTCTGCTGGTG 1440

QY 481 ValLeuProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPhe 500
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Db 1441 GTGCTGCCCTGCCTGCCTCAACCCACTGCTGTACTGTCTTTCAACCCCACTTC 1500

QY 501 ArgAspAspLeuArgArgProArgAlaGlyAspSerGlyProLeuAlaTyrAla 520
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Db 1501 CGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT 1560

QY 521 AlaAlaGlyGluLeuGluYsSerSerCysAspSerThrGlnAlaLeuValAlaPheSer 540
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Db 1561 GCGGCCGGGAGCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT 1620

QY 541 AspValAspLeuIleLeuGluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyr 560
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Db 1621 GATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGCGGCCCTTGGGCTGGAGACCTAT 1680

QY 561 GlyPheProSerValThrIleSerCysGlnGlnProGlyAlaProArgLeuGluGly 580
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Db 1681 GGCTTCCCCTCAGTGACCCCTCATCTCCTGTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGC 1740

QY 581 SerHisCysValGluProGluGlyAsnHisPheGlyAsnProGlnProSerMetAspGly 600
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Db 1741 AGCCATTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCCAACCTCCATGGATGGA 1800

QY 601 GluLeuLeuLeuArgAlaGluGlySerThrProAlaGlyGlyGlyLeuSerGlyGlyGly 620
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Db 1801 GAACTGCTGCTGAGGCGACAGGGATCTACGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGC 1860

QY 621 GlyPheGlnProSerGlyLeuAlaPheAlaSerHisVal 633
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Db 1861 GGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACACGTG 1899

RESULT 2
ADN02244

ID ADN02244 standard; cDNA; 1899 BP.

XX

AC ADN02244;

XX

DT 17-JUN-2004 (first entry)

XX

DE Human partial large G protein-coupled receptor, LGR6, CDS #1.

XX

KW Human; ss; large G protein-coupled receptor 6; LGR6; heart failure;
ischaemic heart disease; myocardial infarction; hypertension;
pericarditis; atherosclerosis; hepatic failure; viral hepatitis; cancer;
intracerebral haemorrhage; brain abscess; Alzheimer's disease;
Pick disease; Parkinson's disease; Huntington's disease;
amyotrophic lateral sclerosis; inflammatory bowel disease;
Crohn's disease; benign prostatic hypertrophy;
systemic lupus erythematosus.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1899

FT /*tag= a

FT /partial

FT /note= "No start or stop codon shown"

FT /product= "Partial LGR6"

XX US2003166047-A1.

PN

XX

PD 04-SEP-2003.

XX

PF 08-MAY-2001; 2001US-00851595.

XX

PR 06-MAY-1999; 99US-0132896P.

PR 08-MAY-2000; 2000US-00566588.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Gu W;

XX

DR WPI; 2003-898067/82.

XX

PT New isolated LGR6 nucleic acids and polypeptides, useful for diagnosing
and treating LGR6-mediated disorders, such as myocardial infarction,
hypertension, atherosclerosis, viral hepatitis, cancer and/or Alzheimer's
disease.

PT

XX

PS Claim 1; SEQ ID NO 6; 145pp; English.

XX

CC The invention relates to an isolated LGR6 (large G protein-coupled
receptor) nucleic acid molecule comprising the mouse and human cDNA
sequences appearing as ADN02239, ADN02241, ADN02242, ADN02244, ADN02245,
CC ADN02247, ADN02248 and ADN02250. Also included are a host cell or a non-
human mammalian host cell containing an LGR6 nucleic acid (and producing
CC LGR6), an isolated LGR6 polypeptide appearing as ADN02240, ADN02243,
CC ADN02246 and ADN02249, an antibody which selectively binds to LGR6, a
CC method for detecting the presence of LGR6 in a sample, a kit (comprising
CC a compound which selectively binds to LGR6, or hybridises to LGR6 nucleic
CC acid, and instructions for use), a method for detecting LGR6 nucleic acid
CC in a sample, a method for identifying a compound which binds to LGR6, a
CC method for modulating the activity of LGR6 and a method for identifying a
CC compound that modulates the activity of LGR6. The methods and
CC compositions of the present invention are useful for diagnosing and
CC treating large G-protein coupled receptor 6 (LGR6)-mediated or -related
CC disorders, such as heart failure, ischaemic heart disease, myocardial
CC infarction, hypertension, pericarditis, atherosclerosis, hepatic failure,
CC viral hepatitis, cancer, intracerebral haemorrhage, brain abscess,
CC Alzheimer's disease, Pick disease, Parkinson's disease, Huntington's
CC disease, amyotrophic lateral sclerosis, inflammatory bowel disease,
CC Crohn's disease, benign prostatic hypertrophy and systemic lupus
CC erythematosus. The present sequence is a partial human CDS for LGR6.

XX

SQ Sequence 1899 BP; 302 A; 624 C; 563 G; 409 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 8.45e-259 Length: 1899

Score: 3305.00 Matches: 632

Percent Similarity: 99.84% Conservative: 0

Best Local Similarity: 99.84% Mismatches: 1

Query Match: 99.94% Indels: 0

DB: 11 Gaps: 0

US-10-664-667-5 (1-633) x ADN02244 (1-1899)

QY 1 AsnThrThrHisTyrArgGluSerTrpTyrAlaCysArgTyrArgSerGlyIleProGly 20
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Db 1 AATACGACTCACTATAGGAAAGCTGGTACGCCCTGCAGGTACCGGTCCGGAATTCGCGG 60
|||||

QY 21 SerThrHisAlaSerValGluArgSerGlnGlyLeuSerLeuProAlaHisProAlaSer 40
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Db 61 TCGACCCACGGCTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCTCT 120
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QY 41 LeuAlaAlaLeuAlaAlaSerAsnThrThrAlaSerGlyLysLeuGlu***AspThrPhe 60
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Db 121 CTTGCTGCCCTAGCGCCTCCAAACACACCATCTGGGAAATTGGAGCTNGACACCTTC 180
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QY 61 SerGlnLeuSerSerLeuGlnAlaLeuAspLeuSerTrpAsnAlaIleArgSerIleHis 80
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Db 181 AGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGTGGAAACGCCATCCGGTCCATCCAC 240
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QY 81 ProGluAlaPheSerThrLeuHisSerLeuValLysLeuAspLeuThrAspAsnGlnLeu 100
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QY 101 ThrThrLeuProLeuAlaGlyLeuGlyLeuMetHisLeuLysLeuLysGlyAsnLeu 120
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Db 301 ACCACACTGCCCCCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 360
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QY 121 AlaLeuSerGlnAlaPheSerLysAspSerPheProLysLeuArgIleLeuGluValPro 140
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QY	141	TyrAlaTyrGlnCysCysProTyrGlyMetCysAlaSerPhePheLysAlaSerGlyGln	160	QY	501	ArgAspAspLeuArgArgLeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAla	520
Db	421	TATGCTACCAAGTGTGTCCTATGGGATGTGCCAGCTTCTTCAAGGCCCTTGGGCAG	480	Db	1501	CGGGATGACCTTCGGGGCTTCGGCCCCCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT	1560
QY	161	TrpGluAlaGluAspLeuHisLeuAspAspGluGluSerSerLysArgProLeuGlyLeu	180	QY	521	AlaAlaGlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuValAlaPheSer	540
Db	481	TGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCTC	540	Db	1561	GCGGCCGGGAGCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT	1620
QY	181	LeuAlaArgGlnAlaGluAsnHisTyrAspGlnAspLeuAspGluLeuGlnLeuGluMet	200	QY	541	AspValAspLeuLeuLeuGluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyr	560
Db	541	CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG	600	Db	1621	GATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGCGGCCCTGGGCTGGAGACCTAT	1680
QY	201	GluAspSerLysProHisProSerValGlnCysSerProThrProGlyProPheLysPro	220	QY	561	GlyPheProSerValThrLeuIleSerCysGlnGlnProGlyAlaProArgLeuGluGly	580
Db	601	GAGGACTCAAAGCCACACCCAGTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC	660	Db	1681	GGCTTCCCCTCAGTGACCCCTCATCTCCTGTCCAGCAGCCAGGGCCCCCAGGCTGGAGGGC	1740
QY	221	CysGluTyrLeuPheGluSerTrpGlyIleArgLeuAlaValTrpAlaIleValIleLeuLeu	240	QY	581	SerHisCysValGluProGluGlyAsnHisPheGlyAsnProGlnProSerMetAspGly	600
Db	661	TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCGTGGCCGTGTGGGCCATCGTGTGCTC	720	Db	1741	AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGA	1800
QY	241	SerValLeuCysAsnGlyLeuValLeuLeuThrValPheAlaGlyGlyProAlaProLeu	260	QY	601	GluLeuLeuLeuArgAlaGluGlySerThrProAlaGlyGlyLeuSerGlyGlyGly	620
Db	721	TCCGTGCTCTGCAATGGACTGGTGTGCTGACCGGTTCGTGGCGGCCTGCCCCCTG	780	Db	1801	GAACTGCTGCTGAGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGTGGC	1860
QY	261	ProProValLysPheValValGlyAlaIleAlaGlyAlaAsnThrLeuThrGlyIleSer	280	QY	621	GlyPheGlnProSerGlyLeuAlaPheAlaSerHisVal	633
Db	781	CCCCCGGTCAAGTTTGTGTAGGTGCGATTGCAAGCGCCCAACACCTTGACTGGCATTTCC	840	Db	1861	GGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTTCACACGTG	1899
QY	281	CysGlyLeuLeuAlaSerValAspAlaLeuThrPheGlyGlnPheSerGluTyrGlyAla	300	RESULT 3			
Db	841	TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTGGTCAAGTTCTCTGAGTACGGAGCC	900	ADK19409			
QY	301	ArgTrpGluThrGlyLeuGlyCysArgAlaThrGlyPheLeuAlaValLeuGlySerGlu	320	ID	ADK19409	standard; cDNA; 1899 BP.	
Db	901	CGCTGGGAGACGGGGCTAGGCTGCCGGCCACTGGCTTCTGGCAGTACTTGGGTGGAG	960	XX			
QY	321	AlaSerValLeuLeuLeuThrLeuAlaAlaValGlnCysSerValSerValSerCysVal	340	AC	ADK19409;		
Db	961	GCATCGGTGCTGCTCACTCTGGCCGCACTGCGCAGTGCAGTGCAGCGTCTCCGTCTCTGTGTC	1020	XX			
QY	341	ArgAlaTyrGlyLysSerProSerLeuGlySerValArgAlaGlyValLeuGlyCysLeu	360	DT	17-JUN-2004	(first entry)	
Db	1021	CGGGCCTATGGGAAGTCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCTAGGCTGCCTG	1080	XX			
QY	361	AlaLeuAlaGlyLeuAlaAlaLeuProLeuAlaSerValGlyGluTyrGlyAlaSer	380	DE		ORF of cDNA encoding human LGR6 polypeptide #1.	
Db	1081	GCACTGGCAGGGCTGGCCGCCGCACTGCCCTGGCTCAGTGGGAGAATACGGGGCCTCC	1140	XX		G-protein coupled receptor; GPCR; large G-protein coupled receptor 6;	
QY	381	ProLeuCysLeuProTyrAlaProProGluGlyGlnProAlaAlaLeuGlyPheThrVal	400	KW		LGR6; weight disorder; neural disorder; endocrine disorder;	
Db	1141	CCACTCTGCCCTACCGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGGCTCACCCGTG	1200	KW		cardiovascular disorder; anorectic; anabolic; immunomodulator;	
QY	401	AlaLeuValMetMetAsnSerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeu	420	KW		neuroprotective; nootropic; antiparkinsonian; anti-HIV; anticonvulsant;	
Db	1201	GCCCTGGTGATGATGAACCTCCTTCTGTTTCCCTGGTCGTGGCCGTGCATCAAAACTG	1260	KW		antithyroid; osteopathic; cardiant; vasotropic; hypotensive;	
QY	421	TyrCysAspLeuProArgGlyAspPheGluAlaValTrpAspCysAlaMetValArgHis	440	XX		antiarteriosclerotic; antiarrhythmic; human; gene; ss.	
Db	1261	TACTGTGACCTGCCGGGGCGGACCTTTGAGGCCGTGTGGGACTGCGCCATGTTGAGGCAC	1320	OS		Homo sapiens.	
QY	441	ValAlaTrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPhe	460	XX		Location/Qualifiers	
Db	1321	GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTC	1380	FT		1. .1899	
QY	461	AlaSerMetLeuGlyLeuPheProValThrProGluAlaValLysSerValLeuLeuVal	480	FT		/*tag= a	
Db	1381	GCCTCCATGCTGGGCCTCTTCCCTGTCAAGCCCGAGGCCGTCAAGTCTGTCTGCTGGTG	1440	FT		/partial	
QY	481	ValLeuProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPhe	500	FT		/product= "LGR6 polypeptide #1"	
Db	1441	GTGCTGCCCCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCCACTTC	1500	FT		/note= "This sequence lacks both start and stop codons"	
				FT		/transl_except= (pos:169. .171,aa:Xaa)	
				XX		/note= "Xaa= Unknown"	
				PN		US2004058377-A1.	
				XX		25-MAR-2004.	
				XX		18-SEP-2003; 2003US-00664667.	
				XX		06-MAY-1999; 99US-0132896P.	
				PR		08-MAY-2000; 2000US-00566588.	
				PR		08-MAY-2001; 2001US-00851595.	
				XX		(MILL-) MILLENNIUM PHARM INC.	
				PA		Gu W;	
				PI			
				XX		WPI; 2004-268789/25.	
				DR		P-PSDB; ADK19408.	
				XX			

PT New large G-protein coupled receptor 6 nucleic acid molecules and
PT polypeptides, useful for diagnosing, preventing or treating diseases
PT associated with aberrant nucleic acid or protein activity, e.g. obesity,
PT anorexia or cachexia.

XX Claim 2; SEQ ID NO 6; 145pp; English.

XX The present invention relates to the isolation of novel members of the G-
CC protein coupled receptor (GPCR) family designated as large G-protein
CC coupled receptor 6 (LGR6), and the polynucleotide sequences encoding
CC them. The invention also discloses LGR6 fusion proteins, antigenic
CC peptides, anti-LGR6 antibodies, recombinant expression vectors, host
CC cells, and non-human transgenic animals in which an LGR6 gene has been
CC introduced or disrupted. The LGR6 polynucleotide sequences, polypeptide
CC sequences, and antibodies are useful for diagnosing, treating or
CC preventing diseases associated with aberrant LGR6 expression or activity,
CC such as weight disorders (e.g. obesity, anorexia nervosa or cachexia),
CC neural disorders (e.g. central nervous system disorder, including
CC Alzheimer's disease, Parkinson's disease, AIDS-related dementia, multiple
CC sclerosis and Huntington's disease), endocrine disorders (e.g.
CC hypothyroidism, hyperthyroidism or acromegaly), or cardiovascular
CC disorders (e.g. ischaemia-reperfusion injury, coronary artery disease,
CC myocardial infarction, arrhythmia, atherosclerosis, hypertension or
CC congestive heart failure). The LGR6 polynucleotide and polypeptide
CC sequences are also useful as targets for developing modulating agents
CC that regulate a variety of cellular processes, e.g. neural and endocrine
CC processes and thermogenesis. They can be used in screening assays (e.g.
CC chromosome mapping, tissue typing or in forensic biology), or in
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials or pharmacogenomics). The present sequence
CC encodes a human LGR6 polypeptide.

XX
SQ Sequence 1899 BP; 302 A; 624 C; 563 G; 409 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 8.45e-259 Length: 1899
Score: 3305.00 Matches: 632
Percent Similarity: 99.84% Conservative: 0
Best Local Similarity: 99.84% Mismatches: 1
Query Match: 99.94% Indels: 0
DB: 12 Gaps: 0

US-10-664-667-5 (1-633) x ADK19409 (1-1899)

QY 1 AsnThrThrHisTyrArgGluSerTrpTyrAlaCysArgTyrArgSerGlyIleProGly 20
Db 1 AATACGACTCACTATAGGAAAGCTGGTACGCTGCAGGTACCGTCCGGAATCCCCGG 60
QY 21 SerThrHisAlaSerValGluArgSerGlnGlyLeuSerLeuProAlaHisProAlaSer 40
Db 61 TCGACCCACGGCTCCGTGGAGCGGAGCCAGGGTCTGAGCCCTGCGGGCTCATCCAGCCT 120
QY 41 LeuAlaAlaLeuAlaAlaSerAsnThrThrAlaSerGlyIleLeuGlu***AspThrPhe 60
Db 121 CTTGCTGCCCTAGCGGCCTCCAAACACACCGCATCTGGGAAATTGGAGCTNGACACCTTC 180
QY 61 SerGlnLeuSerSerLeuGlnAlaLeuAspLeuSerTrpAsnAlaIleArgSerIleHis 80
Db 181 AGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCAC 240
QY 81 ProGluAlaPheSerThrLeuHisSerLeuValLysLeuAspLeuThrAspAsnGlnLeu 100
Db 241 CCTGAGGCCTTCTCCACCCCTGCATCCCTGGTCAAGCTGGACCTGACAGACAACCCAGT 300
QY 101 ThrThrLeuProLeuAlaGlyLeuGlyLeuMetHisLeuLysLeuLysGlyAsnLeu 120
Db 301 ACCACACTGCCCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 360
QY 121 AlaLeuSerGlnAlaPheSerLysAspSerPheProLysLeuArgIleLeuGluValPro 140
Db 361 GCTCTCTCCAGGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCT 420
QY 141 TyrAlaTyrGlnCysCysProTyrGlyMetCysAlaSerPhePheLysAlaSerGlyGln 160

Db 421 TATGCCTACCAGTGCTCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAG 480
QY 161 TrpGluAlaGluAspLeuHisLeuAspGluGluSerSerLysArgProLeuGlyLeu 180
Db 481 TGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCTC 540
QY 181 LeuAlaArgGlnAlaGluAsnHisTyrAspGlnAspLeuAspGluLeuGlnLeuGluMet 200
Db 541 CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG 600
QY 201 GluAspSerLysProHisProSerValGlnCysSerProThrProGlyProPheLysPro 220
Db 601 GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGGCC 660
QY 221 CysGluTyrLeuPheGluSerTrpGlyIleArgLeuAlaValTrpAlaIleValLeuLeu 240
Db 661 TGTGAGTACCTCTTTGAAAGCTGGGCATCCGCCTGGCGTGTGGCCATCGTGTGCTC 720
QY 241 SerValLeuCysAsnGlyLeuValLeuLeuThrValPheAlaGlyGlyProAlaProLeu 260
Db 721 TCCGTGCTCTGCAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGCCCTGCCCCCTG 780
QY 261 ProProValLysPheValValGlyAlaIleAlaGlyAlaAsnThrLeuThrGlyIleSer 280
Db 781 CCCCCGGTCAAGTTTGTGTAGGTGGATTGCAGGGCGCCAAACACTTGACTGGCATTTCC 840
QY 281 CysGlyLeuLeuAlaSerValAspAlaLeuThrPheGlyGlnPheSerGluTyrGlyAla 300
Db 841 TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCC 900
QY 301 ArgTrpGluThrGlyLeuGlyCysArgAlaThrGlyPheLeuAlaValLeuGlySerGlu 320
Db 901 CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCTGGCAGTACTTGGGTCCGAG 960
QY 321 AlaSerValLeuLeuThrLeuAlaAlaValGlnCysSerValSerValSerCysVal 340
Db 961 GCATCGGTGCTGCTGCTCACTCTGGCCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTC 1020
QY 341 ArgAlaTyrGlyLysSerProSerLeuGlySerValArgAlaGlyValLeuGlyCysLeu 360
Db 1021 CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCTTAGGCTGCC 1080
QY 361 AlaLeuAlaGlyLeuAlaAlaAlaLeuProLeuAlaSerValGlyGluTyrGlyAlaSer 380
Db 1081 GCACCTGGCAGGGCTGGCCCGCCGACCTGCCCTGGCCTCAGTGGGAGAAATACGGGGCTCC 1140
QY 381 ProLeuCysLeuProTyrAlaProProGluGlyGlnProAlaAlaLeuGlyPheThrVal 400
Db 1141 CCACTCTGCCTGCCCTAGCGGCCACCTGAGGGTCAAGGGTCAAGCAGCAGCCCTGGGCTT 1200
QY 401 AlaLeuValMetMetAsnSerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeu 420
Db 1201 GCCCTGGTGATGATGAATCCTTCTGTTTCCTGGTCTGTCGGCGGTGCCTACATCAAAC 1260
QY 421 TyrCysAspLeuProArgGlyAspPheGluAlaValTrpAspCysAlaMetValArgHis 440
Db 1261 TACTGTGACCTGCCCGGGGGGACCTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCAC 1320
QY 441 ValAlaTrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPhe 460
Db 1321 GTGGCCTGGCTCATCTTCGACAGACGGGCTCCTTACTGTCCCCGTGGCCTTCCCTCAGCT 1380
QY 461 AlaSerMetLeuGlyLeuPheProValThrProGluAlaValLysSerValLeuVal 480
Db 1381 GCCTCCATGTGGGCCTCTCCCTGTACGCCCGAGCGCGTCAAGTCTGTCTCCTGCTGGTG 1440
QY 481 ValLeuProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPhe 500
Db 1441 GTGCTGCCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCACTTC 1500
QY 501 ArgAspAspLeuArgLeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAla 520

Db 1501 CGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT 1560

QY 521 AlaAlaGlyGluLeuGluLySSerSerCysAspSerThrGlnAlaLeuValAlaPheSer 540
|||||

Db 1561 GCGGCCGGGAGCTGGAGAAGAGCTCCTGTGATCTACCCAGGCCCTGGTAGCCTTCTCT 1620
|||||

QY 541 AspValAspLeuIleLeuGluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyr 560
|||||

Db 1621 GATGTGATCTCATTTCTGAAGCTTCTGAAGCTGGCGGCCCTGGGCTGGAGACCTAT 1680
|||||

QY 561 GlyPheProSerValThrLeuIleSerCysGlnGlnProGlyAlaProArgLeuGluGly 580
|||||

Db 1681 GGCTTCCCTCAGTGACCTCATCTCCTGTGACGACGAGGGCCCCCAGGCTGGAGGGC 1740
|||||

QY 581 SerHisCysValGluProGluGlyAsnHisPheGlyAsnProGlnProSerMetAspGly 600
|||||

Db 1741 AGCCATTGTGTAGAGCCAGAGGGAACCACTTTGGGAACCCCAACCTCCATGGATGA 1800
|||||

QY 601 GluLeuLeuArgAlaGluGlySerThrProAlaGlyGlyGlyLeuSerGlyGlyGly 620
|||||

Db 1801 GAACTGCTGTGAGGGCAGAGGGATCTACGCCAGAGGTGGAGGCTTGTCTCAGGGGTGC 1860
|||||

QY 621 GlyPheGlnProSerGlyLeuAlaPheAlaSerHisVal 633
|||||

Db 1861 GGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACACGTG 1899
|||||

RESULT 4

AAI67922

ID AAI67922 standard; cdna; 2486 BP.

XX

AC AAI67922;

XX

DT 13-MAR-2002 (first entry)

XX

DE Human LGR6 polypeptide encoding cdna (clone fahr).

XX

KW Large G-protein coupled receptor 6; LGR6; GPCR; immunomodulator;
anti-HIV; cytostatic; nootropic; neuroprotective; antiparkinsonian;
anticonvulsant; neuroleptic; antidepressant; tranquilizer; antimigraine;
osteopathic; antiarteriosclerotic; vasotropic; hypotensive; cardiac;
antiarrhythmic; anorectic; gene therapy; human; ss.

XX

OS Homo sapiens.

XX

FH Key

FT CDS

FT 2..1903

FT Location/Qualifiers

FT /*tag= a

FT /product= "LGR6 polypeptide"

FT /transl_except= (pos: 170..172, aa: Xaa)

FT /note= "Xaa = unknown"

XX

XX WO200185768-A2.

PN

XX

PD 15-NOV-2001.

XX

XX 08-MAY-2001; 2001WO-US015002.

PF

XX

XX 08-MAY-2000; 2000US-00566588.

PR

XX

XX (MILL-) MILLENNIUM PHARM INC.

PA

XX

PI Gu W;

XX

XX WPI; 2002-055584/07.

DR

DR P-PSDB; AAG66139.

XX

XX Novel isolated large G-protein coupled receptor 6 polypeptide, useful for
diagnosing and treating weight disorder, metabolic disorder, central
nervous system disorder, endocrine disorder and cardiovascular disorder.

XX

PS Example 1; Fig 4; 198pp; English.

XX

CC The invention provides isolated large G-protein coupled receptor 6 (LGR6)

CC polypeptides and polynucleotides encoding them. The LGR6 polypeptides and
polynucleotides are useful as targets for developing modulating agents
CC that regulate a variety of cellular process, e.g. neural and endocrine
processes, as well as thermogenesis. They are useful for developing novel
CC diagnostic and therapeutic agents for LGR6 associated disorders such as
weight disorders (anorexia, obesity), eating disorders, acquired
CC immunodeficiency syndrome (AIDS)-related wasting, cancer-related wasting,
CC metabolic disorders, central nervous system disorders (e.g. Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, Gilles de la
CC Tourette's syndrome, multiple sclerosis, amyotrophic lateral sclerosis,
CC epilepsy, Jakob-Creutzfeldt disease, depression, schizophrenia,
CC obsessive-compulsive disorder, anxiety, panic disorder, migraine),
CC endocrine disorders (hypo and hyperthyroidism, dwarfism, gigantism,
CC acromegaly), and cardiovascular disorders (atherosclerosis, restenosis,
CC hypertension, myocardial infarction, arrhythmia). The LGR6 polypeptides,
polynucleotides and antibodies are useful in screening assays, detection
CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials and pharmacogenomics), and in methods of
CC treatment (e.g. therapeutic and prophylactic). The present sequence
CC represents a human LGR6 polypeptide encoding cdna
XX

SQ Sequence 2486 BP; 455 A; 773 C; 692 G; 565 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 1.21e-258 Length: 2486

Score: 3305.00 Matches: 632

Percent Similarity: 99.84% Conservative: 0

Best Local Similarity: 99.84% Mismatches: 1

Query Match: 99.94% Indels: 0

DB: 6 Gaps: 0

US-10-664-667-5 (1-633) x AAI67922 (1-2486)

QY 1 AsnThrThrHisTyrArgGluSerTrpTyrAlaCysArgTyrArgSerGlyIleProGly 20
|||||

Db 2 AATACGACTCACTATAGGGAAGCTGGTAGCCTGCAGGTACCGTACCGATTCGGAATTCCTGGG 61
|||||

QY 21 SerThrHisAlaSerValGluArgSerGlnGlyLeuSerLeuProAlaHisProAlaSer 40
|||||

Db 62 TCGACCCACGCTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGTTCATCCAGCCTCT 121
|||||

QY 41 LeuAlaAlaLeuAlaAlaSerAsnThrThrAlaSerGlyLysLeuGlu***AspThrPhe 60
|||||

Db 122 CTTGCTGCCCTAGCGGCCCTCCAACACACACCGCATCTGGGAAATTTGGAGCTNGACACCTTC 181
|||||

QY 61 SerGlnLeuSerSerLeuGlnAlaLeuAspLeuSerTrpAsnAlaIleArgSerIleHis 80
|||||

Db 182 AGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCAC 241
|||||

QY 81 ProGluAlaPheSerThrLeuHisSerLeuValLysLeuAspLeuThrAspAsnGlnLeu 100
|||||

Db 242 CCTGAGGCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGCAGACAAACCAGCTG 301
|||||

QY 101 ThrThrLeuProLeuAlaGlyLeuGlyLeuMetHisLeuLysLeuLysGlyAsnLeu 120
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Db 302 ACCACACTGCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 361
|||||

QY 121 AlaLeuSerGlnAlaPheSerLysAspSerPheProLysLeuArgIleLeuGluValPro 140
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Db 362 GCTCTCTCCAGGCCTTCTCCAAGGACAGTTTCCCAAACCTGAGGATCTTGAGGTGCCT 421
|||||

QY 141 TyrAlaTyrGlnCysCysProTyrGlyMetCysAlaSerPhePheLysAlaSerGlyGln 160
|||||

Db 422 TATGCCTACCAGTGTGTCCCTATGGATGTGTGCCAGCTTCTTCAAGCCTCTGGGCAG 481
|||||

QY 161 TrpGluAlaGluAspLeuHisLeuAspGluGluSerSerLysArgProLeuGlyLeu 180
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Db 482 TGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCTC 541
|||||

QY 181 LeuAlaArgGlnAlaGluAsnHisTyrAspGlnAspLeuAspGluLeuGlnLeuGluMet 200
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Db 542 CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTTGATGAGCTCAGCTGGAGATG 601
|||||

Qy 201 GluAspSerLysProHisProSerValGlnCysSerProThrProGlyProPheLysPro 220
Db 602 GAGGACTCAAAGCCACACCCCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC 661
Qy 221 CysGluTyrLeuPheGluSerTrpGlyIleArgLeuAlaValTrpAlaIleValLeuLeu 240
Db 662 TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGTGTC 721
Qy 241 SerValLeuCysAsnGlyLeuValLeuLeuThrValPheAlaGlyGlyProAlaProLeu 260
Db 722 TCCGTGCTCTGCAATGGACTGGTGTGCTGACCGTGTTCGTGGGGGCTGCCCCCTG 781
Qy 261 ProProValLysPheValValGlyAlaIleAlaGlyAlaAsnThrLeuThrGlyIleSer 280
Db 782 CCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCACACCTTGACTGGCATTTCC 841
Qy 281 CysGlyLeuLeuAlaSerValAspAlaLeuThrPheGlyGlnPheSerGluTyrGlyAla 300
Db 842 TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCC 901
Qy 301 ArgTrpGluThrGlyLeuGlyCysArgAlaThrGlyPheLeuAlaValLeuGlySerGlu 320
Db 902 CGCTGGGAGACGGGGCTAGGTCGCCGGCCACTGGCTTCTTGGCAGTACTTGGGTCGGAG 961
Qy 321 AlaSerValLeuLeuThrLeuAlaAlaValGlnCysSerValSerValSerCysVal 340
Db 962 GCATCGGTGCTGTGCTCACTCTGGCCGCACTGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTC 1021
Qy 341 ArgAlaTyrGlyLysSerProSerLeuGlySerValArgAlaGlyValLeuGlyCysLeu 360
Db 1022 CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCGTG 1081
Qy 361 AlaLeuAlaGlyLeuAlaAlaLeuProLeuAlaSerValGlyGluTyrGlyAlaSer 380
Db 1082 GCACTGGCAGGGCTGGCCCGCACTGCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCC 1141
Qy 381 ProLeuCysLeuProTyrAlaProProGluGlyGlnProAlaAlaLeuGlyPheThrVal 400
Db 1142 CCACTCTGCCTGCCCTACGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTG 1201
Qy 401 AlaLeuValMetMetAsnSerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeu 420
Db 1202 GCCCTGGTGATGATGAACCTCTCTGTTTCTGTGTCGTGGCCGTGCCTACATCAAACTG 1261
Qy 421 TyrCysAspLeuProArgGlyAspPheGluAlaValTrpAspCysAlaMetValArgHis 440
Db 1262 TACTGTGACCTGCCCGGGGCGACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGCAC 1321
Qy 441 ValAlaTrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPhe 460
Db 1322 GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCGTGGCCTTCCTCAGCTTC 1381
Qy 461 AlaSerMetLeuGlyLeuPheProValThrProGluAlaValLysSerValLeuLeuVal 480
Db 1382 GCCTCCATGTGGGCCCTCTTCCTGTTCACGCCCGAGGCCGTCAAGTCTGTCTGTGGTG 1441
Qy 481 ValLeuProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPhe 500
Db 1442 GTGCTGCCCTGCCTGCCTCAACCCACTGTGTACTGTCTTTCAAACCCCCACTTC 1501
Qy 501 ArgAspAspLeuArgArgLeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAla 520
Db 1502 CGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGGCCCTAGCCTATGCT 1561
Qy 521 AlaAlaGlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuValAlaPheSer 540
Db 1562 GCGSCGGGGAGCTGGAGAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT 1621
Qy 541 AspValAspLeuIleLeuGluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyr 560
Db 1622 GATGTGGATCTCATTTCTGGAGCTTCTGAAGCTGGGCGGCCCTGGGCTGGAGACCTAT 1681

Qy 561 GlyPheProSerValThrLeuIleSerCysGlnGlnProGlyAlaProArgLeuGluGly 580
Db 1682 GGCTTCCCCTCAGTGACCCCTCATCTCCTGTAGCAGCCAGGGGCCCCCAGGCTGGAGGGC 1741
Qy 581 SerHisCysValGluProGluGlyAsnHisPheGlyAsnProGlnProSerMetAspGly 600
Db 1742 AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGA 1801
Qy 601 GluLeuLeuLeuArgAlaGluGlySerThrProAlaGlyGlyLeuSerGlyGlyGly 620
Db 1802 GAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGGTGGC 1861
Qy 621 GlyPheGlnProSerGlyLeuAlaPheAlaSerHisVal 633
Db 1862 GGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACACGTG 1900
RESULT 5
ADN02242
ID ADN02242 standard; cDNA; 2486 BP.
XX
AC ADN02242;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human partial large G protein-coupled receptor, LGR6, cDNA #1.
XX
KW Human; ss; large G protein-coupled receptor 6; LGR6; heart failure;
KW ischaemic heart disease; myocardial infarction; hypertension;
KW pericarditis; atherosclerosis; hepatic failure; viral hepatitis; cancer;
KW intracerebral haemorrhage; brain abscess; Alzheimer's disease;
KW Pick disease; Parkinson's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; inflammatory bowel disease;
KW Crohn's disease; benign prostatic hypertrophy;
KW systemic lupus erythematosus.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 2..1903
FT /*tag= a
FT /partial
FT /note= "No start codon shown"
FT /product= "Partial LGR6"
XX
PN US2003166047-A1.
XX
XX
PD 04-SEP-2003.
XX
PF 08-MAY-2001; 2001US-00851595.
XX
PR 06-MAY-1999; 99US-0132896P.
PR 08-MAY-2000; 2000US-00566588.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX
PI Gu W;
XX
DR WPI; 2003-898067/82.
DR P-PSDB; ADN02243.
XX
PT New isolated LGR6 nucleic acids and polypeptides, useful for diagnosing
PT and treating LGR6-mediated disorders, such as myocardial infarction,
PT hypertension, atherosclerosis, viral hepatitis, cancer and/or Alzheimer's
PT disease.
XX
PS Claim 1; SEQ ID NO 4; 145pp; English.
XX
CC The invention relates to an isolated LGR6 (large G protein-coupled
CC receptor) nucleic acid molecule comprising the mouse and human cDNA
CC sequences appearing as ADN02239, ADN02241, ADN02242, ADN02244, ADN02245,
CC ADN02247, ADN02248 and ADN02250. Also included are a host cell or a non-
CC human mammalian host cell containing an LGR6 nucleic acid (and producing
CC LGR6), an isolated LGR6 polypeptide appearing as ADN02240, ADN02243,

CC ADN02246 and ADN02249, an antibody which selectively binds to LGR6, a
CC method for detecting the presence of LGR6 in a sample, a kit (comprising
CC a compound which selectively binds to LGR6, or hybridises to LGR6 nucleic
CC acid, and instructions for use), a method for detecting LGR6 nucleic acid
CC in a sample, a method for identifying a compound which binds to LGR6, a
CC method for modulating the activity of LGR6 and a method for identifying a
CC compound that modulates the activity of LGR6. The methods and
CC compositions of the present invention are useful for diagnosing and
CC treating large G-protein coupled receptor 6 (LGR6)-mediated or -related
CC disorders, such as heart failure, ischaemic heart disease, myocardial
CC infarction, hypertension, pericarditis, atherosclerosis, hepatic failure,
CC viral hepatitis, cancer, intracerebral haemorrhage, brain abscess,
CC Alzheimer's disease, Pick disease, Parkinson's disease, Huntington's
CC disease, amyotrophic lateral sclerosis, inflammatory bowel disease,
CC Crohn's disease, benign prostatic hypertrophy and systemic lupus
CC erythematosus. The present sequence is a partial human cDNA for LGR6.

XX
SQ Sequence 2486 BP; 455 A; 773 C; 692 G; 565 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 1-21e-258 Length: 2486
Score: 3305.00 Matches: 632
Percent Similarity: 99.84% Conservative: 0
Best Local Similarity: 99.84% Mismatches: 1
Query Match: 99.94% Indels: 0
DB: 11 Gaps: 0

US-10-664-667-5 (1-633) x ADN02242 (1-2486)

QY 1 AsnThrThrHisTyrArgGluSerTrpTyrAlaCysArgTyrArgSerGlyIleProGly 20
Db 2 AATACGACTCACTATAGGGAAGCTGGTACGCCTGCAGGTACCGTCCGGAATCCCGGG 61
QY 21 SerThrHisAlaSerValGluArgSerGlnGlyLeuSerLeuProAlaHisProAlaSer 40
Db 62 TCGACCCACGGCTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGTCACTCAGCCTCT 121
QY 41 LeuAlaAlaLeuAlaAlaSerAsnThrThrAlaSerGlyLysLeuGlu***AspThrPhe 60
Db 122 CTGTGCTGCCCTAGCGGCCTCCAAACACACCGCATCTGGGAAATTGGAGCTNGACACCTTC 181
QY 61 SerGlnLeuSerSerLeuGlnAlaLeuAspLeuSerTrpAsnAlaIleArgSerIleHis 80
Db 182 AGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCAC 241
QY 81 ProGluAlaPheSerThrLeuHisSerLeuValLysLeuAspLeuThrAspAsnGlnLeu 100
Db 242 CCTGAGGCCTTCTCCACCCGTCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTG 301
QY 101 ThrThrLeuProLeuAlaGlyLeuGlyLeuMetHisLeuLysLeuLysGlyAsnLeu 120
Db 302 ACCACACTGCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 361
QY 121 AlaLeuSerGlnAlaPheSerLysAspSerPheProLysLeuArgIleLeuGluValPro 140
Db 362 GCTCTCTCCCAGGCCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCT 421
QY 141 TyrAlaTyrGlnCysCysProTyrGlyMetCysAlaSerPhePheLysAlaSerGlyGln 160
Db 422 TATGCCTACCACTGCTGCTCCCTATGGGATGTGTCCAGCTTCTTCAAGGCCTCTGGGCAG 481
QY 161 TrpGluAlaGluAspLeuHisLeuAspAspGluGluSerSerLysArgProLeuGlyLeu 180
Db 482 TGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTCGGCCTC 541
QY 181 LeuAlaArgGlnAlaGluAsnHisTyrAspGlnAspLeuAspGluLeuGlnLeuMet 200
Db 542 CTTGCCAGACAAGCAGAGAACCACCTATGACCAGGACCTGGATGAGCTCCAGTGGAGATG 601
QY 201 GluAspSerLysProHisProSerValGlnCysSerProThrProGlyProPheLysPro 220
Db 602 GAGGACTCAAAGCCACACCCCACTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC 661

QY 221 CysGluTyrLeuPheGluSerTrpGlyIleArgLeuAlaValTrpAlaIleValLeuLeu 240
Db 662 TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGCCATCGGTGTGCTC 721
QY 241 SerValLeuCysAsnGlyLeuValLeuLeuThrValPheAlaGlyGlyProAlaProLeu 260
Db 722 TCCGTGCTCTGCAATGGACTGGTGTGCTGTCGCGGTGTTCGTGGCGGGCCTGCCCCCTG 781
QY 261 ProProValLysPheValValGlyAlaIleAlaGlyAlaAsnThrLeuThrGlyIleSer 280
Db 782 CCCCCGGTCAAGTTGTGTAGGTGCGATTGCAGGGCCAAACACCTTGACTGGCATTTCC 841
QY 281 CysGlyLeuLeuAlaSerValAspAlaLeuThrPheGlyGlnPheSerGluTyrGlyAla 300
Db 842 TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCC 901
QY 301 ArgTrpGluThrGlyLeuGlyCysArgAlaThrGlyPheLeuAlaValLeuGlySerGlu 320
Db 902 CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTGGAG 961
QY 321 AlaSerValLeuLeuLeuThrLeuAlaAlaValGlnCysSerValSerValSerCysVal 340
Db 962 GCATCGGTGCTGTGCTCACTCTGGCCGCGAGTCAGTGCAGCGTCTCCGTCCTCTGTGTC 1021
QY 341 ArgAlaTyrGlyLysSerProSerLeuGlySerValArgAlaGlyValLeuGlyCysLeu 360
Db 1022 CGGGCCTATGGGAAGTCCCCCTCCCTGGGAGCGGTTTCAGACAGGGGTCTTAGGCTGCCTG 1081
QY 361 AlaLeuAlaGlyLeuAlaAlaAlaLeuProLeuAlaSerValGlyGluTyrGlyAlaSer 380
Db 1082 GCACTGGCAGGGCTGGCCGCCGCACTGCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCC 1141
QY 381 ProLeuCysLeuProTyrAlaProProGluGlyGlnProAlaAlaLeuGlyPheThrVal 400
Db 1142 CCACCTCGCCTGCCCTACGCGCCACCTTGAGGCTCAGCCAGCAGCCCTGGGCTTACCCTG 1201
QY 401 AlaLeuValMetMetAsnSerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeu 420
Db 1202 GCCCTGGTGATGATGAACCTCCTTCTGTTTCCGTGCTGTCGCGGTGCTATCAAACTG 1261
QY 421 TyrCysAspLeuProArgGlyAspPheGluAlaValTrpAspCysAlaMetValArgHis 440
Db 1262 TACTGTGACCTGCCGCGGGCGACTTTTGAGCCGTGTGGACTCGGCCCATGGTGAGGCAC 1321
QY 441 ValAlaTrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPhe 460
Db 1322 GTGGCCTGGCTCATCTTCGCAGACGGGCTCTCTACTGTCCCCTGGCCTTCTTCAGCTTC 1381
QY 461 AlaSerMetLeuGlyLeuPheProValThrProGluAlaValLysSerValLeuLeuVal 480
Db 1382 GCCTCCATGTCTGGGCCTCTTCCCTGTACGCCCGAGGCCGTCAAAGTCTGTCTGTGGTG 1441
QY 481 ValLeuProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPhe 500
Db 1442 GTGCTGCCCTGCTGCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCACTTC 1501
QY 501 ArgAspAspLeuArgArgLeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAla 520
Db 1502 CGGGATGACCTTCGGGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT 1561
QY 521 AlaAlaGlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuValAlaPheSer 540
Db 1562 GCGGCCGGGGAGCTGGAGAAGACTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT 1621
QY 541 AspValAspLeuIleLeuGluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyr 560
Db 1622 GATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGCGGGCCCCCTGGGCTGGAGACCTAT 1681
QY 561 GlyPheProSerValThrLeuIleSerCysGlnGlnProGlyAlaProArgLeuGluGly 580
Db 1682 GGCTTCCCCCTCAGTGACCCCTCATCTCCTGTGTCAGCAGCCAGGGGCCCCAGGCTGGAGGGC 1741
QY 581 SerHisCysValGluProGluGlyAsnHisPheGlyAsnProGlnProSerMetAspGly 600

Db 662 TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCGTGGCGTGTGGGCCATCGTGTGCTC 721

Qy 241 SerValIleuCysAsnGlyLeuValLeuLeuThrValPheAlaGlyGlyProAlaProLeu 260

Db 722 TCCGTGCTCTGCAATGGACTGGTGTCTGACCGTGTTCGTGGCGGCTGCCCCCTG 781

Qy 261 ProProValLysPheValValGlyAlaIleAlaGlyAlaAsnThrLeuThrGlyIleSer 280

Db 782 CCCCCGGTCAAGTTTGTGTAGGTGCGATTGCAGGGCGCAACACCTTGACTGGCATTTCC 841

Qy 281 CysGlyLeuLeuAlaSerValAspAlaLeuThrPheGlyGlnPheSerGluTyrGlyAla 300

Db 842 TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAAGTTCTCTGAGTACGGAGCC 901

Qy 301 ArgTrpGluThrGlyLeuGlyCysArgAlaThrGlyPheLeuAlaValLeuGlySerGlu 320

Db 902 CGCTGGGAGACGGGGCTAGGCTGCCGGCCACTGGCTTCCTGGCAGTACTTGGGTGGAG 961

Qy 321 AlaSerValLeuLeuThrLeuAlaAlaValGlnCysSerValSerValSerCysVal 340

Db 962 GCATCGGTGTCTGCTCACTCTGGCCGCACTGCAGTGCAGTGCAGCGTCTCCGTCTCTGTGTC 1021

Qy 341 ArgAlaTyrGlyLysSerProSerLeuGlySerValArgAlaGlyValLeuGlyCysLeu 360

Db 1022 CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCTTAGSGTGCCTG 1081

Qy 361 AlaLeuAlaGlyLeuAlaAlaLeuProLeuAlaSerValGlyGluTyrGlyAlaSer 380

Db 1082 GCACTGGCAGGGCTGGCCCGCACTGCCCCCTGGCCTCAGTGGGAGAATACGGGCGCTCC 1141

Qy 381 ProLeuCysLeuProTyrAlaProProGluGlyGlnProAlaAlaLeuGlyPheThrVal 400

Db 1142 CCACTCTGCCTGCCCTACGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTG 1201

Qy 401 AlaLeuValMetMetAsnSerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeu 420

Db 1202 GCCGTGGTGATGATGAACCTCTCTGTTCCCTGTCGTGGCCGGTGCCTACATCAAACTG 1261

Qy 421 TyrCysAspLeuProArgGlyAspPheGluAlaValTrpAspCysAlaMetValArgHis 440

Db 1262 TACTGTGACCTGCCCGGGGCGACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGCAC 1321

Qy 441 ValAlaTrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPhe 460

Db 1322 GTGGCCTGGCTCATCTTCGAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTC 1381

Qy 461 AlaSerMetLeuGlyLeuPheProValThrProGluAlaValLysSerValLeuVal 480

Db 1382 GCCTCCATGTGGGCCTCTTCCCTGTCTACGCCCGAGCGCGTCAAGTCTGTCTGTCTGGTG 1441

Qy 481 ValLeuProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPhe 500

Db 1442 GTGCTGCCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCACTTC 1501

Qy 501 ArgAspAspLeuArgArgLeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAla 520

Db 1502 CGGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCTATGCT 1561

Qy 521 AlaAlaGlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuValAlaPheSer 540

Db 1562 CGGCGCGGGAGCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT 1621

Qy 541 AspValAspLeuIleLeuGluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyr 560

Db 1622 GATGTGGATCTCATTTCTGAAGCTTCTGAAGCTGGGCGGCCCCCTGGGCTGGAGACCTAT 1681

Qy 561 GlyPheProSerValThrIleIleSerCysGlnGlnProGlyAlaProArgLeuGluGly 580

Db 1682 GGCTTCCCCCTCAGTGACCCCTCATCTCCTGTCTCAGCAGCAGGGGCCCCCAGGCTGGAGGC 1741

Qy 581 SerHisCysValGluProGluGlyAsnHisPheGlyAsnProGlnProSerMetAspGly 600

Db 1742 AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCCAACCCCTCCATGGATGGA 1801

Qy 601 GluLeuLeuLeuArgAlaGluGlySerThrProAlaGlyGlyLeuSerGlyGlyGly 620

Db 1802 GAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGTGGC 1861

Qy 621 GlyPheGlnProSerGlyLeuAlaPheAlaSerHisVal 633

Db 1862 GGCTTTCAGCCCTCTGGCTTGGCCTTGGCCTTTCGCTTCACACGTG 1900

RESULT 7

AAF98722 AAF98722 standard; DNA; 2322 BP.

XX AAF98722;

XX 02-JUL-2001 (first entry)

XX Human late stage ovarian tumour polynucleotide marker 37.

XX Human; ovarian cancer; identification; detection; characterisation; tumour; kinase; marker; cytostatic; antisense gene therapy; ds.

OS Homo sapiens.

XX WO200118542-A2.

XX 15-MAR-2001.

PF 01-SEP-2000; 2000WO-US024199.

XX 03-SEP-1999; 99US-0152547P.

PR 16-MAR-2000; 2000US-0190347P.

PR 21-MAR-2000; 2000US-0191321P.

PR 31-MAY-2000; 2000US-0208382P.

PR 20-JUL-2000; 2000US-00220467.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Thompson P, Lillie J;

XX WPI; 2001-211428/21.

XX Detection, assessment, prevention and therapy of ovarian cancer, comprises detecting changes in the expression of a variety of markers.

PS Claim 1; Page 1188-1189; 1198pp; English.

XX The present invention describes a method for assessing whether a patient is afflicted with ovarian cancer by comparing: (1) the expression of a marker (I) (see AAF98594 to AAF98730), in a patient sample; and (2) the normal level of expression of (I) in a control non-ovarian cancer sample, where a significant difference between the level of expression in (a) and (b) is an indication that the patient is afflicted with ovarian cancer. (I) have cytostatic activities and can be used in antisense gene therapy. The method, compositions and kits from the present invention can be used for: (1) assessing and treating ovarian cancer; (2) making isolated hybridoma, which produces an antibody useful for ovarian cancer assessment; and (3) inhibiting ovarian cancer in a patient. AAF98573 to AAF98593 represent human kinase marker primers and probes which are used in the exemplification of the present invention

SQ Sequence 2322 BP; 407 A; 733 C; 652 G; 530 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.46e-246 Length: 2322

Score: 3150.00 Matches: 609

Percent Similarity: 99.84% Conservative: 1

Best Local Similarity: 99.67% Mismatches: 1

Query Match: 99.25% Indels: 1

DB: 5 Gaps: 0

US-10-664-667-5 (1-633) x AAF98722 (1-2322)

Qy 23 HisAlaSerValGluArgSerGlnGlyLeuSerLeuProAlaHisProAlaSerLeuAla 42
Db 2 CACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCTCTTGCT 61
Qy 43 AlaLeuAlaAlaSerAsnThrThrAlaSerGlyLysLeuGlu***AspThrPheSerGln 62
Db 62 GCCCTAGCGGCCTCCAAACACACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAG 120
Qy 63 LeuSerSerLeuGlnAlaLeuAspLeuSerTrpAsnAlaIleArgSerIleHisProGlu 82
Db 121 CTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAG 180
Qy 83 AlaPheSerThrLeuHisSerLeuValLysLeuAspLeuThrAspAsnGlnLeuThrThr 102
Db 181 GCCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACACACAACCCAGCTGACCACA 240
Qy 103 LeuProLeuAlaGlyLeuGlyGlyLeuMetHisLeuLysLeuLysGlyAsnLeuAlaLeu 122
Db 241 CTGCCCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTC 300
Qy 123 SerGlnAlaPheSerLysAspSerPheProLysLeuArgIleLeuGluValProTyrAla 142
Db 301 TCCCAGGCTTCTCCAAGGACAGATTCCCAAAACTGAGGATCTTGAAGGTGCCTTATGCC 360
Qy 143 TyrGlnCysCysProTyrGlyMetCysAlaSerPhePheLysAlaSerGlyGlnTrpGlu 162
Db 361 TACCAGTGTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCTCTGGGCAGTGGGAG 420
Qy 163 AlaGluAspLeuHisLeuAspAspGluGluSerLysArgProLeuGlyLeuLeuAla 182
Db 421 GCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGCCTCCTTGCC 480
Qy 183 ArgGlnAlaGluAsnHisTyrAspGlnAspLeuAspGluLeuGlnLeuGluMetGluAsp 202
Db 481 AGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGAC 540
Qy 203 SerLysProHisProSerValGlnCysSerProThrProGlyProPheLysProCysGlu 222
Db 541 TCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGGCCCTTCAAGCCCTGTGAG 600
Qy 223 TyrLeuPheGluSerTrpGlyIleArgLeuAlaValTrpAlaIleValLeuLeuSerVal 242
Db 601 TACCTCTTTGAAAGCTGGGCGCATCCGCTGGCCGTGTGGCCATCGTGTGCTCTCCGTG 660
Qy 243 LeuCysAsnGlyLeuValLeuLeuThrValPheAlaGlyGlyProAlaProLeuProPro 262
Db 661 CTCTGCAATGGACTGGTGTCTGTCACCGTGTTCGCTGGCGGCGCTGCCCCCTGCCCCCG 720
Qy 263 ValLysPheValValGlyAlaIleAlaGlyAlaAsnThrLeuThrGlyIleSerCysGly 282
Db 721 GTCAAGTTGTGGTAGGTGCGATTGCGAGGGCGCCAAACACCTTGACTGGCATTTCTGTGGC 780
Qy 283 LeuLeuAlaSerValAspAlaLeuThrPheGlyGlnPheSerGluTyrGlyAlaArgTrp 302
Db 781 CTTCTAGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGG 840
Qy 303 GluThrGlyLeuGlyCysArgAlaThrGlyPheLeuAlaValLeuGlySerGluAlaSer 322
Db 841 GAGACGGGGCTAGGCTGCCGGCCACTGGCTTCTTGGCAGTACTTGGGTCGGAGGCATCG 900
Qy 323 ValLeuLeuLeuThrLeuAlaAlaValGlnCysSerValSerValSerCysValArgAla 342
Db 901 GTGCTGTGCTCACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCC 960
Qy 343 TyrGlyLysSerProSerLeuGlySerValArgAlaGlyValLeuGlyCysLeuAlaLeu 362
Db 961 TATGGGAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTG 1020
Qy 363 AlaGlyLeuAlaAlaAlaLeuProLeuAlaSerValGlyGluTyrGlyAlaSerProLeu 382
Db 1021 GCAGGGCTGGCCCGCCACTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCTTCCCCACTC 1080
Qy 383 CysLeuProTyrAlaProProGluGlyGlnProAlaAlaLeuGlyPheThrValAlaLeu 402

Db 1081 TGCTGCCCCTACGCGCCACCTGAGGGTTCAGCCAGCAGCCCTGGGCTTACCGTGGCCCTG 1140
Qy 403 ValMetMetAsnSerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeuTyrCys 422
Db 1141 GTGATGATGAACCTCCTTCTGTCTTCTGGTCTGTGGCCGGTGCTACATCAAACTGTACTGT 1200
Qy 423 AspLeuProArgGlyAspPheGluAlaValTrpAspCysAlaMetValArgHisValAla 442
Db 1201 GACCTGCCGCGGGCGACATTGAGGCCGTGTGGGACTGCGCATGGTGAGGCACGTGGCC 1260
Qy 443 TrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPheAlaSer 462
Db 1261 TGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCCGTGGCCTTCCTCAGCTTCGCCTCC 1320
Qy 463 MetLeuGlyLeuPheProValThrProGluAlaValLysSerValLeuLeuValValLeu 482
Db 1321 ATGCTGGGCCTCTTCCCTGTACGCCCGAGGCCGTCAAAGTCTGTCTGCTGCTGGTGTGCTG 1380
Qy 483 ProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPheArgAsp 502
Db 1381 CCCTGCTGCCTGCCTCAACCCACTGCTGTACTGCTCTTCAACCCCCCACTTCCGGGAT 1440
Qy 503 AspLeuArgArgLeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAlaAlaAla 522
Db 1441 GACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGSCCCTAGCCTATGCTGCGGCC 1500
Qy 523 GlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuValAlaPheSerAspVal 542
Db 1501 GGGGAGCTGGAGAAAGAGCTCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTG 1560
Qy 543 AspLeuIleLeuGluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyrGlyPhe 562
Db 1561 GATCTCATTTCTGGAAGCTTCTGAAGCTGGCGGCCCCCTGGGCTGGAGACCTATGGCTTC 1620
Qy 563 ProSerValThrLeuIleSerCysGlnGlnProGlyAlaProArgLeuGluGlySerHis 582
Db 1621 CCCTCAGTGACCTCATCTCTGTTCAGCAGCCAGGGGCCCCAGGCTGGAGGGCAGCCAT 1680
Qy 583 CysValGluProGluGlyAsnHisPheGlyAsnProGlnProSerMetAspGlyGluLeu 602
Db 1681 TGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTG 1740
Qy 603 LeuLeuArgAlaGluGlySerThrProAlaGlyGlyLeuSerGlyGlyGlyPhe 622
Db 1741 CTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGTGGCGGCTTT 1800
Qy 623 GlnProSerGlyLeuAlaPheAlaSerHisVal 633
Db 1801 CAGCCCTCTGGCTTGGCCTTTGCTTACACAGTG 1833

RESULT 8

ADQ76775

ID ADQ76775 standard; DNA; 3451 BP.

XX AC ADQ76775;

XX DT 07-OCT-2004 (first entry)

XX DE Human LGR6 splice variant LGR6.2 nucleotide sequence.

XX KW Human; leucine-rich repeat-containing G-protein coupled receptor;

XX KW receptor; LGR6.2; cytosstatic; immunomodulator; muscular-gen.;

XX KW gynaecological; antiinfertility; endocrine-gen.; anabolic; hypertensive;

XX KW vulnery; dermatological; gene therapy; gene; ds.

OS Homo sapiens.

XX PH Key Location/Qualifiers

FT CDS 47..1093

FT /*tag= b

FT /product= "Human LGR6.2"

FT sig_peptide 47..103

```
FT mat_peptide /*tag= a
FT 104..1090
FT /*tag= c
XX
PN WO2004058818-A2.
XX
PD 15-JUL-2004.
XX
PF 23-DEC-2003; 2003WO-EP051091.
XX
PR 26-DEC-2002; 2002US-0436001P.
XX
PA (ISTF ) APS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Muda M;
XX
DR WPI; 2004-534126/51.
XX
PT Novel isolated leucine-rich repeat-containing G-protein coupled receptor-
PT 6 splicing variant 1 and 2 polypeptides, useful for treating or
PT preventing endometriosis, female or male infertility, Addison's disease,
PT Cushing's disease, cancers.
XX
PS Claim 1; SEQ ID NO 4; 85pp; English.
XX
CC The present nucleotide sequence encodes human LGR6.2, a novel splice
CC variant of leucine-rich repeat-containing G-protein coupled receptor 6
CC (LGR6-SV). It was initially identified as an expressed sequence tag
CC clone. The LGR6.2 coding sequence consists of the same exons present in
CC another splice variant, LGR6.1 ADQ76773, plus an extended exon that
CC introduces a stop codon resulting in truncation of the coding sequence,
CC removing the transmembrane domains and the cytoplasmic C-terminal domain
CC of LGR6.1. Thus, LGR6.2 is a secreted, probably soluble, N-terminal
CC extracellular domain version of LGR6.1 and probably functions as an
CC antagonist of the LGR6.1 signalling pathway. Tissue distribution studies
CC indicate a high level of expression in ovary and pituitary tissues. The N
CC -terminal extracellular domain of LGR6.2 can be used as an antagonist of
CC the LGR6 signalling pathway. The invention provides LGR6.1 and LGR6.2
CC polypeptides and nucleic acids, as well as selective binding agents,
CC vectors, host cells and methods for producing LGR6-SV polypeptides. Also
CC provided are pharmaceutical compositions and methods for the diagnosis,
CC treatment, amelioration and/or prevention of diseases, disorders and
CC conditions associated with LGR6-SV polypeptides. LGR6-SV polypeptides and
CC nucleic acids can be used for diagnosing or treating: cancers such as
CC hepatocellular carcinoma, adenomatous polyposis, malignant transformation
CC of epithelial cells, colorectal cancer, breast cancer, ovarian cancer,
CC etc.; cachexia and muscular dystrophy; miscarriage, endometriosis,
CC uterine cancer, and female infertility; Cushing's disease and Addison's
CC disease; male infertility and testicular cancer; leukaemia; and diseases
CC and conditions affecting the kidney. They may also be useful for treating
CC diseases and conditions involving cell proliferation and differentiation,
CC such as tissue damage and degeneration, ageing, wound healing, cancer,
CC hyperplasia and hypertrophy.
XX
SQ Sequence 3451 BP; 728 A; 1063 C; 920 G; 740 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.94e-245 Length: 3451
Score: 3140.00 Matches: 611
Percent Similarity: 97.61% Conservative: 1
Best Local Similarity: 97.45% Mismatches: 11
Query Match: 94.95% Indels: 5
DB: 12 Gaps: 1

US-10-664-667-5 (1-633) x ADQ76775 (1-3451)

QY 7 GluSerTrpTyrAlaCysArgTyrArgSerGlyTleProGlySerThrHisAlaSerVal 26
Db 1027 GAGAAAGTGGGGGCTCTACTTTCTTCTCCAGTGTCTGGGG-----GGCATG 1074
QY 27 GluArgSerGlnGlyLeuSerLeuProAlaHisProAlaSerLeuAlaLeuAlaAla 46
Db 1075 GAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCTCTTGCTGCCCTAGCGGCC 1134
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QY 47 SerAsnThrThrAlaSerGlyLysLeuGlu***AspThrPheSerGlnLeuSerSerLeu 66
Db 1135 TCCAACACAAACCGCATCTGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAGCTCCCTG 1193
QY 67 GlnAlaLeuAspLeuSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThr 86
Db 1194 CAAGCCCTGGATCTTAGCTGGAAAGCCCATCCGGTCCATCCACCTGAGGCCCTTCTCCACC 1253
QY 87 LeuHisSerLeuValLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAla 106
Db 1254 CTGCACTCCCTGGTCAAGCTGGACCTGACACCAACACAGCTGACCACTGCCCCCTGGCT 1313
QY 107 GlyLeuGlyGlyLeuMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPhe 126
Db 1314 GGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCCCTTC 1373
QY 127 SerLysAspSerPheProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCys 146
Db 1374 TCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCAGTGCTGT 1433
QY 147 ProTyrGlyMetCysAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeu 166
Db 1434 CCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGCTGAAGACCTT 1493
QY 167 HisLeuAspAspGluGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGlu 186
Db 1494 CACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCTCCTTGCCAGACAAGCAGAG 1553
QY 187 AsnHistyrAspGlnAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHis 206
Db 1554 AACCACATATGACAGGACCTGGATGAGTCCAGCTGGAGATGGAGACTCAAAGCCACAC 1613
QY 207 ProSerValGlnCysSerProThrProGlyProPheLysProCysGluTyrLeuPheGlu 226
Db 1614 CCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAA 1673
QY 227 SerTrpGlyIleArgLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGly 246
Db 1674 AGCTGGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTTGCAATGGA 1733
QY 247 LeuValLeuLeuThrValPheAlaGlyGlyProAlaProLeuProProValLysPheVal 266
Db 1734 CTGGTGTCTGTACCGTGTTCGCTGGCGGCTGCCCCCTGCCCCCGGTCAAGTTTGTG 1793
QY 267 ValGlyAlaIleAlaGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSer 286
Db 1794 GTAGGTGCGATTGCAGGCGCCAACACCTTGACTGGCATTTCTGTGGCCTTCTAGCCTCA 1853
QY 287 ValAspAlaLeuThrPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeu 306
Db 1854 GTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTA 1913
QY 307 GlyCysArgAlaThrGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeu 326
Db 1914 GGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGTCCGAGGCATCGGTGCTGCTGCTC 1973
QY 327 ThrLeuAlaAlaValGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSer 346
Db 1974 ACTCTGGCCCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCCTATGGGAAGTCC 2033
QY 347 ProSerLeuGlySerValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAla 366
Db 2034 CCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGGCACCTGGCAGGGCTGGCC 2093
QY 367 AlaAlaLeuProLeuAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyr 386
Db 2094 GCGGCACTGCCCTGGCCTTCAGTGGGAGATAACGGGGCCTCCCCACTCTGCCTGCCCTAC 2153
QY 387 AlaProProGluGlyGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsn 406
Db 2154 GCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAAC 2213
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QY 407 SerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArg 426
Db 2214 TCCTTCTGTTCTGTCGTGGCCGGTGCCTACATCAAACGTGACTGTGACCTGCCGCG 2273
QY 427 GlyAspPheGluAlaValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePhe 446
Db 2274 GCGAGCTTTGAGCCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCTGGCTCATCTTC 2333
QY 447 AlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeu 466
Db 2334 GCAGACGGGCTCCTCTACTGTCCCGTGGCTTCCTCAGCTTCGCCCTCCATGCTGGGCCTC 2393
QY 467 PheProValThrProGluAlaValLysSerValLeuLeuValValLeuProLeuProAla 486
Db 2394 TTCCCTGTACGCCCGGAGCCCGTCAAGTCTGTCTGCTGGTGGTGTGCCCTGCCCTGCC 2453
QY 487 CysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPheArgAspLeuArgArg 506
Db 2454 TGCCTCAACCCACTGCTGTACTGCTCTTCAACCCCACTTCGGGATGACCTTCGGCGG 2513
QY 507 LeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAlaAlaGlyGluLeuGlu 526
Db 2514 CTTCGGCCCGCGCAGGGACTCAGGGCCCTAGCCTATGCTGCGCGCGGAGCTGGAG 2573
QY 527 LysSerSerCysAspSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeu 546
Db 2574 AAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATCTG 2633
QY 547 GluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThr 566
Db 2634 GAAGCTTCTGAAGCTGGCGGCCCTGGCTGGAGACCTATGGCTTCCCCTCAGTGACC 2693
QY 567 LeuIleSerCysGlnGlnProGlyAlaProArgLeuGluGlySerHisCysValGluPro 586
Db 2694 CTCATCTCTGTGACAGCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCA 2753
QY 587 GluGlyAsnHisPheGlyAsnProGlnProSerMetAspGlyGluLeuLeuAlaGala 606
Db 2754 GAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGTGAGGGCA 2813
QY 607 GluGlySerThrProAlaGlyGlyLeuSerGlyGlyGlyPheGlnProSerGly 626
Db 2814 GAGGGATACGCCCAGCAGGTGGAGGCTGTGAGGGGTGGCGGCTTTCAGCCCTCTGGC 2873

QY 627 LeuAlaPheAlaSerHisVal 633
Db 2874 TTGGCCTTTGCTTCACACGTG 2894

RESULT 9
AAI67925
ID AAI67925 standard; cDNA; 2208 BP.

XX AAI67925;

DT 13-MAR-2002 (first entry)

DE Human LGR6 polypeptide coding sequence.

XX Large G-protein coupled receptor 6; LGR6; GPCR; immunomodulator;
KW anti-HIV; cytostatic; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; neuroleptic; antidepressant; tranquilizer; antimigraine;
KW osteopathic; antiarteriosclerotic; vasotropic; hypotensive; cardiac;
KW antiarrhythmic; anorectic; gene therapy; human; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1. .2208
FT /*tag= a
FT /product= "LGR6 polypeptide"

XX WO200185768-A2.

XX

PD 15-NOV-2001.
XX
PF 08-MAY-2001; 2001WO-US015002.
XX
PR 08-MAY-2000; 2000US-00566588.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gu W;
XX
DR WPI; 2002-055584/07.
DR P-PSDB; AAG66140.
XX
PT Novel isolated large G-protein coupled receptor 6 polypeptide, useful for
PT diagnosing and treating weight disorder, metabolic disorder, central
PT nervous system disorder, endocrine disorder and cardiovascular disorder.
XX
PS Claim 2; Fig 8; 198pp; English.
XX

CC The invention provides isolated large G-protein coupled receptor 6 (LGR6)
CC polypeptides and polynucleotides encoding them. The LGR6 polypeptides and
CC polynucleotides are useful as targets for developing modulating agents
CC that regulate a variety of cellular process, e.g. neural and endocrine
CC processes, as well as thermogenesis. They are useful for developing novel
CC diagnostic and therapeutic agents for LGR6 associated disorders such as
CC weight disorders (anorexia, obesity), eating disorders, acquired
CC immunodeficiency syndrome (AIDS)-related wasting, cancer-related wasting,
CC metabolic disorders, central nervous system disorders (e.g. Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, Gilles de la
CC Tourette's syndrome, multiple sclerosis, amyotrophic lateral sclerosis,
CC epilepsy, Jakob-Creutzfeldt disease, depression, schizophrenia,
CC obsessive-compulsive disorder, anxiety, panic disorder, migraine),
CC endocrine disorders (hypo and hyperthyroidism, dwarfism, gigantism,
CC acromegaly), and cardiovascular disorders (atherosclerosis, restenosis,
CC hypertension, myocardial infarction, arrhythmia). The LGR6 polypeptides,
CC polynucleotides and antibodies are useful in screening assays, detection
CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials and pharmacogenomics), and in methods of
CC treatment (e.g. therapeutic and prophylactic). The present sequence
CC represents a human LGR6 polypeptide coding sequence

XX
SQ Sequence 2208 BP; 396 A; 710 C; 631 G; 471 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.31e-237 Length: 2208
Score: 3045.50 Matches: 602
Percent Similarity: 92.61% Conservative: 12
Best Local Similarity: 90.80% Mismatches: 19
Query Match: 92.09% Indels: 32
DB: 6 Gaps: 4

US-10-664-667-5 (1-633) x AAI67925 (1-2208)

QY 1 AenThrThrHisTyr-----
Db 224 AACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAG 283
QY 6 ---ArgGluSerTrpTyrAla-----CysArgTyrArg 15
Db 284 GCACCACCAGCCTGGAGATCCTGACCCCTGACCCCGCAGGCATCCGGCTGCTCCCATCGG 343
QY 16 -----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---G1 31
Db 344 GGATGTGCCAACAGCTGCCAGGCTCCGAGTCTCTGGAACTGTCTCACAATCAAATTGAGG 403
QY yLeuSerLeuProAlaHisProAlaSerLeuAlaAlaLeuAlaAlaSerAsnThrThrAl 51
Db 404 AGCTGCCCCAGCCTGCACAGGTGTCAGAAATTGGAGGAAA-TCGGCCTCCAACACACCGC 462
QY 51 aSerGlyLysLeuGlu***AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe 71
Db 463 ATCTGGGAAATTTGGAGCT-GACACCTTCAGCCAGCTCCCTGAGCTCCCTGCAAGCCCTGGATCT 521

QY	71	uSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa	91	431	aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe	451
Db	522	TAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCCTTCTCACCCCTGCACTCCCTGGT	581	1602	CGTGTGGACTGCGCATGGTGAGGCACGTGGCTGGCTCATCTTCGACAGCGGCTCCT	1661
QY	91	lLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyGlyLe	111	451	uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr	471
Db	582	CAAGCTGGACCTGACAGACAACACAGTGACCACACTGCCCTGGCTGGACTTGGGGGCTT	641	1662	CTACTGTCCCGTGGCCTTCTCAGCTTCGCCCTCAGTGTGGCCTCTTCCCTGTACGCC	1721
QY	111	uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh	131	471	oGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe	491
Db	642	GATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCCTTCTCCAAGGACAGTTT	701	1722	CGAGGCCGTCAAGTCTGTCTGTGGTGGTGTGCCCTGCCTGCCTGCCTCAACCCACT	1781
QY	131	eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy	151	491	uLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgLeuArgProArgAl	511
Db	702	CCCAAACTGAGGATCCTGGAGGTGCTTATGCCCTACCACTGCTGCCCTATGGGATGTG	761	1782	GCTGTACCTGCTCTTCAACCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCGCGC	1841
QY	151	sAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspAspGl	171	511	aGlyAspSerGlyProLeuAlaTyrAlaAlaAlaGlyLeuGluLeuGlyLysSerCysAs	531
Db	762	TGCCAGCTTCTTCAAGGCCCTCTGGCAGTGGAGGCTGAAGACCTTCACCTTGATGATGA	821	1842	AGGGGACTCAGGGCCCTAGCCTATGCTGGCGGGGAGCTGGAGAAGAGCTCTGTGA	1901
QY	171	uGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspGl	191	531	pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl	551
Db	822	GGAGTCTTCAAAAAGGCCCTTGGGCCCTCCTTGCCAGACAAGCAGAGAACCACCTATGACCA	881	1902	TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTTCTGGAAGCTTCTGAAGC	1961
QY	191	nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy	211	551	aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysGl	571
Db	882	GGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCACTGTCCAGTG	941	1962	TGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCCCTCAGTGACCCCTCATCTCCTGTCA	2021
QY	211	sSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGlyIleAr	231	571	nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisPh	591
Db	942	TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGSCATCG	1001	2022	GCAGCCAGGGGCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTT	2081
QY	231	gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh	251	591	eGlyAsnProGlnProSerMetAspGlyGlyLeuLeuLeuArgAlaGlySerThrPr	611
Db	1002	CCTGGCGGTGGGCCATCGTTGTCTCCGTGCTCTGCAATGGACTGGTGTGTGAC	1061	2082	TGGGAACCCCAACCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGATCTACGCC	2141
QY	251	rValPheAlaGlyGlyProAlaProLeuProProValLysPheValValGlyAlaIleAl	271	611	oAlaGlyGlyGlyLeuSerGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSe	631
Db	1062	CGTGTGCTGGCGGCCCTGCCCCCTGCCCCCTGCAAGTTTGTGTAGGTGCGATTGC	1121	2142	AGCAGGTGGAGGCTTGTACAGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTGTCTTC	2201
QY	271	aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuTh	291	631	rHisVal	633
Db	1122	AGGCGCAACACACTTGACTGGCATTTCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGAC	1181	2202	ACACGTG	2208
QY	291	rPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaTh	311	RESULT 10		
Db	1182	CTTTTGGTCAGTTCTCTGAGTACGAGCCCGCTGGGAGACGGGCTAGGCTGCCGGGCCAC	1241	ADN02247		
QY	311	rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa	331	ID	ADN02247	standard; cDNA; 2208 BP.
Db	1242	TGGCTTCTTGGCAGTACTTGGGTGGAGGCATCGGTGTGCTGTCTCCTGCTGCTGCTGCTG	1301	XX	ADN02247;	
QY	331	lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe	351	XX	17-JUN-2004	(first entry)
Db	1302	GCAGTGCAGCGTCTCCGTCTCCTGTGTCGGGCCCTATGGAAAGTCCCCCTCCCTGGGCAG	1361	DE	Human	partial large G protein-coupled receptor, LGR6, CDS #2.
QY	351	rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe	371	XX	Human; ss;	large G protein-coupled receptor 6; LGR6; heart failure;
Db	1362	CGTTCGAGCAGGGGTCCCTAGGCTGCCTGGCAGTGGCAGGGCTGGCCGCACTGCCCTT	1421	KW	ischaemic heart disease;	myocardial infarction; hypertension;
QY	371	uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluGl	391	KW	pericarditis;	atherosclerosis; hepatic failure; viral hepatitis; cancer;
Db	1422	GGCCTCAGTGGGAGAAATACGGGGCTTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGGG	1481	KW	intracerebral haemorrhage;	brain abscess; Alzheimer's disease;
QY	391	yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe	411	KW	Pick disease;	Parkinson's disease; Huntington's disease;
Db	1482	TCAGCCAGCAGCCCTTGGGCTTACCGTGGCCCTGGTGATGATGAACCTCTTCTTCTCCT	1541	KW	amyotrophic lateral sclerosis;	inflammatory bowel disease;
QY	411	uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluAl	431	KW	Crohn's disease;	benign prostatic hypertrophy;
Db	1542	GGTGTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCGCGGGCGGACTTTGAGGC	1601	XX	systemic lupus erythematosus.	
				XX	Homo sapiens.	
				XX	Key	Location/Qualifiers
				FT	CDS	1. .2208
				FT		/*tag= a
				FT		/partial
				FT		/note= "No start or stop codon shown"
				XX		/product= "partial LGR6"
				PN		US2003166047-A1.

XX 04-SEP-2003.
PD
XX PF 08-MAY-2001; 2001US-00851595.
XX 06-MAY-1999; 99US-0132896P.
PR 08-MAY-2000; 2000US-00566588.
XX (MILL-) MILLENNIUM PHARM INC.
PA Gu W;
XX WPI; 2003-898067/82.
DR P-PSDB; ADN02246.
XX
PT New isolated LGR6 nucleic acids and polypeptides, useful for diagnosing
PT and treating LGR6-mediated disorders, such as myocardial infarction,
PT hypertension, atherosclerosis, viral hepatitis, cancer and/or Alzheimer's
PT disease.
XX
PS Claim 1; SEQ ID NO 9; 145pp; English.
XX
CC The invention relates to an isolated LGR6 (large G protein-coupled
CC receptor) nucleic acid molecule comprising the mouse and human cDNA
CC sequences appearing as ADN02239, ADN02241, ADN02242, ADN02244, ADN02245,
CC ADN02247, ADN02248 and ADN02250. Also included are a host cell or a non-
CC human mammalian host cell containing an LGR6 nucleic acid (and producing
CC LGR6), an isolated LGR6 polypeptide appearing as ADN02240, ADN02243,
CC ADN02246 and ADN02249, an antibody which selectively binds to LGR6, a
CC method for detecting the presence of LGR6 in a sample, a kit (comprising
CC a compound which selectively binds to LGR6, or hybridises to LGR6 nucleic
CC acid, and instructions for use), a method for detecting LGR6 nucleic acid
CC in a sample, a method for identifying a compound which binds to LGR6, a
CC method for modulating the activity of LGR6 and a method for identifying a
CC compound that modulates the activity of LGR6. The methods and
CC compositions of the present invention are useful for diagnosing and
CC treating large G-protein coupled receptor 6 (LGR6)-mediated or -related
CC disorders, such as heart failure, ischaemic heart disease, myocardial
CC infarction, hypertension, pericarditis, atherosclerosis, hepatic failure,
CC viral hepatitis, cancer, intracerebral haemorrhage, brain abscess,
CC Alzheimer's disease, Pick disease, Parkinson's disease, Huntington's
CC disease, amyotrophic lateral sclerosis, inflammatory bowel disease,
CC Crohn's disease, benign prostatic hypertrophy and systemic lupus
CC erythematosus. The present sequence is a partial human CDS for LGR6.
XX
SQ Sequence 2208 BP; 396 A; 710 C; 631 G; 471 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.31e-237 Length: 2208
Score: 3045.50 Matches: 602
Percent Similarity: 92.61% Conservative: 12
Best Local Similarity: 90.80% Mismatches: 19
Query Match: 92.09% Indels: 32
DB: 11 Gaps: 4

US-10-664-667-5 (1-633) x ADN02247 (1-2208)

QY 1 AsnThrThrHisTyr----- 5
DB 224 AACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGAGTTTCCAGATCTCAAG 283
QY 6 ---ArgGluSerTrpTyrAla-----CysArgTyrArg 15
DB 284 GCACCACCAGCCTGGAGATCCTGACCCTGACCCGGCAGGATCCGGCTGCTCCCATCGG 343
QY 16 -----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---G1 31
DB 344 GGATGTGCCAACAGCTGCCAGGCTCCGAGTCTTGAACTGTCTCACAATCAAATTGAGG 403
QY 31 yLeuSerLeuProAlaHisProAlaSerLeuAlaAlaLeuAlaAlaSerAsnThrThrAl 51
DB 404 AGCTGCCAGCCTGCACAGGTGTCAGAAATTGGAGAAA-TCGGCCTCCAACAACCGC 462

QY 51 aSerGlyLysLeuGlu***AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe 71
DB 463 ATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCT 521
QY 71 uSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa 91
DB 522 TAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGGCTTCTCCACCCTGCACCTCCCTGGT 581
QY 91 lLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyLe 111
DB 582 CAAGCTGGACCTGACAGACAACACAGCTGACCACACTGCCCCCTGGCTGGACTTGGGGGCTT 641
QY 111 uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh 131
DB 642 GATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCCTTCTCCAAGGACAGTTT 701
QY 131 eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy 151
DB 702 CCCAAAACCTGAGGATCCTGGAGGTGCCTTATGCCCTACCAGTGCTGTCCCTATGGGATGTG 761
QY 151 sAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspAspGl 171
DB 762 TGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGTGAAGACCTTACCTTGTATGATGA 821
QY 171 uGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspGl 191
DB 822 GGAGTCTTCAAAAAGGCCCTGGGCCTCCTTGGCCAGACAAGCAGAGAACCACTATGACCA 881
QY 191 nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy 211
DB 882 GGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCAGTGTCCAGTG 941
QY 211 sSerProThrProGlyPropheLysProCysGluTyrLeuPheGluSerTyrGlyIleAr 231
DB 942 TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCG 1001
QY 231 gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh 251
DB 1002 CCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTGCAATGGACTGGTGTCTGTGAC 1061
QY 251 rValPheAlaGlyGlyProAlaProLeuProValLysPheValValGlyAlaIleAl 271
DB 1062 CGTGTTCGTGGCGGGCTGCCCCCTGCCCCCGGTCAAGTTTGTGTAGGTGCGATTGC 1121
QY 271 aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuTh 291
DB 1122 AGGCGCCAACACACCTTGACTGGCATTTCTCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGAC 1181
QY 291 rPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaTh 311
DB 1182 CTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGAGACGGGGCTAGGCTGCCGGGCCAC 1241
QY 311 rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa 331
DB 1242 TGGCTTCTTGGCAGTACTTGGGTGGAGGCATCGGTGCTGCTGTCTCACTCTGGCCGCGAGT 1301
QY 331 lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe 351
DB 1302 GCAGTGCAGCGTCTCCGTCTCTGTGTCCGGGCCCTATGGGAAGTCCCCCTCCCTGGGCAG 1361
QY 351 rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe 371
DB 1362 CGTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCCGCACTGCCCT 1421
QY 371 uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluGl 391
DB 1422 GGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCTGCCCTACGGCCACCTGAGGG 1481
QY 391 yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe 411
DB 1482 TCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGTGATGATGAACCTCCTTCTGTTCT 1541
QY 411 uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluAl 431

Db 1542 GGTGTCGGCGGTGCCTACATCAAACTGTA CTGTGACCTGCCGCGGGCGACTTTGAGGC 1601
Qy 431 aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe 451
Db 1602 CGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGCAGACGGGCTCCT 1661
Qy 451 uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr 471
Db 1662 CTACTGTCCCGTGGCCTTCCTCAGCTTCGCTCCATGCTGGGCCTCTTCCCTGTCAAGCC 1721
Qy 471 oGluAlaValLysSerValLeuValValLeuProLeuProAlaCysLeuAsnProLe 491
Db 1722 CGAGGCGGTCAAGTCTGTCTGTGGTGTGCTGCCCTGCCTGCCTCAACCCACT 1781
Qy 491 uLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgArgLeuArgProArgAl 511
Db 1782 GCTGTACCTGCTCTTCAACCCCACTTCGGGATGACCTTGGCGGCTTCGGCCCGCGGC 1841
Qy 511 aGlyAspSerGlyProLeuAlaTyrAlaAlaAlaGlyGluLeuGluLysSerSerCysAs 531
Db 1842 AGGGACTCAGGGCCCCTAGCCTATGCTGCGCGGGGAGCTGGAGAAGAGCTCCTGTGA 1901
Qy 531 pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl 551
Db 1902 TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTTCTGGAAGCTTCTGAAGC 1961
Qy 551 aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysGl 571
Db 1962 TGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCCTCAGTGACCTCATCTCTGTCA 2021
Qy 571 nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyValAsnHisPh 591
Db 2022 GCAGCCAGGGCCCCCAGGCTGGAGGCGAGCCATTGTGTAGAGCCAGAGGGGAACCACTT 2081
Qy 591 eGlyAsnProGlnProSerMetAspGlyGluLeuLeuLeuArgAlaGluGlySerThrPr 611
Db 2082 TGGAAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCTGAGGGCGAGAGGATCTAGGCC 2141
Qy 611 oAlaGlyGlyGlyLeuSerGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSe 631
Db 2142 AGCAGGTGGAGGCTTGTACGGGGGTGGCGGCTTTCAGGCCCTCTGGCTTGGCCTTGCTTC 2201
Qy 631 rHisVal 633
Db 2202 ACACGTG 2208

RESULT 11
ADK19412
ID ADK19412 standard; cDNA; 2208 BP.
XX
AC ADK19412;
XX
DT 17-JUN-2004 (first entry)
XX
DE ORF of partial cDNA encoding human LGR6 polypeptide #2.
XX
KW G-protein coupled receptor; GPCR; large G-protein coupled receptor 6;
KW LGR6; weight disorder; neural disorder; endocrine disorder;
KW cardiovascular disorder; anorectic; anabolic; immunomodulator;
KW neuroprotective; nootropic; antiparkinsonian; anti-HIV; anticonvulsant;
KW antithyroid; osteopathic; cardiant; vasotropic; hypotensive;
KW antiarteriosclerotic; antiarrhythmic; human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..2208
FT /tag= a
FT /partial
FT /product= "LGR6 polypeptide #2"
FT /note= "This sequence lacks both start and stop codons"
XX

PN US2004058377-A1.
XX
PD 25-MAR-2004.
XX
PF 18-SEP-2003; 2003US-00664667.
XX
PR 06-MAY-1999; 99US-0132896P.
PR 08-MAY-2000; 2000US-00566588.
PR 08-MAY-2001; 2001US-00851595.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gu W;
XX
DR WPI; 2004-268789/25.
DR P-PSDB; ADK19411.
XX
PT New large G-protein coupled receptor 6 nucleic acid molecules and
PT polypeptides, useful for diagnosing, preventing or treating diseases
PT associated with aberrant nucleic acid or protein activity, e.g. obesity,
PT anorexia or cachexia.
XX
PS Claim 2; SEQ ID NO 9; 145pp; English.
XX
CC The present invention relates to the isolation of novel members of the G-
CC protein coupled receptor (GPCR) family designated as large G-protein
CC coupled receptor 6 (LGR6), and the polynucleotide sequences encoding
CC them. The invention also discloses LGR6 fusion proteins, antigenic
CC peptides, anti-LGR6 antibodies, recombinant expression vectors, host
CC cells, and non-human transgenic animals in which an LGR6 gene has been
CC introduced or disrupted. The LGR6 polynucleotide sequences, polypeptide
CC sequences, and antibodies are useful for diagnosing, treating or
CC preventing diseases associated with aberrant LGR6 expression or activity,
CC such as weight disorders (e.g. obesity, anorexia nervosa or cachexia),
CC neural disorders (e.g. central nervous system disorder, including
CC Alzheimer's disease, Parkinson's disease), endocrine disorders (e.g.
CC schizophrenia and Huntington's disease), or cardiovascular
CC disorders (e.g. ischaemia-reperfusion injury, coronary artery disease,
CC myocardial infarction, arrhythmia, atherosclerosis, hypertension or
CC congestive heart failure). The LGR6 polynucleotide and polypeptide
CC sequences are also useful as targets for developing modulating agents
CC that regulate a variety of cellular processes, e.g. neural and endocrine
CC processes and thermogenesis. They can be used in screening assays (e.g.
CC chromosome mapping, tissue typing or in forensic biology), or in
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials or pharmacogenomics). The present sequence
CC encodes a human LGR6 polypeptide.
XX
SQ Sequence 2208 BP; 396 A; 710 C; 631 G; 471 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.31e-237 Length: 2208
Score: 3045.50 Matches: 602
Percent Similarity: 92.61% Conservative: 12
Best Local Similarity: 90.80% Mismatches: 19
Query Match: 92.09% Indels: 32
DB: 12 Gaps: 4
US-10-664-667-5 (1-633) x ADK19412 (1-2208)
Qy 1 AsnThrThrHisTyr-----CysArgTyrArg 15
Db 224 AACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTCCAGATCTCAAAG 283
Qy 6 ---ArgGluSerTrpTyrAla-----CysArgTyrArg 15
Db 284 GCACCACCAGCCTGGAGATCCTGACCTGACCCGCGCAGGCATCCGGCTGCTCCCATCGG 343
Qy 16 -----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---G1 31
Db 344 GGATGTGCCAACAGCTGCCAGGCTCCGAGTCTCGAACTGTCTCAACAATCAATTGAGG 403

XX WO200185768-A2.
PN
XX
PD 15-NOV-2001.
XX
XX 08-MAY-2001; 2001WO-US015002.
PF
XX 08-MAY-2000; 2000US-00566588.
PR
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX
XX Gu W;
PI
XX WPI; 2002-055584/07.
DR
DR P-PSDB; AAG66140.
XX
PT Novel isolated large G-protein coupled receptor 6 polypeptide, useful for
PT diagnosing and treating weight disorder, metabolic disorder, central
PT nervous system disorder, endocrine disorder and cardiovascular disorder.
XX
PS Claim 2; Fig 8; 198pp; English.
PS
XX The invention provides isolated large G-protein coupled receptor 6 (LGR6)
CC polypeptides and polynucleotides encoding them. The LGR6 polypeptides and
CC polynucleotides are useful as targets for developing modulating agents
CC that regulate a variety of cellular process, e.g. neural and endocrine
CC processes, as well as thermogenesis. They are useful for developing novel
CC diagnostic and therapeutic agents for LGR6 associated disorders such as
CC weight disorders (anorexia, obesity), eating disorders, acquired
CC immunodeficiency syndrome (AIDS)-related wasting, cancer-related wasting,
CC metabolic disorders, central nervous system disorders (e.g. Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, Gilles de la
CC Tourette's syndrome, multiple sclerosis, amyotrophic lateral sclerosis,
CC epilepsy, Jakob-Creutzfeldt disease, depression, schizophrenia,
CC obsessive-compulsive disorder, anxiety, panic disorder, migraine),
CC endocrine disorders (hypo and hyperthyroidism, dwarfism, gigantism,
CC acromegaly), and cardiovascular disorders (atherosclerosis, restenosis,
CC hypertension, myocardial infarction, arrhythmia). The LGR6 polypeptides,
CC polynucleotides and antibodies are useful in screening assays, detection
CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials and pharmacogenomics), and in methods of
CC treatment (e.g. therapeutic and prophylactic). The present sequence
CC represents a partial cDNA sequence of human LGR6 polypeptide
XX
SQ Sequence 2711 BP; 530 A; 837 C; 740 G; 604 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.73e-237 Length: 2711
Score: 3045.50 Matches: 602
Percent Similarity: 92.61% Conservative: 12
Best Local Similarity: 90.80% Mismatches: 19
Query Match: 92.09% Indels: 32
DB: 6 Gaps: 4

US-10-664-667-5 (1-633) x AAI67924 (1-2711)

QY 1 AsnThrThrHisTyr----- 5
DB 224 AACTCCACACACTATCTCTGAATGGTGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAG 283
QY 6 ---ArgGluSerTrpTyrAla-----CysArgTyrArg 15
DB 284 GCACCACCAGCCTGGAGATCCTGTACCTGACCCGCGCAGGCATCCGGCTGCTCCCATCGG 343
QY 16 -----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---G1 31
DB 344 GGATGTGCCAACAGCTGCCCGAGGCTCCGAGTCTCTGGAACGTGTCTCACAATCAATTGAGG 403
QY 31 yLeuSerLeuProAlaHisProAlaSerLeuAlaAlaLeuAlaAlaSerAsnThrThrAl 51
DB 404 AGCTGCCAGCCTGCACACAGGTGTCAGAAATTGGAGGAAA-TCGGCCTCCACACACACCGC 462

QY 51 aSerGlyLysLeuGlu***AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe 71
DB 463 ATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAGTCCCTGCAAGCCCTGGATCT 521
QY 71 uSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa 91
DB 522 TAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCTTCTCCACCCTGCACTCCCTGGT 581
QY 91 lLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyLe 111
DB 582 CAAGCTGGACCTGACAGACAACCAGCTGACCACACTGCCCTGGCTGGACTTGGGGCTT 641
QY 111 uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh 131
DB 642 GATGCATCTGAAGCTCAAAGGAAACCTTGCTCTCTCCAGGCCTTCTCCAAGGACAGTTT 701
QY 131 eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy 151
DB 702 CCCAAAACCTGAGGATCCTGGAGGTGCCTTATGCCTACCACTGCTGTCCCTATGGGATGTG 761
QY 151 sAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspG1 171
DB 762 TGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGCTGAAGACCTTCACTTGATGATGA 821
QY 171 uGluSerSerLysArgProLeuGlyLeuLeuAlaAargGlnAlaGluAsnHisTyrAspG1 191
DB 822 GGAGTCTTCAAAAAGGCCCTCTGGGCCTCTTCCAGACAAGCAGAGAACCACTATGACCA 881
QY 191 nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy 211
DB 882 GGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCAGTGTCCAGTG 941
QY 211 sSerProThrProGlyPropheLysProCysGluTyrLeuPheGluSerTrpGlyIleAr 231
DB 942 TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGCATCCG 1001
QY 231 gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh 251
DB 1002 CCTGGCCGTGGGCCCATCGTGTGTCTCTCCGTCTCTGCAATGGACTGGTGTCTGTGAC 1061
QY 251 rValPheAlaGlyGlyProAlaProLeuProProValLysPheValValGlyAlaIleAl 271
DB 1062 CGTGTTCGCTGGCGGGCCTGCCCCCTGCCCCCGGTCAAGTTTGTGTAGTGTGCGATTGC 1121
QY 271 aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuTh 291
DB 1122 AGGCGCCACACCTTGACTGGCATTTCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGAC 1181
QY 291 rPheGlyGlnPheSerGluTyrGlyAlaAargTrpGluThrGlyLeuGlyCysArgAlaTh 311
DB 1182 CTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGGGCCAC 1241
QY 311 rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa 331
DB 1242 TGGCTTCCTGGCAGTACTTGGGTCCGAGGATCGGTGCTGTGCTACTCTGGCCCGCAGT 1301
QY 331 lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe 351
DB 1302 GCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCTATGGGAAGTCCCCCTCCCTGGGCAG 1361
QY 351 rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe 371
DB 1362 CGTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCGCACCTGCCCT 1421
QY 371 uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluGl 391
DB 1422 GGCCTCAGTGGAGAATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCACCTGAGGG 1481
QY 391 yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe 411
DB 1482 TCAGCCAGCAGCCCTGGGCTTCAACCGTGGCCCTGGTGATGATGAACCTCTTGTTCCT 1541
QY 411 uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluAl 431

Db 1542 GGTGGCGCGTGCCTACATCAAACTGTACTGTGACCTGCCGGCGACTTTGAGGC 1601

Qy 431 aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe 451

Db 1602 CGTGCGGACTGCGCCATGTTGAGGCACGTGGCCTGGCTCATCTTCGACAGCGGCTCT 1661

Qy 451 uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr 471

Db 1662 CTACTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCATGTGTGGCCTCTTCCCTGTACGCC 1721

Qy 471 oGluAlaValLysSerValLeuValValLeuProLeuProAlaCysLeuAsnProLe 491

Db 1722 CGAGCGCGTCAAGTCTGTCTGTGGTGTGCTGCCCTGCCTGCCTCAACCCACT 1781

Qy 491 uLeuTyrLeuLeuPheAsnProHisPheArgAspLeuArgArgLeuArgProArgAl 511

Db 1782 GCTGTACCTGCTCTTCAACCCCACTTCGGGATGACCTTCGGCGGCTTCGGCCCGCGC 1841

Qy 511 aGlyAspSerGlyProLeuAlaTyrAlaAlaGlyGluLeuGluLysSerSerCysAs 531

Db 1842 AGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGAGCTGGAGAGAGCTCCTGTGA 1901

Qy 531 pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl 551

Db 1902 TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTTGGAAGCTTCTGAAGC 1961

Qy 551 aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysGl 571

Db 1962 TGGCGGCCCCCTGGGCTGGAGACTATGGCTTCCCCTCAGTGACCCCTCATCTCCTGTCA 2021

Qy 571 nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisPh 591

Db 2022 GCAGCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTT 2081

Qy 591 eGlyAsnProGlnProSerMetAspGlyGlyLeuLeuLeuArgAlaGluGlySerThrPr 611

Db 2082 TGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGTGAGGCAGAGGGATCTACGCC 2141

Qy 611 oAlaGlyGlyLeuSerGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlase 631

Db 2142 AGCAGGTGAGGCTTGTTCAGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTGTCTC 2201

Qy 631 rHisVal 633

Db 2202 ACACGTG 2208

RESULT 13

ADN02245
ID ADN02245 standard; cDNA; 2711 BP.

XX AC ADN02245;

XX DT 17-JUN-2004 (first entry)

DE XX Human partial large G protein-coupled receptor, LGR6, CDNA #2.

KW Human; ss; large G protein-coupled receptor 6; LGR6; heart failure;
KW ischaemic heart disease; myocardial infarction; hypertension;
KW pericarditis; atherosclerosis; hepatic failure; viral hepatitis; cancer;
KW intracerebral haemorrhage; brain abscess; Alzheimer's disease;
KW Pick disease; Parkinson's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; inflammatory bowel disease;
KW Crohn's disease; benign prostatic hypertrophy;
KW systemic lupus erythematosus.

XX OS Homo sapiens.

FH Key Location/Qualifiers
FT CDS 1..2211

FT /*tag= a

FT /partial

FT /note= "No start codon shown"

FT XX /product= "Partial LGR6"

PN US2003166047-A1.

XX PD 04-SEP-2003.

XX PF 08-MAY-2001; 2001US-00851595.

XX PR 06-MAY-1999; 99US-0132896P.

XX PR 08-MAY-2000; 2000US-00566588.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Gu W;

XX DR WPI; 2003-898067/82.

XX DR P-PSDB; ADN02246.

PT New isolated LGR6 nucleic acids and polypeptides, useful for diagnosing and treating LGR6-mediated disorders, such as myocardial infarction, hypertension, atherosclerosis, viral hepatitis, cancer and/or Alzheimer's disease.

PS Claim 1; SEQ ID NO 7; 145pp; English.

XX The invention relates to an isolated LGR6 (large G protein-coupled receptor) nucleic acid molecule comprising the mouse and human cDNA sequences appearing as ADN02239, ADN02241, ADN02242, ADN02244, ADN02245, ADN02247, ADN02248 and ADN02250. Also included are a host cell or a non-human mammalian host cell containing an LGR6 nucleic acid (and producing LGR6), an isolated LGR6 polypeptide appearing as ADN02240, ADN02243, ADN02246 and ADN02249, an antibody which selectively binds to LGR6, a method for detecting the presence of LGR6 in a sample, a kit (comprising a compound which selectively binds to LGR6, or hybridises to LGR6 nucleic acid, and instructions for use), a method for detecting LGR6 nucleic acid in a sample, a method for identifying a compound which binds to LGR6, a method for modulating the activity of LGR6 and a method for identifying a compound that modulates the activity of LGR6. The methods and compositions of the present invention are useful for diagnosing and treating large G-protein coupled receptor 6 (LGR6)-mediated or -related disorders, such as heart failure, ischaemic heart disease, myocardial infarction, hypertension, pericarditis, atherosclerosis, hepatic failure, viral hepatitis, cancer, intracerebral haemorrhage, brain abscess,

CC Alzheimer's disease, Pick disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, inflammatory bowel disease, Crohn's disease, benign prostatic hypertrophy and systemic lupus erythematosus. The present sequence is a partial human cDNA for LGR6.

SQ Sequence 2711 BP; 530 A; 837 C; 740 G; 604 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.73e-237 Length: 2711
Score: 3045.50 Matches: 602
Percent Similarity: 92.61% Conservative: 12
Best Local Similarity: 90.80% Mismatches: 19
Query Match: 92.09% Indels: 32
DB: 11 Gaps: 4

US-10-664-667-5 (1-633) x ADN02245 (1-2711)

Qy 1 AsnThrThrHisTyr-----CysArgTyrArg 15
|||:::|||||||
Db 224 AACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAG 283
Qy 6 ---ArgGluSerTyrTyrAla-----CysArgTyrArg 15
:::|||||:::
Db 284 GCACCACCAGCCTGGAGATCCTGACCCCTGACCCCGCAGGCATCCGGCTGCTCCCATCGG 343
Qy 16 -----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---G1 31
:::|||||||:::
Db 344 GGATGTGCCAACAGCTGCCCAGGCTCCGAGTCTCGAAGTGTCTCACAAATCAATGAGG 403
Qy 31 yLeuSerLeuProAlaHisProAlaSerLeuAlaAlaLeuAlaAlaSerAsnThrThrAl 51

Db	404	AGCTGCCAGCCTGCACAGGTGTAGAAATTGGAGGAAA -TCGGCCTCCAACACAACCGC	462
Qy	51	aSerGlyLysLeuGlu**AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe	71
Db	463	ATCTGGGAAATTGGAGCT -GACACCTTCAGCCAGCTGAGCTCCCTCGCAAGCCCTGGATCT	521
Qy	71	uSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa	91
Db	522	TAGCTGGAAACGCCATCCGGTCCATCCACCTGAGGCCCTTCTCCACCTGCACCTCCCTGGT	581
Qy	91	lLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyGlyLe	111
Db	582	CAAGCTGGACCTGACAGACAACAGCTGACCACACTGCCCCCTGGCTGGACTTGGGGGCTT	641
Qy	111	uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh	131
Db	642	GATGCATCTGAAGCTCAAAAGGGAACCTTGCTCTCTCCAGGCCCTTCTCCAAGGACAGTTT	701
Qy	131	eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy	151
Db	702	CCCAAACTGAGGATCTCTGGAGTGCCCTTATGCCCTACCAGTGTGTCCCTATGGGATGTG	761
Qy	151	sAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspAspGl	171
Db	762	TGCCAGCTTCTTCAAGGCCCTCTGGGCAGTGGAGGCTGAAGACCTTCACCTTGATGATGA	821
Qy	171	uGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspGl	191
Db	822	GGAGTCTTCAAAAAGGCCCTCTGGGCCTCTTGGCCAGACAAGCAGAGAACCACTATGACCA	881
Qy	191	nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy	211
Db	882	GGACCTGGATGAGCTCCAGTGGAGATGGAGGACTCAAAGCCACACCCAGTGTCCAGTG	941
Qy	211	sSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGlyIleAr	231
Db	942	TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCG	1001
Qy	231	gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh	251
Db	1002	CCTGGCCGTGTGGGCCATCGTGTGTCTCTCCGTGCTCTGCAATGGACTGGTGTGTGTGAC	1061
Qy	251	rValPheAlaGlyGlyProAlaProLeuProValLysPheValValGlyAlaIleAl	271
Db	1062	CGTGTTCGTGGCGGCCTGCCCCCTGCCCCCGTCAAGTTTGTGTAGTGCAGATTGC	1121
Qy	271	aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuTh	291
Db	1122	AGGGCCCAACACCTTGACTGGCATTTCTGTGGCCCTTCTAGCCTCAGTCGATGCCCTGAC	1181
Qy	291	rPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaTh	311
Db	1182	CTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGGCCAC	1241
Qy	311	rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaVa	331
Db	1242	TGGCTTCTTGGCAGTACTTGGGTGGAGGCATCGGTGTGTGTGTCTCACTCTGGCCGCGAGT	1301
Qy	331	lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe	351
Db	1302	GCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCCTATGGGAAGTCCCCCTCCCTGGGCGAG	1361
Qy	351	rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe	371
Db	1362	CGTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCGCACTGCCCT	1421
Qy	371	uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluGl	391
Db	1422	GGCCTCAGTGGGAGATAACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGG	1481
Qy	391	yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe	411

Db	1482	TCAGCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGATGATGAATCACTCCTTCTGTTTCCT	1541
QY	411	uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluAl	431
Db	1542	GGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCGCGGGGCGACTTTGAGGC	1601
QY	431	aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe	451
Db	1602	CGTGTGGGACTGCGCCATGGTGAGGCACGTGGCTTGCTCATCTTCGACAGACGGGCTCCT	1661
QY	451	uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr	471
Db	1662	CTACTGTCCCGTGGCCTTCCTCAGCTTCGCCCTCCATGTGGGCTCCTTCCCTGTACAGCC	1721
QY	471	oGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe	491
Db	1722	CGAGGCGGTCAAGTCTGTCTCTGGTGGTGCTGCCCTGCCCTGCCCTCAACCCACT	1781
QY	491	uLeuTyrLeuLeuPheAsnProHisPheArgAspLeuArgArgLeuArgProArgAl	511
Db	1782	GCTGTACTGCTCTTCAACCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCCGCGC	1841
QY	511	aGlyAspSerGlyProLeuAlaTyrAlaAlaAalaGlyGluLeuGlyLysSerSerCysAs	531
Db	1842	AGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGAGCTGGAGAAGAGCTCCTGTGA	1901
QY	531	pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl	551
Db	1902	TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTTCTGGAAGCTTCTGAAGC	1961
QY	551	aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysGl	571
Db	1962	TGGCGGCCCCCCCTGGGCTGGAGACCTATGGCTTCCCCCTCAGTGACCCCTCATCTCCTGTCA	2021
QY	571	nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisPh	591
Db	2022	GCAGCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAAACCACTT	2081
QY	591	eGlyAsnProGlnProSerMetAspGlyGluLeuLeuLeuArgAlaGluGlySerThrPr	611
Db	2082	TGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTGCTGAGGCAGAGGGATCTACGCC	2141
QY	611	oAlaGlyGlyLeuSerGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSe	631
Db	2142	AGCAGGTGAGGCTTGTACGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTC	2201
QY	631	rHisVal	633
Db	2202	ACACGTG	2208
RESULT 14			
ADK19410			
ID	ADK19410 standard; cDNA; 2711 BP.		
XX			
AC	ADK19410;		
XX			
DT	17-JUN-2004 (first entry)		
XX			
DE	Partial cDNA encoding human LGR6 polypeptide #2.		
XX			
KW	G-protein coupled receptor; GPCR; large G-protein coupled receptor 6;		
KW	LGR6; weight disorder; neural disorder; endocrine disorder;		
KW	cardiovascular disorder; anorectic; anabolic; immunomodulator;		
KW	neuroprotective; nootropic; antiparkinsonian; anti-HIV; anticonvulsant;		
KW	antithyroid; osteopathic; cardiant; vasotropic; hypotensive;		
KW	antiarteriosclerotic; antiarrhythmic; human; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
CDS	1..2211		
FT	/*tag= a		
FT	/partial		
FT			

FT /product= "LGR6 polypeptide #2"
FT /note= "This sequence lacks a start codon"

PN US2004058377-A1.
XX
PD 25-MAR-2004.
XX
PF 18-SEP-2003; 2003US-00664667.
XX
PR 06-MAY-1999; 99US-0132896P.
PR 08-MAY-2000; 2000US-00566588.
PR 08-MAY-2001; 2001US-00851595.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX

PI Gu W;
XX
XX WPI; 2004-268789/25.
DR P-PSDB; ADK19411.
DR

XX New large G-protein coupled receptor 6 nucleic acid molecules and
PT polypeptides, useful for diagnosing, preventing or treating diseases
PT associated with aberrant nucleic acid or protein activity, e.g. obesity,
PT anorexia or cachexia.

XX Claim 2; SEQ ID NO 7; 145pp; English.

CC The present invention relates to the isolation of novel members of the G-
CC protein coupled receptor (GPCR) family designated as large G-protein
CC coupled receptor 6 (LGR6), and the polynucleotide sequences encoding
CC them. The invention also discloses LGR6 fusion proteins, antigenic
CC peptides, anti-LGR6 antibodies, recombinant expression vectors, host
CC cells, and non-human transgenic animals in which an LGR6 gene has been
CC introduced or disrupted. The LGR6 polynucleotide sequences, polypeptide
CC sequences, and antibodies are useful for diagnosing, treating or
CC preventing diseases associated with aberrant LGR6 expression or activity,
CC such as weight disorders (e.g. obesity, anorexia nervosa or cachexia),
CC neural disorders (e.g. central nervous system disorder, including
CC Alzheimer's disease, Parkinson's disease, AIDS-related dementia, multiple
CC sclerosis and Huntington's disease), endocrine disorders (e.g.
CC hypothyroidism, hyperthyroidism or acromegaly), or cardiovascular
CC disorders (e.g. ischaemia-reperfusion injury, coronary artery disease,
CC myocardial infarction, arrhythmia, atherosclerosis, hypertension or
CC congestive heart failure). The LGR6 polynucleotide and polypeptide
CC sequences are also useful as targets for developing modulating agents
CC that regulate a variety of cellular processes, e.g. neural and endocrine
CC processes and thermogenesis. They can be used in screening assays (e.g.
CC chromosome mapping, tissue typing or in forensic biology), or in
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials or pharmacogenomics). The present sequence
CC encodes a human LGR6 polypeptide.

XX
SQ Sequence 2711 BP; 530 A; 837 C; 740 G; 604 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.73e-237 Length: 2711
Score: 3045.50 Matches: 602
Percent Similarity: 92.61% Conservative: 12
Best Local Similarity: 90.80% Mismatches: 19
Query Match: 92.09% Indels: 32
DB: 12 Gaps: 4

US-10-664-667-5 (1-633) x ADK19410 (1-2711)

Qy 1 AsnThrHisTyr-----
Db 224 AACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTCCAGATCTCAAAG 283
Qy 6 ---ArgGluSerTrpTyrAla-----CysArgTyrArg 15
Db 284 GCACCACGAGCCTGGAGATCCTGACCTGTACCGCGCAGGCATCCGGCTGCTCCCATCGG 343
Qy 16 -----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln----G1 31

Db 344 GGATGTGCCAACACAGCTGCCAGGCTCCGAGTCCTGGAACTGTCTCACAATCAAAATTGAGG 403
Qy 31 yLeuSerLeuProAlaHisProAlaSerLeuAlaAlaLeuAlaAlaSerAsnThrThrAl 51
Db 404 AGCTGCCAGCCTGCACAGGTGTTCAGAAATTGGAGGAAA-TCGGCCTCCAACACACCGC 462
Qy 51 aSerGlyLysLeuGlu***AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe 71
Db 463 ATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAGTCCCTGCAAGCCCTGGATCT 521
Qy 71 uSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa 91
Db 522 TAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCACCTCCCTGGT 581
Qy 91 llysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyGlyLe 111
Db 582 CAAGCTGGACCTGACAGACAACACAGCTGACCACACTGCCCTGGCTGGCTTGGGGGCTT 641
Qy 111 uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh 131
Db 642 GATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCCTTCTCCAAGGACAGTTT 701
Qy 131 eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy 151
Db 702 CCCAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCAGTGTCTCCCTATGGGATGTG 761
Qy 151 sAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspG1 171
Db 762 TGCAGCTTCTTCAAGGCCTCTGGGAGTGGGAGGTGAAGACCTTTCACCTTGATGATGA 821
Qy 171 uGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspG1 191
Db 822 GGAGTCTTCAAAAAGGCCCTGGGCCTCTTGGCCAGACAAGCAGAGAACCACTATGACCA 881
Qy 191 nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy 211
Db 882 GGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCAGTGTCCAGTG 941
Qy 211 sSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGlyIleAr 231
Db 942 TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCG 1001
Qy 231 gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh 251
Db 1002 CCTGGCCGTGFGGCCATCGTGTGTCTCTCCGTGCTCTGCAATGGACTGGTGTGCTGAC 1061
Qy 251 rValPheAlaGlyGlyProAlaProLeuProProValLysPheValValGlyAlaIleAl 271
Db 1062 CGTGTTCGCTGGCGGGCCTGCCCCCTGCCCGGTCAAGTTTGTGGTAGGTGCGATTGC 1121
Qy 271 aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuTh 291
Db 1122 AGCGGCCAACACCTTGACTGGCATTTCTGTGGCCCTTAGCCCTCAGTCGATGCCCTGAC 1181
Qy 291 rPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaTh 311
Db 1182 CTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGGGCCAC 1241
Qy 311 rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa 331
Db 1242 TGGCTTCTTGGCAGTACTTGGGTGCGAGGCATCGGTGCTGCTCAGTCTGCGCCGAGT 1301
Qy 331 lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe 351
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Qy 351 rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe 371
Db 1362 CGTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCCGCTGCCCCCT 1421
Qy 371 uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluG1 391

Db	1422	GGCCTCAGTGGGAGAAATACGGGGCCTCCCACTCTGCCTGCCCTACGCGCCACCTGAGGG	1481
Qy	391	yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe	411
Db	1482	TCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACCTCTCTGTTTCCT	1541
Qy	411	uValValAlaGlyAlaTyriLeLySLeuTyrCysAspLeuProArgGlyAspPheGluAl	431
Db	1542	GGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCGCGGGCGACTTGAGGC	1601
Qy	431	aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe	451
Db	1602	CGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGCAGACGGGCTCCT	1661
Qy	451	uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr	471
Db	1662	CTACTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCATGCTGGGCCTCTTCCCTGTCAAGCC	1721
Qy	471	oGluAlaValLySerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe	491
Db	1722	CGAGGCCGTCAAGTCTGCTGCTGGTGGTGTGCTGCCCTGCCTGCCTCAACCCCACT	1781
Qy	491	uLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgArgLeuArgProArgAl	511
Db	1782	GCTGTACCTGCTCTTCAACCCCACTTCGGGATGACTTCGGCGGCTTCGGCCCCCGGC	1841
Qy	511	aGlyAspSerGlyProLeuAlaTyraAlaAlaGlyGluLeuGluLySersSerCysAs	531
Db	1842	AGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGAGCTGGAGAAGACTCTGTGA	1901
Qy	531	pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl	551
Db	1902	TTCTACCCAGGCCCTGGTAGCCTTCTGTATGTGGATCTCATTTCTGGAAGCTTCTGAAGC	1961
Qy	551	aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysGl	571
Db	1962	TGGGGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTCAGTGACCCCTCATCTCCTGTCA	2021
Qy	571	nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisPh	591
Db	2022	GCAGCCAGGGCCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTT	2081
Qy	591	eGlyAsnProGlnProSerMetAspGlyGluLeuLeuLeuArgAlaGluGlySerThrPr	611
Db	2082	TGGGAACCCCCCAACCTCCATGGATGGAGAACTGCTGTGAGGGCAGAGGGATCTAGGCC	2141
Qy	611	oAlaGlyGlyGlyLeuSerGlyGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlase	631
Db	2142	AGCAGGTGGAGGCTTGTCAAGGGGTGGCGGCTTTTCAGCCCTCTGGCTTGGCCCTTGCTTC	2201
Qy	631	rHisVal	633
Db	2202	ACACGTG	2208
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ID	ADC16710	standard; DNA; 2786 BP.	
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XX	AC	ADC16710;	
XX	AC		
DT	18-DEC-2003	(first entry)	
XX	DE	Human G-protein coupled receptor DNA (SeqID 20).	
XX	KW	human; G-protein coupled receptor; GPCR; TGR41; antimetabolite;	
KW	KW	neuroprotective; cytostatic; antiinflammatory; osteopathic;	
KW	KW	antibacterial; gene therapy; infection; cancer; gene; ds.	
XX	XX		
OS	OS	Homo sapiens.	
XX	XX		
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FT	/note= "Start and stop codons are absent"				
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PN	WO2003040371-A1.				
XX					
PD	15-MAY-2003.				
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PF	05-NOV-2002; 2002WO-JP011485.				
XX					
PR	06-NOV-2001; 2001JP-00340189.				
PR	31-MAY-2002; 2002JP-00159448.				
XX					
PA	(TAKE) TAKEDA CHEM IND LTD.				
XX					
PI	Ikeda N, Miwa M, Ito T, Ohtaki T;				
XX					
DR	WPI; 2003-441575/41.				
DR	P-PSDB; ADC16711.				
XX					
PT	G-protein coupled receptor protein for treatment of infection and cancer				
PT	etc.				
XX					
PS	Disclosure; Page 139-141; 153pp; Japanese.				
XX					
CC	This invention relates to novel cDNA sequences encoding the human G-				
CC	protein coupled receptor (GPCR) proteins known as TGR41, namely TGR41A,				
CC	TGR41V, TGR41A2 and TGR41V2. Specifically, it refers to the recombinant				
CC	DNA vectors, the antibodies against the novel proteins as well as their				
CC	ligands, a screening method for the detection compounds that affect GPCR				
CC	protein binding, and also the resultant diagnostic drugs. The present				
CC	invention describes these compounds as antimetabolites, neuroprotective,				
CC	cytostatic, antiinflammatory, osteopathic and antibacterial. As such,				
CC	through using gene therapy they can be useful in the treatment of				
CC	disorders associated with the central nervous system, endocrine system,				
CC	metabolism, inflammation, circulatory system, respiration, digestion, immune				
CC	system, bone, cartilage, urinary system, transplantation, infection and				
CC	cancer. This polynucleotide is the DNA (SeqID 20) encoding a human GPCR				
CC	protein related to the exemplification of the invention.				
XX					
SQ	Sequence 2786 BP; 507 A; 917 C; 777 G; 585 T; 0 U; 0 Other;				
Alignment Scores:					
Pred. No.:	1.79e-237	Length:	2786		
Score:	3045.50	Matches:	602		
Percent Similarity:	92.61%	Conservative:	12		
Best Local Similarity:	90.80%	Mismatches:	19		
Query Match:	92.09%	Indels:	32		
DB:	10	Gaps:	4		
US-10-664-667-5 (1-633) x ADC16710 (1-2786)					
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		:::			
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Qy	6	--ArgGluSerTrpTyrAla-----			15
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Db	862	GCACCACCAGCCTGGAGATCTCTGACCTGACCCGCGCAGGCATCCGGCTGCTCCCATCGG	921		
Qy	16	-----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---G1	31		
		::: :::			
Db	922	GGATGTGCCAACACAGCTGCCAGGCTCCGAGTCTCGGAACTGTCTCACATCAAAATTGAGG	981		
Qy	31	yLeuSerLeuProAlaHisProAlaSerLeuAlaAlaLeuAlaAlaSerAsnThrThrAl	51		
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Db	982	AGCTGCCCAGCCTGCACAGGTGTGAGAAATTGGAGGAAA-TCGGCCTCCACACACACCGC	1040		
Qy	51	aSerGlyLysLeuGlu***AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe	71		
Db	1041	ATCTGGGAAATTGGAGCT-GACACCTTCAGCAGCTGAGCTCCCTGCAAGCCCTGGATCT	1099		
Qy	71	uSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa	91		

Db 1100 TAGCTGGAAAGCCCATCCGGTCCATCCACCCCTGAGGCCTTCTCCACCCCTGCACTCCCTGGT 1159
Qy 91 lLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyGlyLe 111
Db 1160 CAAGCTGGACCTGACAGACAACCAAGCTGACCACTGCCCCCTGGCTGGACTTGGGGGCTT 1219
Qy 111 uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh 131
Db 1220 GATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCCTTCTCCAAGGACAGTTT 1279
Qy 131 eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy 151
Db 1280 CCCAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCACTGCTGTCCCTATGGGATGIG 1339
Qy 151 sAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspAspG1 171
Db 1340 TGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGCTGAAGACCTTCACCTTGATGATGA 1399
Qy 171 uGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspG1 191
Db 1400 GGAGTCTTCAAAAAGGCCCTCTGGGCCTCTTGCAGACAAAGCAGAACCACTATGACCA 1459
Qy 191 nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy 211
Db 1460 GGACCTGGATGACTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCACTGTCCAGTG 1519
Qy 211 sSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGlyIleAr 231
Db 1520 TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCG 1579
Qy 231 gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh 251
Db 1580 CCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTCTCTGCAATGGACTGGTGTGTGTGAC 1639
Qy 251 rValPheAlaGlyGlyProAlaProLeuProProValLysPheValValGlyAlaIleAl 271
Db 1640 CGTGTTCGTGGCGGCCCTGCCCCCTGCCCGCTCAAGTTTGTGGTAGGTGCGATTGC 1699
Qy 271 aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuTh 291
Db 1700 AGGCGCCAAACACCTTGACTGGCATTTCTCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGAC 1759
Qy 291 rPheGlyGlnPheSerGluTyrGlyAlaAargTrpGluThrGlyLeuGlyCysArgAlaTh 311
Db 1760 CTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGGGCCAC 1819
Qy 311 rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa 331
Db 1820 TGGCTTCCTGGCAGTACTTGGGTGCGAGGCATCGGTGCTGCTGCTCACTCTGGCCGCAGT 1879
Qy 331 lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe 351
Db 1880 GCAGTGCAGCGTCTCCGTCTCTGTTCGGGCCCTATGGGAAGTCCCCCTCCCTGGGCAG 1939
Qy 351 rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe 371
Db 1940 CGTTCAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCCGCACCTGCCCT 1999
Qy 371 uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluG1 391
Db 2000 GGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCCTGCCCTACGGCCACCTGAGGG 2059
Qy 391 yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe 411
Db 2060 TCAGCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGATGATGAACCTCTTCTGTTCCT 2119
Qy 411 uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluAl 431
Db 2120 GGTCGTGGCCGGTGCTTACATCAAACTGTACTGTGACCTGCCGGGGCGACTTTGAGGC 2179
Qy 431 aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe 451

Db 2180 CGTGTGGGACTGCGCCCATGSGTAGGCACGCTGGCCTGGCTCATCTTCGCAGACGGGCTCCT 2239
Qy 451 uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr 471
Db 2240 CTACTGTCCCGTGGCCTTCTTCAGCTTTGCCCTCCATGCTGGGCCCTCTTCCCTGTACGCC 2299
Qy 471 oGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe 491
Db 2300 CGAGGCCGTCAAGTCTGTCTGTCTGGTGGTGTGCTGCCCTGCCCTGCCTCAACCCACT 2359
Qy 491 uLeuTyrLeuLeuPheAsnProHisPheArgAspLeuArgArgLeuArgProArgAl 511
Db 2360 GCTGTACCTGCTCTTCAACCCCACTTCCGGGATGACCTTCGGGGCTTCGGCCCCCGCGC 2419
Qy 511 aGlyAspSerGlyProLeuAlaTyrAlaAlaGlyGluLeuGluLysSerSerCysAs 531
Db 2420 AGGGACTCAGGGCCCCCTAGCCTATGCTCGGCCCGGGAGCTGGAGAAGAGCTCCTGTGA 2479
Qy 531 pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl 551
Db 2480 TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTTCTGGAAGCTTCTGAAGC 2539
Qy 551 aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysG1 571
Db 2540 TGGCGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTCAGTGACCCCTCATCTCCTGTCA 2599
Qy 571 nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisPh 591
Db 2600 GCAGCCAGGGGCCCCCAAGGCTGGAGGCGAGCCATTGTGTAGAGCCAGAGGGGAACCACTT 2659
Qy 591 eGlyAsnProGlnProSerMetAspGlyGluLeuLeuLeuArgAlaGluGlySerThrPr 611
Db 2660 TGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGGATCTACGCC 2719
Qy 611 oAlaGlyGlyGlyLeuSerGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSe 631
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Qy 631 rHisVal 633
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Search completed: April 14, 2005, 19:24:43
Job time : 665 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 14, 2005, 18:37:28 ; Search time 3621 Seconds
(without alignments)
6654.151 Million cell updates/sec

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Perfect score: 3307
Sequence: 1 NTHYRESWYACRYRSGIPG.....GGLSGGGGFQPSGLAFASHV 633

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10664667 @CGN 1 1 2607 @runat_13042005_184539_7277 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3140	95.0	3509	BC038795	BC038795 Homo sapi
2	2621	79.3	2822	3 AK052873	AK052873 Mus muscu
3	2582.5	78.1	3583	3 AK085901	AK085901 Mus muscu
4	1275	38.6	2724	9 AY411732	AY411732 Homo sapi
5	1231	37.2	2724	9 AY411734	AY411734 Mus muscu
6	1075.5	32.5	812	4 BG916782	BG916782 602816031
7	1062	32.1	819	4 BG863804	BG863804 602798701
8	1037	31.4	982	2 BF159363	BF159363 601770339
9	960	29.0	2593	9 AY411733	AY411733 Pan trogl

10	956	28.9	3035	3	AK044357	AK044357 Mus muscu
11	932.5	28.2	753	4	BG916963	BG916963 602816251
12	929	28.1	3855	3	AK040883	AK040883 Mus muscu
13	914	27.6	690	2	BB636845	BB636845 BB636845
14	887.5	26.8	869	2	BF158974	BF158974 601766476
15	803	24.3	680	7	CN258480	CN258480 170005321
16	794	24.0	640	7	CO351740	CO351740 DR AOV NR
17	763	23.1	3006	3	AK033699	AK033699 Mus muscu
18	690	20.9	1104	1	AL530798	AL530798 AL530798
19	646	19.5	800	4	BG196708	BG196708 RST15934
20	614	18.6	776	5	BU708439	BU708439 UI-M-FCO-
21	609	18.4	461	2	BE149368	BE149368 RC1-HT025
22	600	18.1	671	4	BM795259	BM795259 K-EST0077
23	565	17.1	880	5	BQ216343	BQ216343 AGENCOURT
24	540	16.3	798	4	BI143698	BI143698 602907345
25	535	16.2	651	2	BB621262	BB621262 BB621262
26	513.5	15.5	695	6	BY731701	BY731701 BY731701
27	507.5	15.3	788	7	CF734172	CF734172 UI-M-HB0-
28	493.5	14.9	1719	2	BF144122	BF144122 601788812
29	484	14.6	764	5	BU387687	BU387687 603582771
30	475	14.4	607	5	BQ572012	BQ572012 UI-M-FB0-
31	471	14.2	310	7	Z44115	Z44115 HSC1SG111 n
32	469.5	14.2	807	3	AK016357	AK016357 Mus muscu
33	469.5	14.2	816	6	BY716002	BY716002 BY716002
34	465	14.1	471	5	BX281802	BX281802 BX281802
35	465	14.1	771	5	BQ425502	BQ425502 AGENCOURT
36	461	13.9	839	4	BI150746	BI150746 602914834
37	439.5	13.3	2360	3	AK016635	AK016635 Mus muscu
38	434	13.1	600	4	BI989071	BI989071 4024-89 M
39	430.5	13.0	604	4	BM538630	BM538630 ha98a06.g
40	429.5	13.0	2079	9	AY399755	AY399755 Mus muscu
41	427	12.9	594	5	BX482638	BX482638 DKFZp686M
42	419	12.7	807	4	BI182677	BI182677 UNL-P-FN-
43	416	12.6	868	2	BE868472	BE868472 601444469
44	414.5	12.5	2088	9	AY399753	AY399753 Homo sapi
45	411.5	12.4	1060	1	AL541959	AL541959 ALS41959

ALIGNMENTS

RESULT 1	BC038795	BC038795	3509 bp	mRNA	linear	HTC 19-NOV-2003
LOCUS	Homo sapiens	Homo sapiens	leucine-rich repeat-containing G protein-coupled			
DEFINITION	receptor 6, mRNA (cdna clone IMAGE:5220507), with apparent retained intron.					
ACCESSION	BC038795					
VERSION	BC038795.1	GI:24433474				
KEYWORDS	HTC.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 3509)					
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Uesdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettaman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.					
TITLE	Generation and initial analysis of more than 15,000 full-length					

JOURNAL MEDLINE	human and mouse cDNA sequences				
PUBMED	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
REFERENCE	22388257				
AUTHORS	12477932				
TITLE	2 (bases 1 to 3509)				
JOURNAL	Strausberg,R.				
	Direct Submission				
	Submitted (25-OCT-2002) National Institutes of Health, Mammalian				
	Gene Collection (MGC), Cancer Genomics Office, National Cancer				
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,				
	USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk				
	Email: cgabs-r@mail.nih.gov				
	Tissue Procurement: Life Technologies, Inc.				
	cDNA Library Preparation: Life Technologies, Inc.				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
	DNA Sequencing by: National Institutes of Health Intramural				
	Sequencing Center (NISC),				
	Gaithersburg, Maryland;				
	Web site: http://www.nisc.nih.gov/				
	Contact: nisc_mgc@nhgri.nih.gov				
	Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,				
	Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,				
	Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,				
	Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,				
	Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,				
	McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,				
	Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,				
	Young,A., Zhang,L.-H. and Green,E.D.				
	Clone distribution: MGC clone distribution information can be found				
	through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov				
	Series: IRAK Plate: 64 Row: n Column: 17				
	This clone was selected for full length sequencing because it				
	passed the following selection criteria: Hexamer frequency ORF				
	analysis				
	This clone has the following problem: retained intron.				
FEATURES	Location/Qualifiers				
source	1..3509				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:5220507"				
	/tissue_type="Pancreas, Spleen, adult pooled"				
	/clone_lib="NIH MGC_120"				
	/lab_host="DH10B"				
	/note="Vector: pCMV-SPORT6"				
ORIGIN					
Alignment Scores:					
Pred. No.:	1.03e-281	Length:	3509		
Score:	3140.00	Matches:	611		
Percent Similarity:	97.61%	Conservative:	1		
Best Local Similarity:	97.45%	Mismatches:	11		
Query Match:	94.95%	Indels:	5		
DB:	3	Gaps:	1		
US-10-664-667-5 (1-633) x BC038795 (1-3509)					
QY	7	GluSerTrpTyrAlaCysArgTyrArgSerGlyIleProGlySerThrHisAlaSerVal	26		
					:::
Db	1024	GAGAAAGTGGGGGCTCTACTTTCTCCTCCAGTGTCTGGGG-----GGCATG	1071		
QY	27	GluArgSerGlnGlyLeuSerLeuProAlaHisProAlaSerLeuAlaLeuAlaAla	46		
Db	1072	GAGCGGAGCCAGGGTCTGAGCCTGCCGCTCATCCAGCCTCTCTTGCTGCCCTAGCGGC	1131		
QY	47	SerAsnThrThrAlaSerGlyLysLeuGlu***AspThrPheSerGlnLeuSerSerLeu	66		
Db	1132	TCCAACACACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAGCTCCCTG	1190		
QY	67	GlnAlaLeuAspLeuSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThr	86		

Db	1191	CAAGCCCTGGATCTTAGCTGGAAAGCCCATCCGGTCCATCCACCCCTGAGGCCCTTCTCCACC	1250		
QY	87	LeuHisSerLeuValLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAla	106		
Db	1251	CTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACACTGCCCTGGCT	1310		
QY	107	GlyLeuGlyGlyLeuMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPhe	126		
Db	1311	GGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCTTC	1370		
QY	127	SerLysAspSerPheProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCys	146		
Db	1371	TCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCAAGTGTGT	1430		
QY	147	ProTyrGlyMetCysAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeu	166		
Db	1431	CCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCAGTGGGAGGCTGAAGACCTT	1490		
QY	167	HisLeuAspAspGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGlu	186		
Db	1491	CACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCCTCCTTGCCAGACAAGCAGAG	1550		
QY	187	AsnHisTyrAspGlnAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHis	206		
Db	1551	AACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGACTCAAAGCCACAC	1610		
QY	207	ProSerValGlnCysSerProThrProGlyProPheLysProCysGluTyrLeuPheGlu	226		
Db	1611	CCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAA	1670		
QY	227	SerTrpGlyIleArgLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGly	246		
Db	1671	AGCTGGGGCATCGCCTGGCCGTGTGGGCCCATCGTGTGTCTCCGTGCTCTGCAATGGA	1730		
QY	247	LeuValLeuLeuThrValPheAlaGlyGlyProAlaProLeuProProValLysPheVal	266		
Db	1731	CTGGTGTCTGTGACCGTGTTCGTGGCGGGCGCTGCCCCCTGCCCCCGGTCAAGTTTGTG	1790		
QY	267	ValGlyAlaIleAlaGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSer	286		
Db	1791	GTAGGTGCGATTGACGGCGCCAAACACCTTGACTGGCATTTCTGTGGCCTTCTAGCCTCA	1850		
QY	287	ValAspAlaLeuThrPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeu	306		
Db	1851	GTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTA	1910		
QY	307	GlyCysArgAlaThrGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeu	326		
Db	1911	GGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTGGAGGCATCGGTGCTGCTGCTC	1970		
QY	327	ThrLeuAlaAlaValGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSer	346		
Db	1971	ACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCCTATGGGAAGTCC	2030		
QY	347	ProSerLeuGlySerValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAla	366		
Db	2031	CCCTCCCTGGGCAGCGTTCGAGCAGGGGTCTTAGGCTGCCTGGCACCTGGCAGGGCTGGCC	2090		
QY	367	AlaAlaLeuProLeuAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyr	386		
Db	2091	GCCGCACCTGCCCTGGCCTCAGTGGGAGATAACGGGGCCTCCCCACTCTGCTGCCCTAC	2150		
QY	387	AlaProProGluGlyGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsn	406		
Db	2151	GCGCCACCTGAGGTCAGCCAGCAGCCCTGGGCTTCCCGTGGCCCTGGTGATGATGAAC	2210		
QY	407	SerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArg	426		
Db	2211	TCCTTCTGTTTCTGGTCGTGGCCGGTGCCTACATCAAACCTGTACTGTGACCTGCCGCGG	2270		
QY	427	GlyAspPheGluAlaValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePhe	446		

Db 2271 GCGGACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGCACGTGGCCTCATCTTC 2330

QY 447 AlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeu 466
|||||

Db 2331 GCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCATGCTGGGCCTC 2390

QY 467 PheProValThrProGluAlaValLysSerValLeuLeuValValLeuProLeuProAla 486
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Db 2391 TTCCTGTGCACGCCCGAGGCGTCAAGTCTGTCTGTGGTGTGCTGCCCTGCCTGCC 2450

QY 487 CysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPheArgAspLeuArgArg 506
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Db 2451 TGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCACTTCCGGATGACCTTCGGCGG 2510

QY 507 LeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAlaAlaGlyGluLeuGlu 526
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Db 2511 CTTGGCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGCGGCCGGGAGCTGGAG 2570

QY 527 LysSerSerCysAspSerThrGlnAlaLeuValAlaPheSerAspValAspLeuLeu 546
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Db 2571 AAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTCTCTGATGTGGATCTCATTTCTG 2630

QY 547 GluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThr 566
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Db 2631 GAAGCTTCTGAAGCTGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCTCAGTGACC 2690

QY 567 LeuLeSerCysGlnGlnProGlyAlaProArgLeuGluGlySerHisCysValGluPro 586
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Db 2691 CTCATCTCCTGTGCAGCAGCGCGGCCCCCCCAGGCTGGAGGCAGCCATTGTGTAGAGCCA 2750

QY 587 GluGlyAsnHisPheGlyAsnProGlnProSerMetAspGlyGluLeuLeuLeuArgAla 606
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Db 2751 GAGGGGAACCACTTTGGGAACCCCAACCTCCATGGATGGAGAACTGCTGCTGAGGGCA 2810

QY 607 GluGlySerThrProAlaGlyGlyGlyLeuSerGlyGlyGlyPheGlnProSerGly 626
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Db 2811 GAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGGTGGCGGCTTTCAGCCCTCTGGC 2870

QY 627 LeuAlaPheAlaSerHisVal 633
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Db 2871 TTGGCCTTTGCTTCACACGTG 2891

RESULT 2

AK052873

LOCUS

DEFINITION

AK052873 2822 bp mRNA linear HTC 03-APR-2004

Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830015D13 product:CDNA FLJ14471 FIS, CLONE MAMMA1001030, WEAKLY SIMILAR TO LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR homolog [Homo sapiens], full insert sequence.

ACCESSION

AK052873

VERSION

AK052873.1 GI:26095426

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

AUTHORS

Carninci,P. and Hayashizaki,Y.

TITLE

High-efficiency full-length cDNA cloning

JOURNAL

Meth. Enzymol. 303, 19-44 (1999)

MEDLINE

99279253

PUBMED

10349636

REFERENCE

2

AUTHORS

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL

Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE

20499374

PUBMED

11042159

REFERENCE

3

AUTHORS

Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,

Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kaashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

PUBMED

11076861

REFERENCE

4

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE

Functional annotation of a full-length mouse cDNA collection

JOURNAL

Nature 409, 685-690 (2001)

REFERENCE

5

AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL

Nature 420, 563-573 (2002)

REFERENCE

6

AUTHORS

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, tel:81-45-503-9222, Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/

URL:http://fantom.gsc.riken.jp/.

FEATURES

source

Location/Qualifiers

1. .2822

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM DB:D830015D13"

/db_xref="taxon:10090"

/clone="D830015D13"

/tissue type="heart"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev stage="16 days neonate"

1. .2822

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misc_feature

Alignment Scores:

Pred. No.: 2,41e-233 Length: 2822

Score: 2621.00 Matches: 518

Percent Similarity: 89.12% Conservative: 31

Best Local Similarity: 84.09% Mismatches: 63

Query Match:	79.26%	Indels:	6
DB:	3	Gaps:	1
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QY	19	ProGlySerThrHisAlaSerValGluArgSerGlnGlyLeuSerLeuProAlaHisPro	38
Db	404	CCTGGAGCTGTCTCATAATCA-----GATCGAGGAGTTACCCAGCCTGCACAGGTG	454
QY	39	AlaSerLeuAlaAlaLeuAlaAlaSerAsnThrThrAlaSerGlyLysLeuGlu***Asp	58
Db	455	TCAGAACTGGAGGAAA-TTGGCCTCCGACATAACCGGATCAAGGAAATTGGT-GCAGAT	512
QY	59	ThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLeuSerTrpAsnAlaIleArgSer	78
Db	513	ACCTTCAGCCAGCTGGGCTCCTTGCAAGCTTTAGACCTGAGTTGGAATGCCATCCGTGCC	572
QY	79	IleHisProGluAlaPheSerThrLeuHisSerLeuValLysLeuAspLeuThrAspAsn	98
Db	573	ATCCACCCTGAGGCTTTCTCAACCTTCGATCCTTGGTTAAGCTGGACCTGACTGACAAC	632
QY	99	GlnLeuThrThrLeuProLeuAlaGlyLeuGlyLeuMetHisLeuLysLeuLysGly	118
Db	633	CAGTGACCACACTGCCCTTGGCTGGGCTGGGAGGCTGATGCACCTGAAGCTCAAAGGG	692
QY	119	AsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPheProLysLeuArgIleLeuGlu	138
Db	693	AACTTGGCCCTGTCTCAGGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAG	752
QY	139	ValProTyrAlaTyrGlnCysCysProTyrGlyMetCysAlaSerPhePheLysAlaSer	158
Db	753	GTGCCCTACGCCTACCACTGCTGTGCTACGGCATCTGTGCCAGCTTCTTCAAGACCTCT	812
QY	159	GlyGlnTrpGluAlaGluAspLeuHisLeuAspAspGluGluSerSerLysArgProLeu	178
Db	813	GGGCAGTGGCAGGCCGAGGACTTTCATCCAGAGGAAGAGGAGGCCACCAAGAGGCCCTG	872
QY	179	GlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspGlnAspLeuAspGluLeuGlnLeu	198
Db	873	GGTCTCCTTGTGGACAAGCTGAGAACCACTATGACCTAGACCTGGATGAGCTCCAGATG	932
QY	199	GluMetGluAspSerLysProHisProSerValGlnCysSerProThrProGlyProphe	218
Db	933	GGGACAGAGGACTCAAAGCCACACCCAGTGTCAGTGCAGGCCCTGTTCAGGCCCTTTC	992
QY	219	LysProCysGluTyrLeuPheGluSerTrpGlyIleArgLeuAlaValTrpAlaIleVal	238
Db	993	AAGCCCTGCGAGCACCTCTTTGAGAGCTGGGGCATCCGCTTGTGTGGGCATCGTG	1052
QY	239	LeuLeuSerValLeuCysAsnGlyLeuValLeuLeuThrValPheAlaGlyGlyProAla	258
Db	1053	TTACTCTCCGTACTCTGTAAACGGCTGGTGCTGCTGACAGTCTTTGCCAGCGGACCCAGC	1112
QY	259	ProLeuProProValLysPheValValGlyAlaIleAlaGlyAlaAsnThrLeuThrGly	278
Db	1113	CCGCTGTCCCCCGTCAAGCTTGTGGTGGGTGCGATGGCAGGCGCCAAACGCCCTGTCTGGGC	1172
QY	279	IleSerCysGlyLeuLeuAlaSerValAspAlaLeuThrPheGlyGlnPheSerGluTyr	298
Db	1173	ATTTCTGTGGTCTCTGGCCTCGGTGGACGCCTTGACCTATGGTCAGTTGCTGAGTAT	1232
QY	299	GlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaThrGlyPheLeuAlaValLeuGly	318
Db	1233	GGAGCCCGCTGGGAGAGCGGTCTGGGCTGCCAGGCTACGGGCTTCTTGGCTGTCTGGGT	1292
QY	319	SerGluAlaSerValLeuLeuLeuThrLeuAlaAlaValGlnCysSerValSerValSer	338
Db	1293	TCAGAGGCGTGGTGCTGCTGCTCACACTGGCGCGCTGCAGTGCAGCATCTCCGTGACC	1352
QY	339	CysValArgAlaTyrGlyLysSerProSerLeuGlySerValArgAlaGlyValLeuGly	358
Db	1353	TGCGTCCGAGCCTACGGGAAGCGCCGCTCGCCTTGGCAGCGTCCGCGCAGGCGCACTGGGA	1412

QY	359	CysLeuAlaLeuAlaGlyLeuAlaAlaAlaLeuProLeuAlaSerValGlyGluTyrGly	378
Db	1413	TGCCTGGCGCTGGCCGGCTGGCCGACACTGCCCTGGCTGGCTCGGTGGAGAGTATGGC	1472
QY	379	AlaSerProLeuCysLeuProTyrAlaProProGluGlyGlnProAlaAlaLeuGlyPhe	398
Db	1473	GCCTCCCCACTGTGCTGCCCTACGCCCCACCGAGGGCCGCGGCTGCCCTGGGCTTC	1532
QY	399	ThrValAlaLeuValMetMetAsnSerPheCysPheLeuValValAlaGlyAlaTyrIle	418
Db	1533	GCTGTAGCCCTGGTGATGATGAACTCGCTCTGCTTCTTGGTGGCCGCGCCTACATC	1592
QY	419	LysLeuTyrCysAspLeuProArgGlyAspPheGluAlaValTrpAspCysAlaMetVal	438
Db	1593	AAGCTCTACTGTGACCTGCCACGGGGTGACTTTGAGGCCGTGTGGGACTGCGCCATGGTG	1652
QY	439	ArgHisVal-AlaTrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPheLe	458
Db	1653	CGCCACGTGGCGCTGGCTCATCTTTGCAGATGGCCTCCTCTACTGCCCGTGGCCTTCCT	1712
QY	458	uSerPheAlaSerMetLeuGlyLeuPheProValThrProGluAlaValLysSerValLe	478
Db	1713	CAGCTTTGCCCTCTATGCTGGCCTCTTCCCTGTCAACCCGAGGCTGTCAAGTCAGTCCT	1772
QY	478	uLeuValValLeuProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnPr	498
Db	1773	TCTGGTGGTGCCTCTGCCTGCCTGCCTCAACCCACTGCTCTACTGCTCTTCAACCC	1832
QY	498	oHisPheArgAspAspLeuArgArgLeuArgProArgAlaGlyAspSerGlyProLeuAl	518
Db	1833	TCACCTCCGGGATGACCTTCGGCGGCTCTGGCCAAGCCCTCGGTCCCAGGGCCCCCTAGC	1892
QY	518	aTyrAlaAlaAlaGlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuValAl	538
Db	1893	CTACGCTGCAGCCGGTGAGCTGGAGAAAGACTCTCGACTCCACCCAAGCGCTGGTGGC	1952
QY	538	apheSerAspValAspLeuIleLeuGluAlaSerGluAlaGlyArgProProGlyLeuGl	558
Db	1953	TTTCTCAGATGGGATCTTATTCTGGAAGCTTCTGAGGCTGGGCAGCCTCTGGGCTAGA	2012
QY	558	uThrTyrGlyPheProSerValThrLeuIleSerCysGlnGlnProGlyAlaProArgLe	578
Db	2013	GACCTATGGCTTCCCTTCAGTGACCTCATCTCCGACATCAGCGGGGGCTACCAAGCT	2072
QY	578	uGluGlySerHisCysValGluProGluGlyAsnHisPheGlyAsnProGlnProSerMe	598
Db	2073	GGAGGGAAACCATTTTGTAGAGTCTGATGGAACCAAGTTTGGGAACCCACACCTCCCAT	2132
QY	598	tAspGlyGluLeuLeuArgAlaGluGlySerThrProAlaGlyGlyLeuSerGl	618
Db	2133	GAAGGGAGAACTGCTGCTGAAGGCAGGGAGCCACTTTTGGCAGGCTGTGGCTCTTCCGT	2192
QY	618	yGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSerHisVal	633
Db	2193	GGGTGGAGCCCTCTGGCCCTCTGGCTCTCTCTTTTGCCCTCTCACTTG	2238
RESULT 3			
AK085901			
LOCUS			
DEFINITION			
AK085901 3583 bp mRNA linear HTC 03-APR-2004			
Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched			
library, clone:D830026M09 product:CDNA FLJ14471 FIS, CLONE			
MAMMA1001030, WEAKLY SIMILAR TO LUTROPIN-CHORIOGONADOTROPIC HORMONE			
RECEPTOR homolog [Homo sapiens], full insert sequence.			
AK085901			
VERSION			
AK085901.1 GI:26103061			
KEYWORDS			
HTC; CAP trapper.			
SOURCE			
Mus musculus (house mouse)			
ORGANISM			
Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
1			
REFERENCE			
Carninci,P. and Hayashizaki,Y.			
AUTHORS			
High-efficiency full-length cDNA cloning			
TITLE			

Db 1872 :||||| ||||||| |||||||:|||||:|||||:||||| ||||| |||||:||||| 1931

Qy 278 yIleSerCysGlyLeuLeuAlaSerValAspAlaLeuThrPheGlyGlnPheSerGluTy 298

Db 1932 CATTTCTGTGTCTCCTGGCCTCGGTGGACGCCTTGACCTATGGTCAGTTTCGCTGAGTA 1991

Qy 298 rGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaThrGlyPheLeuAlaValLeuG1 318

Db 1992 TGGAGCCCGCTGGGAGAGCGGTCTGGGCTGCCAGGCTACGGGCTTCCTGGCTGTCCTGGG 2051

Qy 318 ySerGluAlaSerValLeuLeuThrLeuAlaAlaValGlnCysSerValSerValSe 338

Db 2052 TTCAGAGCGTCGGTGTCTGTCTCACACTGGCGCGCTGAGTGCAGCATCTCCGTGAC 2111

Qy 338 rCysValArgAlaTy rGlyLySerPro-SerLeuGlySerValArgAlaGlyValLeuG 358

Db 2112 CTGGCTCCGAGCCTACGGGAAGCGCGCTCGCCTGGCAGCGTCCGGCAGGCGCACTTG 2171

Qy 358 lyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLeuAlaSerValGlyGluTy rG 378

Db 2172 GATGCTGCCGCTGGCCGGCTGGCCCGCAGCACTGCCGCTGGCTCGTGGGAGAGTATG 2231

Qy 378 lyAlaSerProLeuCysLeuProTy rAlaProProGluGlyGlnProAla-AlaLeuGly 397

Db 2232 GCGCTCCCCACTCTGCCTGCCCTACGCCCCACCCAGGCGCGCGCTGCCCTGGCGGC 2291

Qy 398 PheThrValAlaLeuValMetMetAsnSerPheCysPheLeuValValAlaGlyAlaTy r 417

Db 2292 TTCGTGTAGCCCTGGTGATGATGAACCTCGCTCTGCTTCTGTGTGGTGGCCGCGCTAC 2351

Qy 418 IleLy sLeuTy rCysAspLeuProArgGlyAspPheGluAlaValTrpAspCysAlaMet 437

Db 2352 ATCAAGCTCTACTGTGACCTGCCACGGGTGACTTTGAGGCCGTGTGGGACTCGGCCATG 2411

Qy 438 ValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLeuTy rCysProValAlaPhe 457

Db 2412 GTGCGCCACGTGGCCTGGCTCATCTTTGCAGATGGCCTCTCTACTGCCCCCGTGGCCTTC 2471

Qy 458 LeuSerPheAlaSerMetLeuGlyLeuPheProValThrProGluAlaValLy sSerVal 477

Db 2472 CTCAGCTTTGCCTCTATGCTGGGCCTCTTCCCTGTCAACCCCGAGGCTGTCAAGTCAGTC 2531

Qy 478 LeuLeuValValLeuProLeuProAlaCysLeuAsnProLeuLeuTy rLeuLeuPheAsn 497

Db 2532 CTCTGTGGTGTGCTGCCTCTGCCTGCCTGCCTCAACCCACTGCTCTACCTGCTCTTAAAC 2591

Qy 498 ProHisPheArgAspAspLeuArgArgLeuArgProArgAlaGlyAspSerGlyProLeu 517

Db 2592 CTTCACTTCGGGATGACCTTCGGCGGCTCTGGCCAAAGCCCTCGGTCCCCAGSGCCCTA 2651

Qy 518 AlaTy rAlaAlaAlaGlyGluLeuGluLy sSerSerCysAspSerThrGlnAlaLeuVal 537

Db 2652 GCCTACGCTGCAGCCGGTGAGCTGGAGAAGACTCTTCGCACTCCACTCAAGCGCTGGTG 2711

Qy 538 AlaPheSerAspValAspLeuIleLeuGluAlaSerGluAlaGlyArgProProGlyLeu 557

Db 2712 GCTTTCTCACATGTGGATCTTATTCTGGAAGCTTCTGAGGCTGGGCAAGCCTCTCGGGGTA 2771

Qy 558 GluThrTy rGlyPheProSerValThrLeuIleSerCysGlnGlnProGlyAlaProArg 577

Db 2772 GAGACCTATGGCTTCCCTTCAGTGACCTCATCTCCGACATCAGCCGGGGGTACCAGG 2831

Qy 578 leuGluGlySerHisCysValGluProGluGlyAsnHisPheGlyAsnProGlnProSer 597

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Qy 598 MetAspGlyGluLeuLeuLeuArgAlaGluGlySerThrProAlaGlyGlyLeuSer 617

Db 2892 ATGAAGGGAGAACTGCTGTGAAGGCAGAGGGAGCCACTTTGGCAGGCTGTGCTCTTCC 2951

Qy 618 GlyGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSerHisVal 633

Db 2952 GTGGGTGGAGCCCTCTGGCCCTCTGGCTCTCTGGCTCTCTTTCCTCTCACTTG 2999

RESULT 4

AY411732 2724 bp DNA linear GSS 16-DEC-2003

LOCUS Homo sapiens GPR49 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

DEFINITION AY411732

ACCESSION AY411732

VERSION AY411732.1 GI:39767700

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2724)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2724)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

Location/Qualifiers

source

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/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

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/locus_tag="HCM4322"

ORIGIN

Alignment Scores:

Pred. No.: 1.51e-107 Length: 2724

Score: 1275.00 Matches: 250

Percent Similarity: 64.92% Conservative: 96

Best Local Similarity: 46.90% Mismatches: 157

Query Match: 38.55% Indels: 30

DB: 9 Gaps: 8

US-10-664-667-5 (1-633) x AY411732 (1-2724)

Qy 54 LysLeuGlu***AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLeuSerTrp 73

Db 1162 GAAATTAAAGTTGACACTTTCAGCAGTTCCTAGCCTCCGATCGCTGAATTGGCTTG 1221

Qy 74 AsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuValLysLeu 93

Db 1222 AACAAAATTGCTATTATTACCCCAATGCATTTCCACTTTGCCATCCCTAATAAAGCTG 1281

Qy 94 AspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyLeuMetHis 113

Db 1282 GACCTATCGTCCAACCTCCTGTCTCTTTTCCATAACTGGGTTACATGGTTAAACTCAC 1341

Qy 114 LeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPheProLys 133

Db 1342 TTAAAATTACAGGAAATCATGCTTACAGAGCTTGATATCATCTGAAAAACTTCCAGAA 1401

Qy 134 LeuArgIleLeuGluValProTy rAlaTy rGlnCysCysProTy rGlyMetCysAlaSer 153

Db 1402 CTCAAGGTTATAGAAATGCCTTATGCTTACCAGTGTGTCATTGGAGTGTGTGAGAAT 1461

QY 154 PhePheLysAlaSerGlyGlnTrp-----GluAlaGluAspLeuHis 167
Db 1462 GCCTATAAGATTCTAATCAATGAATAAAGGTGACAAACAGCAGTATGGACGACCTTCAT 1521
QY 168 LeuAspAspGluGluSerSerLysArgProLeuGlyLeuLeuAlaAargGlnAlaGluAen 187
Db 1522 -----AAGAAAGATGCTGGAATGTTTCAGGCTCAAGATGAA--- 1557
QY 188 HisTyrAspGlnAspLeuAspGluLeuGlnLeuGluMet---GluAspSerLysProHis 206
Db 1558 -----CGTGACCTTGAAGATTTCCTGCTTGACTTTTGAGAAAGACCTGAAAGCCCTT 1608
QY 207 ProSerValGlnCysSerProThrProGlyProPheLysProCysGluTyrLeuPheGlu 226
Db 1609 CATTGAGTCAGTGTTCACCTTCCCGAGGCCCTTCAAACCCCTGTGAACACCTGCTTGAT 1668
QY 227 SerTrpGlyIleArgLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGly 246
Db 1669 GGCTGGCTGATCAGAATTGGAGTGTGGACCATAGCAGTTCTGGCACTTACTTGTATGCT 1728
QY 247 LeuValLeuLeuThrValPheAlaGlyGlyProAlaProLeuProProValLysPheVal 266
Db 1729 TTGGTGACTTCAACAGTTTTTCAGA---TCCCCTCTGTACATTTCCCCCATTAACCTGTA 1785
QY 267 ValGlyAlaIleAlaGlyAlaAenThrLeuThrGlyIleSerCysGlyLeuLeuAlaSer 286
Db 1786 ATTGGGGTCATCGCAGCAGTGAAACATGCTCACGGGAGTCTCCAGTGCCTGTGGCTGGT 1845
QY 287 ValAspAlaLeuThrPheGlyGlnPheSerGluTyrGlyAlaAargTrpGluThrGlyLeu 306
Db 1846 GTGGATGCGTTCACCTTTTGGCAGCTTTGCACGACATGGTGCGCTGGTGGGAGAAATGGGGTT 1905
QY 307 GlyCysArgAlaThrGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeu 326
Db 1906 GGTTCGCATGTCAATTGGTTTTTTGTCCATTTTGTGCTTCAGAATCATCTGTTTTCTGCTT 1965
QY 327 ThrLeuAlaAlaValGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSer 346
Db 1966 ACTCTGGCAGCCCTGGAGCGTGGGTCTCTGTGAAATATTTCTGCAAAATTTGAAACGAAA 2025
QY 347 ProSerLeuGlySerValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAla 366
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QY 367 AlaAlaLeuProLeuAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyr 386
Db 2086 GCGCAGTTCCCTGCTGGTGGCAGCAAGTATGGCGCTCCCTCTCTGCTGCCTTTG 2145
QY 387 AlaProProGluGlyGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsn 406
Db 2146 -----CCTTTTGGGAGCCCGACCATGGGCTACATGCTGCTCTCATCTTGCTCAAT 2199
QY 407 SerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArg 426
Db 2200 TCCCTTTGCTTCTCATGATGACCATTTGCCTACACCAAGCTCTACTGCAATTTGGACAAG 2259
QY 427 GlyAspPheGluAlaValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePhe 446
Db 2260 GGAGACCTGGAGAATATTTGGGACTGCTCTATGGTAAACACATCTGCCCTGTTGCTCTTC 2319
QY 447 AlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeu 466
Db 2320 ACCAACTGCATCCTAAACTGCCTGTGGCTTTCTTGTCTCTCTCTCTTTAATAAACCTT 2379
QY 467 PheProValThrProGluAlaValLysSerValLeuLeuValValLeuProLeuProAla 486
Db 2380 ACATTATCAGTCCTGAAGTAATTAAGTTTATCCCTTCTGGTGGTAGTCCCACTTCTCGCA 2439
QY 487 CysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgArg 506
Db 2440 TGTCTCAATCCCTTCTCTACATCTTGTTCATCTCAATCCTTAAGGAGGATCTGGTGAGC 2499
QY 507 LeuArgProArgAla-----GlyAspSerGlyProLeuAlaTyrAlaAla 521

Db 2500 CTGAGAAAGCAAAACCTACGTTCTGGACAAGATCAAAAACACCAAGCTTGATGTCAATTAAC 2559
QY 522 AlaGlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuValAlaPheSerAsp 541
Db 2560 TCTGATGATGTCGAAAAACAGTCTCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGC 2619
QY 542 ValAspLeuIleLeuGluAlaSerGluAlaGlyArgPro-----ProGlyLeu 557
Db 2620 TCCAGCATCACTTATGACCTGCCTCCCAGTTCCTGGTGCATCACCAGCTTATCCAGTGACT 2679
QY 558 GluThrTyrGlyPheProSerValThrLeuIleSerCys 570
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RESULT 5
AY411734 2724 bp DNA linear GSS 16-DEC-2003
LOCUS
DEFINITION Mus musculus GPR49 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY411734
VERSION AY411734.1 GI:39767702
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2724)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2724)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
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gene <1..>2724
/gene="GPR49"
ORIGIN /locus_tag="HCM4322"
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Score: 1231.00 Matches: 245
Percent Similarity: 65.84% Conservative: 102
Best Local Similarity: 46.49% Mismatches: 162
Query Match: 37.22% Indels: 18
DB: 9 Gaps: 8
US-10-664-667-5 (1-633) x AY411734 (1-2724)
QY 54 LysLeuGlu**AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLeuSerTrp 73
Db 1162 GAAATTAAGGGCAGCACACTTTTCAGCAGTTGTTTAACCTCCGATCTCTGAACCTAGCATGG 1221
QY 74 AsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuValLysLeu 93
Db 1222 AATAAAATTGCTATCATTCACCCCAATGCGTTTTTCTACGTTGCCGTTCTCTAATAAAGTTG 1281

Alignment Scores:		1.03e-89	Length:	812
Pred. No.:		1075.50	Matches:	223
Score:		88.41%	Conservative:	21
Percent Similarity:		80.80%	Mismatches:	27
Best Local Similarity:		32.52%	Indels:	8
Query Match:		4	Gaps:	3
DB:				
US-10-664-667-5 (1-633) x BG916782 (1-812)				
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Qy	151	CysAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspAsp	170	
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Qy	171	GluGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAsp	190	
Db	121	GAGGAGGCACCAAGAGGCCCTGGGTCTCCTTGTGTGACAAGCTGAGAACCACTATGAC	180	
Qy	191	GlnAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGln	210	
Db	181	CTAGACCTGGATGAGCTCCAGATGGGGACAGAGGACTCAAAGCCAAACCCAGTTCAG	240	
Qy	211	CysSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGlyIle	230	
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Qy	251	ThrValPheAlaGlyGlyProAlaProLeuProProValLysPheValValGlyAlaIle	270	
Db	361	ACAGTCTTTGCCAGCGGACCAGC-CGGCTGTCCCCCGTCAAGCTTGTGTGGTGGCGATG	419	
Qy	271	AlaGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeu	290	
Db	420	GCAGCGCCCAACGCCCTGACGGGCATTTCTGTGTTCTCTCGCCTCGGTGGACGCCCTG	479	
Qy	291	ThrPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAla	310	
Db	480	ACCTATGGTCAGTTCGCTGAGTATGGAGCCCGCTGGGAGAGCGGTCTGGGCTGCCAGCT	539	
Qy	311	ThrGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAla	330	
Db	540	ACGGCTTCCTGGCTGTCTGGGTTCAGAGGCGTCCGTGCTGCTGCCTCACACTGGCGGG	599	
Qy	331	ValGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGly	350	
Db	600	GTGAGTGCAGCATCTCTGTGACCTGCGTCCGAGCCTACGGGAAGCGCCGTCGCT-CGC	658	
Qy	351	SerValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuPro	370	
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Qy	371	LeuAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGlu	390	
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Qy	391	GlyGln-ProAlaAlaLeuGlyPheThrValAlaLeuValMetMet	405	
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RESULT 7
BG863804
LOCUS
DEFINITION BG863804 819 bp mRNA linear EST 29-MAY-2001
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mRNA sequence.
ACCESSION BG863804

VERSION BG863804.1 GI:14214342
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 819)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10863 Row: a column: 01
High quality sequence stop: 758.

FEATURES
Location/Qualifiers
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/clone_lib="NCI_CGAP_Mam4"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."

ORIGIN
Alignment Scores:
Pred. No.: 1.91e-88 Length: 819
Score: 1062.00 Matches: 215
Percent Similarity: 87.74% Conservative: 14
Best Local Similarity: 82.38% Mismatches: 29
Query Match: 32.11% Indels: 4
DB: 0
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Qy 46 AlaSerAsnThrThrAlaSerGlyLysLeuGlu***AspThrPheSerGlnLeuSerSer 65
Db 42 GCCTCCGACATAACAGGATCAAGGAAATTGGT-GCAGATACCTTCAGCCAGCTGGGCTCC 100
Qy 66 LeuGlnAlaLeuAspLeuSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSer 85
Db 101 TTGCAAGCTTTAGACCTGAGTTGGAATGCCATCCGTCCATCCACCTGAGGCTTTCTCA 160
Qy 86 ThrLeuHisSerLeuValLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeu 105
Db 161 ACCCTTCGATCCTTGGTTAAGCTGGACCTGACTGACACACAGCTGACCACTGCCCTG 220
Qy 106 AlaGlyLeuGlyGlyLeuMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAla 125
Db 221 GCTGGGCTGGGAGGCTGATGCACCTGAAGCTCAAAGGAACTTGGCCCTGTCTCAGGCC 280
Qy 126 PheSerLysAspSerPheProLysLeuArgIleLeuGluVal-ProTyrAlaTyrGlnCy 145
Db 281 TTCTCCAAGGACAGTTTCCAAAACCTGAGGATCCTCGGAGTGCCCCCTACGCCTACCA 340
Qy 145 sCysProTyrGlyMetCysAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAs 165

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453	Cys	Pro	ValAla	AlaPhe	LeuSerPhe	AlaSerMetLeu	GlyLeuPheProValThrProGlu	472
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473	Ala	Val	LysSer	ValLeu	ValValLeu	ProAlaCys	LeuAsnProLeuLeu	492
2123	ATA	TGA	AGTCTGTT	ACGCTGATATCTT	CCCGCTGCCTTGCCTT	CGCTGAATCCAGT	CTCTG	2182
493	Tyr	Leu	LeuPhe	AsnPro	HisPhe	ArgAspAspLeu	ArgLeuArgProArgAlaGly	512
2183	TAC	GT	TTCTTCA	CCCCAAAGTTAA	AGACGACTGGA	AGCTCCTG	AAGCGCGTGTCA	2242
512	-----	-----	-----	-----	-----	-----	-----	512
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513	-----	-----	Asp	SerGlyPro	LeuAlaTyr	AlaAlaGlyGlu	LeuGluLysSerSer	529
2303	TTCT	ACTAC	GACTGTGG	CATGTATTCC	CACTTGCAGG	GTAACTGACTGTCTGT	GACTGC	2362
530	Cys	Asp	SerThr	GlnAla	LeuValAla	PheSerAsp	ValAspLeuIleLeuGluAlaSer	549
2363	TGT	GAGT	CATTTCTT	CTGACAAA	ACCAGTATCGT	GCAACACTTA	ATA-----	2410
550	Glu	AlaGly	ArgPro	GlyLeu	GluThrTyr	GlyPhePro	SerValThrLeuIleSer	569
2411	-----	-----	-----	-----	AAATGC	ACAGTTGTCT	CTGTATTGACAGTGGCCTCT	2446
570	Cys	GlnGln	ProGly	Ala	575			
2447	TGC	CAGAGG	CCAGAG	GCC	2464			

BG916963
LOCUS
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BG916963
753 bp mRNA linear EST 05-JUN-2001
602816251F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4935180 5',
mRNA sequence.
BG916963
BG916963.1 GI:14297439
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 753)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

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/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="IMAGE:4935180"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam6"

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BG916963 753 bp mRNA linear EST 05-JUN-2001
 602816251F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4935180 5',
 mRNA sequence.
 BG916963
 BG916963.1 GI:14297439
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 753)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM10865 row: f column: 13
 High quality sequences stop: 644.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

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	/sex="male"	
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	/dev_stage="adult"	
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	Alignment Scores:	
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	Best Local Similarity:	85.92% Mismatches: 23
	Query Match:	28.09% Indels: 1
	DB:	3 Gaps: 0
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Qy	422	CysAspLeuProArgGlyAspPheGluAlaValTrpAspCysAlaMetValArgHisVal 441
Db	3	TGTGACCTGCCACGGGTGACTTTGAGGCCGTGTGGGACTGGCCATGGTGGCCACGTG 62
Qy	442	AlaTrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPheAla 461
Db	63	GCCTGGTCATCTTTGCAGATGGCCTCCTCTACTGCCCGGTGGCCTTCCTCAGCTTGCC 122
Qy	462	SerMetLeuGlyLeuPheProValThrProGluAlaValLysSerValLeuLeuValVal 481
Db	123	TCTATGCTGGCCTCTTCCTGTACCCCCGAGGCTGTCAAGTCAGTCCTTCTGGTGGTG 182
Qy	482	LeuProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPheArg 501
Db	183	CTGCCTCTGCCTGCCTGCCTCAACCCACTGCTCTACCTGCTCTTCAACCCCTCACTCCGG 242
Qy	502	AspAspLeuArgArgLeuArgPro-ArgAlaGlyAspSerGlyProLeuAlaTyrAlaAl 521
Db	243	GATGACCTTCGGCGGCTCTGGCCAAGCCCTCGGTCCCCAGGGCCCCCTAGCCTACGCTGC 302
Qy	521	aAlaGlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuValAlaPheSerAs 541
Db	303	AGCCGGTGAGCTGGAGAAGAGTCTCTGCGACTCCACCCCAAGCGCTGGTGGCTTTCAGA 362
Qy	541	pValAspLeuIleLeuGluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyrGl 561
Db	363	TGTGGATCTTATTCTGGAAGCTTCTGAGGCTGGGCAGCCCTCTGGGCTAGAGACCTATGG 422
Qy	561	yPheProSerValThrLeuIleSerCysGlnGlnProGlyAlaProArgLeuGluGlySe 581
Db	423	CTTCCCTTCAGTGACCCCTCATCTCCCGACATCAGCCGGGGGCTACCAGGCTGGAGGAAA 482
Qy	581	rHisCysValGluProGluGlyAsnHisPheGlyAsnProGlnProSerMetAspGlyGl 601
Db	483	CCATTGTGAGAGTCTGATGGAACCAAGTTTGGGAACCCACAACCTCCCATGAAGSGAGA 542
Qy	601	uLeuLeuLeuArgAlaGluGlySerThrProAlaGlyGlyGlyLeuSerGlyGlyGl 621
Db	543	ACTGCTGCTGAAGGCAGAGGGAGCCACTTTTGGCAGGCTGTGGCTCTTCCGTGGGTGGAGC 602

Qy	621	yPheGlnProSerGlyLeuAlaPheAlaSerHisVal 633
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RESULT 13	BB636845	
	LOCUS	
	DEFINITION	BB636845 RIKEN full-length enriched, adult male aorta and vein Mus
	MUSCULUS	musculus cDNA clone A530037C04 5', mRNA sequence.
	ACCESSION	BB636845
	VERSION	BB636845.1 GI:16472635
	KEYWORDS	EST.
	SOURCE	Mus musculus (house mouse)
	ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 690)	
	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.	
	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)	
	Unpublished (2001)	
	Contact: Yoshihide Hayashizaki	
	Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute	
	The Institute of Physical and Chemical Research (RIKEN)	
	1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan	
	Tel: 81-45-503-9222	
	Fax: 81-45-503-9216	
TITLE	Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/	
	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.	
	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)	
	wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.	
	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)	
	Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.	
	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)	
	Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.	
	Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)	
	Please visit our web site (http://genome.gsc.riken.go.jp) for further details.	
FEATURES	e mouse tissues.	
	Location/Qualifiers	
	1..690	
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	/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia	

Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was comried with a primer [5', GAGAGAGAGATCCAAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC 1."

ORIGIN

Alignment Scores:
Pred. No.: 1e-74 Length: 690
Score: 914.00 Matches: 181
Percent Similarity: 88.68% Conservative: 7
Best Local Similarity: 85.38% Mismatches: 24
Query Match: 27.64% Indels: 1
DB: 2 Gaps: 0

US-10-664-667-5 (1-633) x BB636845 (1-690)

QY 422 CysAspLeuProArgGlyAaspPheGluAlaValTrpAspCysAlaMetValArgHisVal 441
Db 1 TGTGACCTGCCACGGGGTGACTTTGAGGCCGTGTGGACTGCGCCATGGTGGCCACGTG 60
QY 442 AlaTrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPheAla 461
Db 61 GCCTGGCTCATCTTTGCAGATGGCCTCCTACTGCCCCGTGGCCTTCTCAGCTTTGCC 120
QY 462 SerMetLeuGlyLeuPheProValThrProGluAlaValLysSerValLeuValVal 481
Db 121 TCTATGCTGGGCCTCTTCCCTGTACCCCCGAGGCTGTCAAGTCAGTCCCTTCTGGTGGTG 180
QY 482 LeuProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPheArg 501
Db 181 CTGCCTCTGCCTGCCTCAACCCACTGCTCTACCTGCTCTTCAACCCCTCACTTCCGG 240
QY 502 AspAspLeuArgArgLeuArgProArgAlaGlyAaspSerGlyProLeuAlaTyrAlaAla 521
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QY 522 AlaGlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuValAlaPheSerAsp 541
Db 301 GCCGGTGAGCTGGAGAAAGAGCTCCTCGACTCCACCCCAAGCGCTGGTGGCTTCTCAGAT 360
QY 542 ValAspLeuIleLeuGluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyrGly 561
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QY 562 PheProSerValThrLeuIleSerCysGlnGlnProGlyAlaProArgLeuGluGlySer 581
Db 421 TTCCCTTCAGTGACCCTCATCTCCGACATCAGCGGGGGGTACCAGGCTGGAGGGAAAC 480
QY 582 HisCysValGluProGluGlyAsnHisPheGlyAsnProGlnProSerMetAspGlyGlu 601
Db 481 CATTTTGATAGTCTGATGAACCAAGTTTGGGAACCCACAACTCCCATGAAGGGAGAA 540
QY 602 LeuLeuArgAlaGluGlySerThrProAlaGlyGlyLeuSerGlyGlyGlyGly 621
Db 541 CTGCTGCTGAAGGCAGAGGGAGCCACTTTGGCAGGCTGTGGCTCTTCCGTGGGTGGAGCC 600
QY 622 PheGlnProSerGlyLeuAlaPheAlaSerHisVal 633
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RESULT 14
BF158974

LOCUS BF158974 869 bp mRNA linear EST 30-OCT-2000
DEFINITION 601766476F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3982506 5', mRNA sequence.
ACCESSION BF158974
VERSION BF158974.1 GI:11039068
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 869)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM9181 row: g column: 19
High quality sequence stop: 640.
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Stem cell origin."
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/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Alignment Scores:
Pred. No.: 4.3e-72 Length: 869
Score: 887.50 Matches: 212
Percent Similarity: 77.78% Conservative: 19
Best Local Similarity: 71.38% Mismatches: 39
Query Match: 26.84% Indels: 32
DB: 2 Gaps: 4

US-10-664-667-5 (1-633) x BF158974 (1-869)

QY 175 LysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspGlnAspLeuAsp 194
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QY 195 GluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCysSerProThr 214
Db 61 GAGCTCCAGATGGGGACAGAGGACTCAAAGCCAAACCCAGTGTCCAGTGCAGCCCTGTT 120
QY 215 ProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGlyIleArgLeuAlaVal 234
Db 121 CCAGGCCCTTCAAGCCCTGCGAGCACCTCTTTGAGAGCTGGGGCATCCGCTTGCTGTG 180
QY 235 TrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuThrValPheAla 254
Db 181 TGGGCCATCGTGTCTCTCCGTACTCTGTAAACGGGCTGGTGTGCTGACAGTCTTTGCC 240
QY 255 GlyGlyProAlaProLeuProProValLysPheValValGlyAlaIleAlaGlyAlaAsn 274
Db 241 AGCGGACCCAGCCCGTGTCCCCCGTCAAGCTTGTGGTGGGTGCGATGGCAGGCGCCAAC 300
QY 275 ThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuThrPheGlyGln 294

Db 301 |||||GCCTGACGGCATTTCTCTGGTCTCTCGCTCGGTGGACGCCCTTGACCTATGCTCAG 360

QY 295 PheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaThrGlyPheLeu 314
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Db 361 TTCGCTGAGTATGGAGCCCGCTGGAGAGCGGTCTGGGTGCCAGGCTACGGGCTTCCTG 420
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QY 315 AlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaValGlnCysSer 334
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Db 421 GCTGTCTGGTTTCAGAGCGGTGGTGTCTGCTGCCTACACTGGCGGCGGTGCAGTCAGC 480
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QY 335 ValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySerValArgAla 354
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Db 481 ATCTCTGTGACCTG-GTCCGAGCCTACGGGAAGGCGCGTCTGCT-GGCAGCGTCCGCGCA 538
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QY 355 GlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLeuAlaSerVal 374
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QY 375 GlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaPro-ProGluGlyGlnProAl 394
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Db 598 GGAGAGTATGGCGCCTCCCATCTGACGTGCCTAAGCCCCCACCCGAGTGGCGGCGGC 657
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QY 394 aAlaLeu-GlyPheThrValAlaLeuValMetMet-----AsnSerPheCysPheL 411
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Db 658 GGCCTGGGGCTTCGCTGTAAACCTTGTTTGATTGATTGACACTCCGCTCTGGCTCCCTGG 717
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QY 411 euValValAlaGlyAlaTyrIleLys-LeuTyrCysAspLeuProArgGlyAspPheGlu 430
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QY 431 AlaVal-----TrpAspCysAlaMetVal 438
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RESULT 15
CN258480
LOCUS CN258480 680 bp mRNA linear EST 16-MAY-2004
DEFINITION 1700532179685 GRN_ES Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN258480
VERSION CN258480.1 GI:47274894
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 680)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation

JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
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FEATURES
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/db_xref="taxon:9606"
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and H9 (p26) maintained in feeder-free conditions"

ORIGIN
Alignment Scores: 2.33e-64 Length: 680
Pred. No.: 803.00 Matches: 171
Score: 89.11% Conservative: 9
Percent Similarity: 84.65% Mismatches: 16
Best Local Similarity: 24.28% Indels: 8
Query Match: 7 Gaps: 2
DB:

US-10-664-667-5 (1-633) x CN258480 (1-680)

QY 12 CysArgTyrArg-----SerGlyIleProGlySer-ThrHisAlaSerValGluAr 28
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Db 79 TGCTCCCATCGGGGATGTGCCAACAGCTGCCAGGCTCCGAGTCTTGGAACCTGTCTCACA 138
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QY 28 gSerGln--GlyLeuSerLeuProAlaHisProAlaSerLeuAlaLeuAlaAlaSe 47
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Db 139 ATCAAATTGAGGAGCTGCCAGCCTGCACAGGTGTACAGAAATTGGAGGAAA-TCGGCCTC 197
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QY 47 rAsnThrThrAlaSerGlyLysLeuGlu**AspThrPheSerGlnLeuSerSerLeuG1 67
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QY 67 nAlaLeuAspLeuSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLe 87
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Db 257 AGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCGAGGCCTTCTCCACCT 316
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QY 87 uHisSerLeuValLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaG1 107
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Db 317 GCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACTGCCCTGGCTGG 376
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QY 107 YLeuGlyGlyLeuMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSe 127
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Db 377 ACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCAGGCTTCTC 436
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QY 127 rLysAspSerPheProLysLeuArgIle-LeuGluValProTyrAlaTyrGlnCysCysP 147
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Db 437 CAAGGACAGTTTCCCAAAACTGAGGATCCTTGGAGGTGCCTTATGCCTACCAGTGTGTC 496
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QY 147 roTyrGlyMetCysAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuH 167
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Db 497 CCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGAGTGGGAGGCTGAAGACCTTC 556
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QY 167 isLeuAspAspGluGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluA 187
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Db 557 ACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTCGGCCTCCTTGGCAGACAAGCAGAGA 616
|||:|||||

QY 187 snHisTyrAspGlnAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisP 207
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Db 617 ACCACTATGACCAGGACTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACC 676
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QY 207 ro 207
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Db 677 CC 678
|||:|||||

Search completed: April 14, 2005, 21:48:37
Job time : 3652 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 14, 2005, 18:46:01 ; Search time 210 Seconds
(without alignments)
4932.206 Million cell updates/sec

Title: US-10-664-667-5
Perfect score: 3307
Sequence: 1 NTHYRESWYACRYRSGIPG.....GGLSGGGGFPQPSGLAFASHV 633

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3040	91.9	2988	4 US-09-799-451-723	Sequence 723, App
2	1275	38.6	2724	4 US-09-170-496D-263	Sequence 263, App
3	1275	38.6	4570	4 US-09-976-594-201	Sequence 201, App
4	1269	38.4	2724	4 US-09-170-496D-277	Sequence 277, App
5	958	29.0	4203	2 US-08-866-757-1	Sequence 1, Appli
6	958	29.0	4203	3 US-09-153-593-1	Sequence 1, Appli
7	957	28.9	2612	4 US-09-495-050A-214	Sequence 214, App
8	759	23.0	453	3 US-09-397-787-240	Sequence 240, App
9	595.5	18.0	723	4 US-09-495-050A-220	Sequence 220, App
10	414.5	12.5	2179	1 US-08-487-886-1	Sequence 1, Appli
11	414.5	12.5	2179	2 US-08-531-070A-1	Sequence 1, Appli
12	414.5	12.5	2179	3 US-08-482-855-1	Sequence 1, Appli

13	414.5	12.5	2179	3 US-08-474-986-1	Sequence 1, Appli
14	414.5	12.5	2393	4 US-09-016-434-1209	Sequence 1209, Ap
15	414.5	12.5	4417	3 US-07-741-453A-57	Sequence 57, Appl
16	408	12.3	2413	4 US-09-016-434-1469	Sequence 1469, Ap
17	404.5	12.2	3549	4 US-09-826-509-586	Sequence 586, App
18	403.5	12.2	2292	4 US-09-826-509-402	Sequence 402, App
19	403.5	12.2	3710	3 US-07-741-453A-62	Sequence 62, Appl
20	398.5	12.1	2292	4 US-09-826-509-394	Sequence 394, App
21	398.5	12.1	2292	4 US-09-826-509-406	Sequence 406, App
22	393.5	11.9	2292	4 US-09-826-509-398	Sequence 398, App
23	391.5	11.8	2292	4 US-09-826-509-414	Sequence 414, App
24	389.5	11.8	2292	4 US-09-826-509-410	Sequence 410, App
25	388.5	11.7	2469	4 US-09-186-350A-54	Sequence 54, Appl
26	387.5	11.7	2292	4 US-09-826-509-418	Sequence 418, App
27	385.5	11.7	2292	4 US-09-826-509-422	Sequence 422, App
28	383.5	11.6	3018	4 US-09-016-434-1468	Sequence 1468, Ap
29	381	11.5	2022	3 US-07-757-342D-9	Sequence 9, Appli
30	381	11.5	2022	4 US-09-461-657B-9	Sequence 9, Appli
31	381	11.5	2022	4 US-09-461-657B-15	Sequence 15, Appl
32	381	11.5	2097	4 US-09-461-657B-14	Sequence 14, Appl
33	381	11.5	2912	4 US-09-461-657B-12	Sequence 12, Appl
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36	354.5	10.7	2703	4 US-09-482-273-75	Sequence 75, Appl
37	349	10.6	1834	4 US-09-461-657B-17	Sequence 17, Appl
38	349	10.6	1909	4 US-09-461-657B-16	Sequence 16, Appl
39	349	10.6	2724	4 US-09-461-657B-13	Sequence 13, Appl
40	349	10.6	2799	4 US-09-461-657B-11	Sequence 11, Appl
41	329	9.9	2709	4 US-09-482-273-101	Sequence 101, App
42	320	9.7	473	2 US-08-866-757-3	Sequence 3, Appli
43	320	9.7	473	3 US-09-153-593-3	Sequence 3, Appli
c 44	318.5	9.6	1298	3 US-08-795-876-32	Sequence 32, Appl
45	318.5	9.6	1300	3 US-08-795-876-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-799-451-723
; Sequence 723, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 723
; LENGTH: 2988
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

; LOCATION: (1)..(2484)									
US-09-799-451-723									
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Best Local Similarity:		96.27%		Mismatches:		14			
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Qy	19	ProGlySer-ThrHisAlaSerValGluArgSerGln--	--GlyLeuSerLeuProAlaHi	37					
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Qy	37	sProAlaSerLeuAlaAlaLeuAlaAlaSerAsnThrThrAlaSerGlyLysLeuGlu**	57						
Db	698	GGTGTCAAGAAATTGGAGGAAA-TCGGCCTCCAACACACCGCATCTGGGAAATTGGAGCT	756						
Qy	57	*AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLeuSerTrpAsnAlaIleAr	77						
Db	757	-GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAAACGCCATCCG	815						
Qy	77	gSerIleHisProGluAlaPheSerThrLeuHisSerLeuValLysLeuAspLeuThrAs	97						
Db	816	GTCCATCCACCCTGAGGCCTTCTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGA	875						
Qy	97	pAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyGlyLeuMetHisLeuLysLeuLy	117						
Db	876	CAACCAGCTGACCACACTGCCCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAA	935						
Qy	117	sGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPheProLysLeuArgIleLe	137						
Db	936	AGGGAACCTTGCTCTCTCCAGGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCT	995						
Qy	137	uGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCysAlaSerPhePheLysAl	157						
Db	996	GGAGGTGCCTTATGCCCTACAGTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGC	1055						
Qy	157	aSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspAspGluGluSerSerLysArgPr	177						
Db	1056	CTCTGGGCAGTGGGAGGCTGAAGACCTTCAACCTTGATGATGAGGAGTCTTCAAAAAGGCC	1115						
Qy	177	oLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspGlnAspLeuAspGluLeuGl	197						
Db	1116	CCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCA	1175						
Qy	197	nLeuGluMetGluAspSerLysProHisProSerValGlnCysSerProThrProGlyPr	217						
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Qy	217	oPheLysProCysGluTyrLeuPheGluSerTrpGlyIleArgLeuAlaValTrpAlaI1	237						
Db	1236	CTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCAT	1295						
Qy	237	eValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuThrValPheAlaGlyGlyPr	257						
Db	1296	CGTGTGCTCTCCGTGCTCTGCAATGGACTGGTGTGCTGTGACCGTGTTCGCTGGCGGGCC	1355						
Qy	257	oAlaProLeuProProValLysPheValValGlyAlaIleAlaGlyAlaAsnThrLeuTh	277						
Db	1356	TGTCCCCCTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCAAACCTTGAC	1415						
Qy	277	rGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuThrPheGlyGlnPheSerGl	297						
Db	1416	TGGCATTTCTGTGGCCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGA	1475						
Qy	297	uTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaThrGlyPheLeuAlaValLe	317						
Db	1476	GTACGGAGCCGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCTCGGCAGTACT	1535						

QY	317	uGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaValGlnCysSerValSerVa	337						
Db	1536	TGGGTCCGAGGCATCGGTGCTGCTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGT	1595						
QY	337	lSerCysValArgAlaTyrGlyLysSerProSerLeuGlySerValArgAlaGlyValLe	357						
Db	1596	CTCCTGTGTCCGGCCTATGGGAAGTCCCCCTCCCTGGCAGCGTTTCGAGCAGGGGTCT	1655						
QY	357	uGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLeuAlaSerValGlyGluTy	377						
Db	1656	AGGCTGCCTGGCACTGGCAGGGCTGGCCGCCGCACTGCCCCCTGAGGAGAAATA	1715						
QY	377	rGlyAlaSerProLeuCysLeuProTyrAlaProProGluGlyGlnProAlaAlaLeuGl	397						
Db	1716	CGGGCCCTCCCACTCTGCCTGCCCTACGGCCACCTGAGGGTCAGCCAGCAGCCCTGGG	1775						
QY	397	yPheThrValAlaLeuValMetMetAsnSerPheCysPheLeuValValAlaGlyAlaTy	417						
Db	1776	CTTCACCGTGGCCTGGTGATGATGAACCTCCTTCTGTTTCTGGTGGCCGGTGCCTA	1835						
QY	417	rIleLysLeuTyrCysAspLeuProArgGlyAspPheGluAlaValTrpAspCysAlaMe	437						
Db	1836	CATCAAACTGTACTGTGACCTGCCCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCAT	1895						
QY	437	tValArgHisValAlaAlaTrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPh	457						
Db	1896	GGTGAGGCACGTGGCCTGGCTCATCTTCGACAGCGGGCTCCTACTGTCCCGTGGCCTT	1955						
QY	457	eLeuSerPheAlaSerMetLeuGlyLeuPheProValThrProGluAlaValLysSerVa	477						
Db	1956	CCTCAGCTTCGCCTCCATGTGGGCCTCTTCCCTGTCAAGCTTCAAGTCTGT	2015						
QY	477	lLeuLeuValValLeuProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAs	497						
Db	2016	CCTGTGTGTGTGCTGCCCTGCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAA	2075						
QY	497	nProHisPheArgAspAspLeuArgArgLeuArgProArgAlaGlyAspSerGlyProLe	517						
Db	2076	CCCCCACTTCGGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCT	2135						
QY	517	uAlaTyrAlaAlaAlaGlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuVa	537						
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QY	537	lAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAlaGlyArgProGlyLe	557						
Db	2196	AGCCTTCTCTGATGTGATCTCATTTCTGAAGCTTCTGAAGCTGGCGGCCCTGGGCT	2255						
QY	557	uGluThrTyrGlyPheProSerValThrLeuIleSerCysGlnGlnProGlyAlaProAr	577						
Db	2256	GGAGACCTATGGCTTCCCTCAGTGACCTCATCTCCTGTGTCAGCAGCCAGGGGCCCCCAG	2315						
QY	577	gLeuGluGlySerHisCysValGluProGluGlyAsnHisPheGlyAanProGlnProSe	597						
Db	2316	GCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTC	2375						
QY	597	rMetAspGlyGluLeuLeuArgAlaGluGlySerThrProAlaGlyGlyLeuSe	617						
Db	2376	CATGGATGGAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGT	2435						
QY	617	rGlyGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSerHisVal	633						
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RESULT 2

US-09-170-496D-263
; Sequence 263, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-


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; LENGTH: 4570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 205542.2
; NAME/KEY: unsure
; LOCATION: 3900, 3919, 3934
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-201

Alignment Scores:
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Best Local Similarity: 46.90%      Mismatches:  157
Query Match:      38.55%      Indels:      30
DB:              4          Gaps:      8

US-10-664-667-5 (1-633) x US-09-976-594-201 (1-4570)

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QY      74 AsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuValLysLeu 93
Db      1483 AACAAAATTGCTATTATTACACCCCAATGCATTTTCCACTTTGCCATCCCTAATAAAGCTG 1542

QY      94 AspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyGlyLeuMetHis 113
Db      1543 GACCTATCGTCCAACCTCTGTCGTCTTTTCCCTATACTGGGTTACATGGTTAACTCAC 1602

QY      114 LeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPheProLys 133
Db      1603 TTAAAAATTAACAGGAATCATGCCTTACAGAGCTTGATATCATCTGAAAACCTTCCAGAA 1662

QY      134 LeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCysAlaSer 153
Db      1663 CTCAAGGTTATAGAAATGCCTTATGCTTACCAGTGTGTGCATTTGGAGTGTGTGAGAAT 1722

QY      154 PhePheLysAlaSerGlyGlnTrp-----GluAlaGluAspLeuHis 167
Db      1723 GCCTATAAGATTCTTAATCAATGGAATAAAGTGACAACAGCAGTATGGACGACCTTCAT 1782

QY      168 LeuAspAspGluGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsn 187
Db      1783 -----AAGAAAGATGCTGGAATGTTTCAGGCTCAAGATGAA-- 1818

QY      188 HisTyrAspGlnAspLeuAspGluLeuGlnLeuGluMet---GluAspSerLysProHis 206
Db      1819 -----CGTGACCTTGAAGATTTCCCTGCTTGACTTTTGAGGAAGACCTGAAAGCCCTT 1869

QY      207 ProSerValGlnCysSerProThrProGlyProPheLysProCysGluTyrLeuPheGlu 226
Db      1870 CATTGAGTGCAGTGTTCACCTTCCCAGGCCCTTCAAAACCCTGTGAACACCTGCTTGAT 1929

QY      227 SerTrpGlyIleArgLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGly 246
Db      1930 GGCTGGCTGATCAGAATTGGAGTGTGGACCATAGCAGTTCTTGGCACTTACTTGTAAATGCT 1989

QY      247 LeuValLeuLeuThrValPheAlaGlyGlyProAlaProLeuProValLysPheVal 266
Db      1990 TTGGTGACTTCAACAGTTTTCAGA--TCCCTCTGTACATTTCCCCCATTAACCTGTTA 2046

QY      267 ValGlyAlaIleAlaGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSer 286
Db      2047 ATTGGGGTTCATCGGAGCAGTGAAACATGCTCACGGGAGTCTCCAGTGCCTGCTGGCTGGT 2106

QY      287 ValAspAlaLeuThrPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeu 306
Db      2107 GTGGATGCGTTCACTTTTGGCAGCTTTGCCAGCATGGTGCCTGGTGGGAGAAATGGGGTT 2166
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QY      307 GlyCysArgAlaThrGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeu 326
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QY      327 ThrLeuAlaIaValGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSer 346
Db      2227 ACTCTGGCAGCCCTGGAGCGTGGGTTCTCTGTGAAATATTCTGCAAAATTTGAAACGAAA 2286

QY      347 ProSerLeuGlySerValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAla 366
Db      2287 GCTCCATTTTCTAGCCTGAAAGTAATCATTTTGTCTGTGCCCTGTGCCCTTGACCATG 2346

QY      367 AlaAlaLeuProLeuAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyr 386
Db      2347 GCCGCAGTTCCCTGCTGGTGGCAGCAGTAAGTATGGCGCTCCCTCTCTGCTGCTTGTG 2406

QY      387 AlaProProGluGlyGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsn 406
Db      2407 -----CCTTTGGGAGGCCAGCACCATGGGCTACATGGTGCCTCTCATCTTGTCTCAAT 2460

QY      407 SerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArg 426
Db      2461 TCCCTTTGCTTCTCATGATGACCAATTGCCATACACCAAGCTCTACTGCAATTTGGACAAG 2520

QY      427 GlyAspPheGluAlaValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePhe 446
Db      2521 GGAGACCTGGAGAATATTTGGGACTGCTCTATGGTAAACACATTGGCCCTGTGTGCTCTTC 2580

QY      447 AlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeu 466
Db      2581 ACCAACTGCATCTCTAAACTGCCCTGTGGCTTCTTGTCTCTCTCTTAAATAAACCTT 2640

QY      467 PheProValThrProGluAlaValLysSerValLeuLeuValValLeuProLeuProAla 486
Db      2641 ACATTTATCAGTCTGAAGTAATTAAGTTTATCTCTTCTGGTGGTAGTCCCACTTCTCTGCA 2700

QY      487 CysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPheArgAspLeuArgArg 506
Db      2701 TGTCTCAATCCCTTCTCTACATCTTGTTCATCCTCAATCCTCACTTTAAGSAGGATCTGGTGAGC 2760

QY      507 LeuArgProArgAla-----GlyAspSerGlyProLeuAlaTyrAlaAla 521
Db      2761 CTGAGAAAGCAAAACCTACGCTCTGGACAAGATCAAAACACCCCAAGCTTGATGTCAATTAAC 2820

QY      522 AlaGlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuValAlaPheSerAsp 541
Db      2821 TCTGATGATGTGCAAAACAGTCTCTGTGACTCAACTCAAGCCTTGGTAAACCTTTACCAGC 2880

QY      542 ValAspLeuIleLeuGluAlaSerGluAlaGlyArgPro-----ProGlyLeu 557
Db      2881 TCCAGCATCACTTATGACCTGCCTCCAGTTCCGAGTTCCGTGCCATCACCAAGCTTATCCAGTGACT 2940

QY      558 GluThrTyrGlyPheProSerValThrIleuIleSerCys 570
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RESULT 4
US-09-170-496D-277
; Sequence 277, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 277
; LENGTH: 2724
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-277

Alignment Scores:
Pred. No.:      7.43e-111      Length:      2724
Score:          1269.00      Matches:      249
Percent Similarity: 64.73%      Conservative: 96
Best Local Similarity: 46.72%      Mismatches:  158
Query Match:     38.37%      Indels:      30
DB:              4              Gaps:         8

US-10-664-667-5 (1-633) x US-09-170-496D-277 (1-2724)

Qy 54 LysLeuGlu**AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLeuSerTrp 73
Db 1162 GAAATTAAGTTGACACTTTCCAGCAGTTGCTTAGCCTCCGATCGCTGAATTTGGCTTG 1221

Qy 74 AsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuValLysLeu 93
Db 1222 AACAAAATTGCTATTATTACCCCAATGCATTTTCCACTTTGCCATCCCTAATAAAGCTG 1281

Qy 94 AspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyGlyLeuMetHis 113
Db 1282 GACCTATCGTCCAACCTCCTGTGCTCTTTTCCATATAACTGGGTACATGGTTAACTCAC 1341

Qy 114 LeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPheProLys 133
Db 1342 TTAAAATAACAGGAAATCATGCCTTACAGAGCTTGATATCATCTGAAACCTTTCCAGAA 1401

Qy 134 LeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCysAlaSer 153
Db 1402 CTCAAGGTTATAGAAATGCCTTATGTCTTACCAGTGTGTGCATTTGGAGTGTGTGAGAT 1461

Qy 154 PhePheLysAlaSerGlyGlnTrp-----GluAlaGluAspLeuHis 167
Db 1462 GCCTATAAGATTCTTAATCAATGGAATAAAGGTGACAAACAGCAGTATGGACGACCTTCAT 1521

Qy 168 LeuAspAspGluGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsn 187
Db 1522 -----AAGAAAGATGCTGGAATGTTTTCAGGCTCAAGATGAA--- 1557

Qy 188 HisTyrAspGlnAspLeuAspGluLeuGlnLeuGluMet---GluAspSerLysProHis 206
Db 1558 -----CGTGACCTTGAAGATTTCCTGCTTGACTTTGAGGAAGACCTGAAAGCCCTT 1608

Qy 207 ProSerValGlnCysSerProThrProGlyProPheLysProCysGluTyrLeuPheGlu 226
Db 1609 CATTCACTGCAGTGTTCACCTTCCCAGGCCCTTCAAACCCCTGTGAACACCTGCTTGAT 1668

Qy 227 SerTrpGlyIleArgLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGly 246
Db 1669 GGCTGGCTGATCAGAAATTGGAGTGTGGACCATAGCAGTTCTGGCACTTACTTGTAAATGCT 1728

Qy 247 LeuValLeuLeuThrValPheAlaGlyGlyProAlaProLeuProProValLysPheVal 266
Db 1729 TTGGTGACTTCAACAGTTTTTTCAGA---TCCCCCTCTGTACATTTCCCCCATTAACCTGTTA 1785

Qy 267 ValGlyAlaIleAlaGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSer 286
Db 1786 ATTGGGTCATCGCAGCAGTGAACATGCTCACGGGAGTCTCCAGTGCCTGCTGGCTGCT 1845

Qy 287 ValAspAlaLeuThrPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeu 306
Db 1846 GTGGATGCGTTCACTTTTGGCAGCTTTGCACGACATGGTGGCTGGTGGGAGAAATGGGGTT 1905

Qy 307 GlyCysArgAlaThrGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeu 326
Db 1906 GGTTGCCATGTTCATTTGGTTTGTTCATTTTGTCTTCCAGATCATCTGTTTTCCTGCTT 1965

Qy 327 ThrLeuAlaAlaValGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSer 346
Db 1966 ACTCTGGCAGCCCTGGAGCGTGGGTTCTCTGTGAAATATTCTGCAAAATTTTGAAACGAAA 2025
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Qy 347 ProSerLeuGlySerValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAla 366
Db 2026 GCTCCATTTTCTAGCCTGAAAGTAATCATTTTGTCTGTGCCCCTGTGCGCTTGACCATG 2085

Qy 367 AlaAlaLeuProLeuAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyr 386
Db 2086 GCCGCAGTTCCTCTGCTGGTGGCAGCAAGTATGGCGCTCCCTCTCTGCTGCCTTTG 2145

Qy 387 AlaProProGluGlyGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsn 406
Db 2146 -----CCTTTTGGGAGCCCGACGACCATGGGCTACATGGTGGCTCTCATCTTGTCTCAAT 2199

Qy 407 SerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArg 426
Db 2200 TCCTTTGCTTCTCATGATGACCATTTGCCCTACACCAAGCTCTACTGCAATTTGGACAAG 2259

Qy 427 GlyAspPheGluAlaValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePhe 446
Db 2260 GGAGACCTGGAGAAATATTGGGACTGCTCTATGAAAAAACACATTTGCCCTGTGTCTCTTC 2319

Qy 447 AlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeu 466
Db 2320 ACCAACTGCATCCTAAACTGCCCTGTGGCTTCTTGTCTCTCTCTCTTTAATAAACCTT 2379

Qy 467 PheProValThrProGluAlaValLysSerValLeuLeuValValLeuProLeuProAla 486
Db 2380 ACATTTATCAGTCCTGAAAGTAATTAAGTTTATCCTTCTGGTGGTAGTCCCACCTTCTCTGCA 2439

Qy 487 CysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgArg 506
Db 2440 TGCTCAATCCCCTTCTCTACATCTTGTTCATCCTCCTCAATCCTCACTTTAAGGAGGATCTGGTGAGC 2499

Qy 507 LeuArgProArgAla-----GlyAspSerGlyProLeuAlaTyrAlaAla 521
Db 2500 CTGAGAAAAGCAAACTTACGCTGTGGACAAGATCAAAACACCCCAAGCTTGTGATGTCAATTAAC 2559

Qy 522 AlaGlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuValAlaPheSerAsp 541
Db 2560 TCTGATGATGTGCAAAAACAGTCTCTGTGACTCAACTCAAGCCTTGGTAACCTTTACCAGC 2619

Qy 542 ValAspLeuIleLeuGluAlaSerGluAlaGlyArgPro-----ProGlyLeu 557
Db 2620 TCCAGCATCACTTATGACCTGCCCTCCCAGTTCCGTTGCCATCACCAGCTTATCCAGTGACT 2679

Qy 558 GluThrTyrGlyPheProSerValThrLeuIleSerCys 570
Db 2680 GAGAGCTGCCATCTTTCTCTGTGGCATTTGTCCCATGT 2718
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RESULT 5
US-08-866-757-1
; Sequence 1, Application US/08866757
; Patent No. 5858716
; GENERAL INFORMATION:
; APPLICANT: ELSHOUBAGY, NABIL A
; APPLICANT: LI, XIAOTONG
; APPLICANT: BERGSMAN, DEREK J
; TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,757
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; FILING DATE: 30-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4203 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-866-757-1

Alignment Scores:
Pred. No.: 7.25e-81 Length: 4203
Score: 958.00 Matches: 211
Percent Similarity: 54.11% Conservative: 85
Best Local Similarity: 38.57% Mismatches: 191
Query Match: 28.97% Indels: 60
DB: 2 Gaps: 9

US-10-664-667-5 (1-633) x US-08-866-757-1 (1-4203)
QY 54 LysLeuGlu**AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLeuSerTrp 73
Db 697 CAAATAAGGAAGGCACCTTCAAGGCCTGATATCTTAAGGATTCTAGATCTGAGTAGA 756
QY 74 AsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuValLysLeu 93
Db 757 AACCTGATACATGAAATTACACAGTAGAGCTTTTGCCACACTTGGGCCAATAAATAACCTA 816
QY 94 AspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyLeuMetHis 113
Db 817 GATGTAAGTTTCAATGATTAACCTTCCTTCCTCGAAGGCCTGAATGGGCTAAATCAA 876
QY 114 LeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPheProLys 133
Db 877 CTGAAACTGGTGGCAACTCAAGCTGAAAGAGCCTTAGCAGCAAAAGACTTTGTTAAC 936
QY 134 LeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCysAlaSer 153
Db 937 CTCAGGTCTTTATCAGTACCATATGCTTATCAGTGTGTGCATTTTGGGTTGTGACTCT 996
QY 154 PhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspAsp----- 170
Db 997 TAT-----GCAAATTAAACACAGAAGATAACAGCCTCCAGGACCACAGTGTG 1044
QY 171 ---GluGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyr 189
Db 1045 GCACAGGAGAAAGGTACTGCTGATGCAGCAAAATGCACAAGCACTCTTGAAAAATGAAGAA 1104
QY 190 AspGlnAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerVal 209
Db 1105 CATAGTCAAATA-----ATTATC 1122
QY 210 GlnCysSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGly 229
Db 1123 CATTGTAACACCTTCAACAGGTGCTTTTAAGCCCTGTGAATATTACTGGGAAGCTGGATG 1182
QY 230 IleArgLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeu 249
Db 1183 ATTGCTCTACTGTGTGTTCAATTTCTTGGTTGCATATTTTTCACACCTGCTGTTATT 1242
QY 250 LeuThrValPheAlaGlyGlyProAlaProLeuProValLysPheValValGlyAla 269
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Db 1243 TTAACAACATTTGCATCTTGTACATCA---CTGCCCTTCGTCCAAATTGTTTATAGGCTTG 1299
QY 270 IleAlaGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAla 289
Db 1300 ATTTCTGTCTAACTTATTTCATGGGAATCTATACTGGCATCCTAACTTTTCTTGATGCT 1359
QY 290 LeuThrPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArg 309
Db 1360 GTGTCTGGGCAGATTTCGTTGAATTTGGCATTTGGTGGAAACTGGCAGTGGCTGCAAA 1419
QY 310 AlaThrGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAla 329
Db 1420 GTAACCTGGGTTTCTTGCAGTTTTCCTCCTCAGAAAAGTGCCATATTTTATTAAATGCTAGCA 1479
QY 330 AlaValGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeu 349
Db 1480 ACTGTCGAAAGAGCTTATCTGCAAAAGATATAATGAAAATGGGAAGAGCAATCATCTC 1539
QY 350 GlySerValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeu 369
Db 1540 AAACAGTTCGGGTTGCTGCCCTTTTGGCTTTCCTAGGTCTACAGTAACAGGCTGTTTT 1599
QY 370 ProLeuAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProPro 389
Db 1600 CCCCTTTTCCATAGAGGGGAATATTCTGCATCACCCCTTTGTTTGCCATT-----CCT 1653
QY 390 GluGlyGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCys 409
Db 1654 ACAGGTGAAACGCCATCATTAGGATTCACTGTAAACGTTAGTGCTATTAAACTCACTAGCA 1713
QY 410 PheLeuValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPhe 429
Db 1714 TTTTATTAAATGCGCGTTATCTACACTAAGCTATACTGCAACTTGGAAAAAGAGGACCTC 1773
QY 430 GluAlaValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGly 449
Db 1774 TCAGAAAAACTCACAATCTAGCATGATTAAAGCATGTCGCTTGGCTAATCTTCACCAATTGC 1833
QY 450 LeuLeuTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProVal 469
Db 1834 ATCTTTTCTGCCCTGTGGCGTTTTTTTCAATTGCACCATTGATCACTGCAATCTCTATC 1893
QY 470 ThrProGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsn 489
Db 1894 AGCCCCGAAATAAATGAAGTCTGTACTCTGATATTTTCCATTGCTGCTGCTGCTGAAT 1953
QY 490 ProLeuLeuTyrLeuLeuPheAsnProHisPheArgAspAsp-----LeuArg 505
Db 1954 CCAGTCCTGTATGTTTCTTCAACCCCAAGCTTTAAAGAGACTGGAAGTTACTGAAGCGA 2013
QY 506 ArgLeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAlaAlaGlyGluLeu 525
Db 2014 CGTGTACCAAGAAAAGTGGATCAGTTTCAGTTTCCATCAGTAGCCCAAGGTGTTGTCTG 2073
QY 526 GluLys-----SerSer 529
Db 2074 GAACAGGATTCTACTACGACTGTGGCATGTACTCACATTTGCAGGGCAACCTGACTGTT 2133
QY 530 CysAspSerThrGlnAlaLeuValAlaPheSerAspValAsp-----LeuIleLeu 546
Db 2134 TGCAGACTGCTGCGAATCGTTTCTTTTAAACAAAGCCAGTATCATGCAACACTTGATA--- 2190
QY 547 GluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThr 566
Db 2191 -----AAATCACACAGCTGTCTGTCATTGGCA 2217
QY 567 LeuIleSerCysGlnGlnPro 573
Db 2218 GTGGCTTCTTGCCAAAGACCT 2238
RESULT 6
US-09-153-593-1
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; Sequence 1, Application US/09153593A
; Patent No. 6174994
; GENERAL INFORMATION:
; APPLICANT: ELSHOURBAGY, NABIL A
; APPLICANT: LI, XIAOTONG
; APPLICANT: BERGSMÄ, DERK J
; TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
; FILE REFERENCE: GH-70055-1
; CURRENT APPLICATION NUMBER: US/09/153,593A
; CURRENT FILING DATE: 1998-09-15
; EARLIER APPLICATION NUMBER: 08/866,757
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4203
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-153-593-1

Alignment Scores:
Pred. No.:      7.25e-81      Length:      4203
Score:          958.00      Matches:      211
Percent Similarity: 54.11%      Conservative: 85
Best Local Similarity: 38.57%      Mismatches: 191
Query Match:      28.97%      Indels:      60
DB:              3          Gaps:      9

US-10-664-667-5 (1-633) x US-09-153-593-1 (1-4203)
QY 54 LysLeuGlu**AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLeuSerTrp 73
Db 697 CAAATAAGGAAGGCACCTTTCAAGCCTGATATCTCTAAGGATTCTAGATCTGAGTAGA 756
QY 74 AsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuValLysLeu 93
Db 757 AACCTGATACATGAATTCACAGTAGAGCTTTTGCCACACTTGGGCCAATAACTAACCTA 816
QY 94 AspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyLeuMetHis 113
Db 817 GATGTAAAGTTTCAATGAATTAACCTTCCTTCCTACGGAAGCCTGAATGGGCTAAATCAA 876
QY 114 LeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPheProLys 133
Db 877 CTGAAACTGGTGGCAACTTCAAGCTGAAAGAGCCTTAGCAGCAAAAGACTTTTGTTAAC 936
QY 134 LeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCysAlaSer 153
Db 937 CTCAGGTCTTTATCAGTACCATATGCTTATCAGTGTCTGTCATTTTGGGGTTGTGACTCT 996
QY 154 PhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspAsp----- 170
Db 997 TAT-----GCAATTTAAACACAGAAGATAACAGCCTCCAGGACCACAGTGTG 1044
QY 171 ---GluGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyr 189
Db 1045 GCACAGGAGAAAGGTACTGCTGATGCAGCAAAATGTCACAAGCACTCTTGAAAAATGAAGAA 1104
QY 190 AspGlnAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerVal 209
Db 1105 CATAGTCAAATA-----ATTATC 1122
QY 210 GlnCysSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGly 229
Db 1123 CATGTACACCTTCAACAGGTGCTTTTAAGCCCTGTGAATATTTACTGGGAAGCTGGATG 1182
QY 230 IleArgLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeu 249
Db 1183 ATTCGTCTTACTGTGGTTCATTTCTTGGTTGCATTATTTTCAACCTGCTTGTATT 1242
QY 250 LeuThrValPheAlaGlyGlyProAlaProLeuProValLysPheValValGlyAla 269
Db 1243 TTAACAACATTTGCATCTCTGTACATCA---CTGCCCTTCGTCCAAATTTGTTATAGGCTTG 1299
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QY 270 IleAlaGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAla 289
Db 1300 ATTTCTGTGCTTAACCTTATTCATGGGAATCTATACTGGCATCCTAACTTTTCTTGATGCT 1359
QY 290 LeuThrPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArg 309
Db 1360 GTGTCTGGGGCAGATTCGCTGAATTTGGCATTTTGGTGGAAACTGGCAGTGGCTGCAAA 1419
QY 310 AlaThrGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAla 329
Db 1420 GTAACCTGGGTTTCTTGCAAGTTTCTCCTCAGAAAGTGCATATTTTATTATGCTAGCA 1479
QY 330 AlaValGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeu 349
Db 1480 ACTGTCGAAAGAAGCTTATCTGCAAAAGATATATGAAAAAATGGGAAGAGCAATCATCTC 1539
QY 350 GlySerValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeu 369
Db 1540 AAACAGTTCGGGTTGCTGCCCTTTTGGCTTTCCTAGTGCTACAGTAACAGGCTGTTT 1599
QY 370 ProLeuAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProPro 389
Db 1600 CCCCTTTCCATAGAGGGGAATATTTCTGCATCACCCCTTTGTTTGGCATTT-----CCT 1653
QY 390 GluGlyGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCys 409
Db 1654 ACAGGTGAAACGCCATCATTAGGATTCACTGTAACTAGTGCTATTAAACTCACTAGCA 1713
QY 410 PheLeuValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPhe 429
Db 1714 TTTTATTAAATGGCCGTTATCTACACTAAGCTATATACTGCAACTTGGAAAAAGAGGACCTC 1773
QY 430 GluAlaValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGly 449
Db 1774 TCAGAAAACTCACAAATCTAGCATGATTAAAGCATGTGCTTGGCTTAATCTTCCACCAATTGC 1833
QY 450 LeuLeuTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProVal 469
Db 1834 ATCTTTTCTGCCCTGTGGCGTTTTCATTTGACCATTTGATCACTGCAATCTCTATC 1893
QY 470 ThrProGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsn 489
Db 1894 AGCCCCGAAATAATGAAGTCTGTTACTCTGATATATTTTCCATTGCTTGCCTTGCCTGAAT 1953
QY 490 ProLeuLeuTyrLeuLeuPheAsnProHisPheArgAspAsp-----LeuArg 505
Db 1954 CCAGTCTGTATGTTTCTTCAACCCAAAGTTTAAAGAAGACTGGAAGTTTACTGAAGCGA 2013
QY 506 ArgLeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAlaAlaAlaGlyGluLeu 525
Db 2014 CGTGTACCAGAAAGTGGATCAGTTTCAGTTTCCATCAGTAGCCAAGGTGGTTGTCTG 2073
QY 526 GluLys-----SerSer 529
Db 2074 GAACAGGATTTCTACTACGACTGTGGCATGTACTACATTTGCAGGGCAACCTGACTGTT 2133
QY 530 CysAspSerThrGlnAlaLeuValAlaPheSerAspValAsp-----LeuIleLeu 546
Db 2134 TGCGACTGTGCGAATCGTTTCTTTTAAACAAAGCCAGTATCATGCAAAACACTTGATA--- 2190
QY 547 GluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThr 566
Db 2191 -----AAATCACACACAGCTGTCTCCTGCATTGGCA 2217
QY 567 LeuIleSerCysGlnGlnPro 573
Db 2218 GTGGCTTCTTGCCAAAGACCT 2238
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RESULT 7
US-09-495-050A-214
; Sequence 214, Application US/09495050A
; Patent No. 6492505

; Patent No. 6468758
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
; FILE REFERENCE: 210121.466C2
; CURRENT APPLICATION NUMBER: US/09/397,787
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 240
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-397-787-240

Alignment Scores:
Pred. No.: 2.3e-63 Length: 453
Score: 759.00 Matches: 149
Percent Similarity: 98.68% Conservative: 0
Best Local Similarity: 98.68% Mismatches: 1
Query Match: 22.95% Indels: 1
DB: 3 Gaps: 0

US-10-664-667-5 (1-633) x US-09-397-787-240 (1-453)

QY 444 LeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPheAlaSerMet 463
Db 3 CTCATCTTCGACAGCGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCATG 62
QY 464 LeuGlyLeuPheProValThrProGluAlaValLyssSerValLeuLeuValValLeuPro 483
Db 63 CTGGGCTCTTCCCTGTACGCCCGGAGCGCTCAAGTCTGTCTGTCTGTGGTGTGCTGCC 122
QY 484 LeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPheArgAspAsp 503
Db 123 CTGCCTGCCTGCCTCAACCCACTGCTGTACCTGTCTTCAACCCCACTTCGGGGATGAC 182
QY 504 LeuArgArgLeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAlaAlaGly 523
Db 183 CTTCGGGGCTTCGGCCCCCGCAGGGGACTCAGGGCCCTTAGCCTATGCTGCGGCGGG 242
QY 524 GluLeuGluLyssSerSerCysAspSerThrGlnAlaLeuValAlaPheSerAspValAsp 543
Db 243 GAGCTGGAGAAGAGCTCCCGTATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGAT 302
QY 544 LeuIleLeuGluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyrGlyPhePro 563
Db 303 CTCATTCTGGAAGCTTCTGAAGCTGGCGGCCCTCGGCTGGAGACCTATGGCTTCCCC 362
QY 564 SerValThrLeuIleSerCysGlnGlnProGlyAlaProArgLeuGluGly-SerHisCy 583
Db 363 TCAGTGACCTCATCTCCTGTACAGCAGCCAGGGCCCCCAGGCTGGAGGGCAAGCCATTG 422
QY 583 sValGluProGluGlyAsnHisPheGlyAsn 593
Db 423 TGTAGAGCCAGAGGGGAACCACTTTGGGAAC 453

RESULT 9

US-09-495-050A-220
; Sequence 220, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31

; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 220
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 2603450CT1
US-09-495-050A-220

Alignment Scores:
Pred. No.: 1.95e-47 Length: 723
Score: 595.50 Matches: 116
Percent Similarity: 67.36% Conservative: 47
Best Local Similarity: 47.93% Mismatches: 76
Query Match: 18.01% Indels: 4
DB: 4 Gaps: 2

US-10-664-667-5 (1-633) x US-09-495-050A-220 (1-723)

QY 234 ValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuThrValPhe 253
Db 6 GTGTGGACCATAGCAGTCTCGCACCTTACTTGTAAATGCTTGGTGACTTCAACAGTTTTC 65
QY 254 AlaGlyGlyProAlaProLeuProProValLyssPheValValGlyAlaIleAlaGlyAla 273
Db 66 AGA--TCCCCTCTGTACATTTCCCCCATTAACCTGTTAAATTGGGTCATCGCAGCAGTG 122
QY 274 AsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuThrPheGly 293
Db 123 AACATGCTCACGGGAGTCTCCAGTGCCGTGCTGGTGGTGGATGCGTTCACTTTTGGC 182
QY 294 GlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaThrGlyPhe 313
Db 183 AGCTTTGCACGACATGGTGCTGGTGGAGAAATGGGGTTGGTTGCCATGTCTATTGGTTT 242
QY 314 LeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaValGlnCys 333
Db 243 TTGTCCATTTTTCCTCAGAAATCATCTGTTTCTGCTTACTCTGGCAGCCCTGGAGCGT 302
QY 334 SerValSerValSerCysValArgAlaTyrGlyLyssSerProSerLeuGlySerValArg 353
Db 303 GGGTTCTCTGTAATATTCTGCAAAATTTGAAACGAAAGCTCCATTTTCTAGCCTGAAA 362
QY 354 AlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLeuAlaSer 373
Db 363 GTAATCATTTTGTCTGTGCCCTGTGGCCTTGACCATGGCCGAGTTTCCCCCTGCTGGGT 422
QY 374 ValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluGlyGlnPro 393
Db 423 GGCAGCAAGTATGGCGCTCCCTCTCTGCTGCCTTTG-----CCTTTTGGGGAGGCC 476
QY 394 AlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLeuValVal 413
Db 477 AGCACCATGGGCTACATGGTCGCTCTCATCTTGTCTCAATTCCTTTTCTCCTCATGATG 536
QY 414 AlaGlyAlaTyrIleLyssLeuTyrCysAspLeuProArgGlyAspPheGluAlaValTrp 433
Db 537 ACCATTGCCTACACCAAGCTCTACTGCAATTTGGACAAGGAGACCTGGAGAATATTGG 596
QY 434 AspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLeuTyrCys 453
Db 597 GACTGCTCTATGGTAAACACATTCCTGTTGCTTCTTCACTCCTCACTCACTCACTGC 656
QY 454 ProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrProGluAla 473
Db 657 CTGTGGCTTCTTGTCTCTCTCTCTTTTAAATAAACCTTACATC-ATCAGTCTCTGAAGTA 715
QY 474 ValLyss 475
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Db 716 ATTAAG 721

RESULT 10

US-08-487-886-1

; Sequence 1, Application US/08487886

; Patent No. 574448

; GENERAL INFORMATION:

; APPLICANT: Kelton, Christie Ann

; APPLICANT: Schweickhardt, Rene Lynn

; APPLICANT: Cheng, Shirley Vui Yen

; APPLICANT: Nugent, No. 574448een Patrice

; TITLE OF INVENTION: Human Follicle Stimulating

; TITLE OF INVENTION: Hormone Receptor

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Stephan P. Williams,

; ADDRESSEE: Ares-Serono, Inc.

; STREET: Exchange Place, 37th floor

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density

; COMPUTER: IBM PS/2, model 55 SX

; OPERATING SYSTEM: MS-DOS version 4.0

; SOFTWARE: VAX/VMS Massll via Kermit to IBM MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,886

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/670,085

; FILING DATE: 15-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Williams, Stephan P.

; REGISTRATION NUMBER: 28546

; REFERENCE/DOCKET NUMBER: US/252

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 723-1300

; TELEFAX: (617) 723-8923

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2179

; TYPE: Nucleic acid

; STRANDEDNESS: Double

; TOPOLOGY: Linear

; MOLECULE TYPE: cDNA to mRNA

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; TISSUE TYPE: Testis

; IMMEDIATE SOURCE:

; LIBRARY: lgt11 cDNA library, Clontech #HL1010b

; CLONE: pFHSR11-11, pFHSR15-6

; FEATURE:

; NAME/KEY: protein coding region

; LOCATION: 75 to 2159

US-08-487-886-1

Alignment Scores:

Pred. No.:	2.08e-29	Length:	2179
Score:	414.50	Matches:	131
Percent Similarity:	42.94%	Conservative:	94
Best Local Similarity:	25.00%	Mismatches:	232
Query Match:	12.53%	Indels:	67
DB:	1	Gaps:	13

US-10-664-667-5 (1-633) x US-08-487-886-1 (1-2179)

QY 55 LeuGlu***AspThrPheSerGlnLeuSer---SerLeuGlnAlaLeuAspLeuSerTrp 73

Db 552 ATTGAAAGAAATCTTTCGTGGGCTGAGCTTTGAAAGTGTGATTCTATGGCTGAATAAG 611

QY 74 AsnAlaIleArgSerIleHisProGluAlaPhe----- 84

Db 612 AATGGGATTCAAGAAATACACAACTGTGCATTCAATGGAACCCAACTAGATGAGCTGAAT 671

QY 85 -----SerThrLeuHisSerLeu----- 90

Db 672 CTAAGCGATAATAATAATTAGAGAATTCCTAATGATGTTTCCACGGAGCCTCTGGA 731

QY 91 ---ValLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGly 109

Db 732 CCAGTCATTCTAGATATTTCAAGAACCAAGGATCCATTCCCTGCCTAGCTATGGCTTAGAA 791

QY 110 GlyLeuMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAsp 129

Db 792 AATCTTAAGAAAGCTGAGGGCCAGGTCGACTTACAACCTTAAAAAGCTGCCTACTCTGGA 851

QY 130 SerPheProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGly 149

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QY 168 -----LeuAspAspGluGluSerSerLysArgProLeu 178

Db 948 TGCAACAAATCTATTTAAGGCAAGAAGTTGATTATATGACTCAGACTAGGGGTGAGAGA 1007

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Db 1008 TCCTCTCTGGCAGAGACAATGAGTCCAGCTACAGCAGAGGATTTGACATGACGTACACT 1067

QY 199 GluMetGluAspSerLysProHisPro-----SerValGlnCysSerProThrProGly 216

Db 1068 GAGTTTGACTATGACTTATGCAATGAAGTGGTTGACGTGACCTGCTCCCTAAGCCAGAT 1127

QY 217 PropheLysProCysGluTyrLeuPheGluSerTrpGlyIleArgLeuAlaValTrpAla 236

Db 1128 GCATTCAACCCATGTGAAGATATCATGCGGGGTACAACATCCTCAGAGTCTGATATGGTTT 1187

QY 237 IleValLeuLeuSerValLeuCysAsnGlyLeuValValGlyAlaIleAlaGlyAlaAsnThrLeu 276

Db 1188 ATCAGCATCCTGGCCATCACTGGGAAC---ATCATAGTGTAGTGTGATCCTAACTACCAGC 1244

QY 257 ProAlaProLeuProValLysPheValValGlyAlaIleAlaGlyAlaAsnThrLeu 276

Db 1245 CAATATAAACTCACAGTCCCCAGGTTCTTATGTGCAACCTGGCCCTTGTGATCTCTGC 1304

QY 277 ThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuThrPheGlyGlnPheSer 296

Db 1305 ATTGGAATCTACCTGTCTCATTTGCATCAGTTGATATCCATACCAGAGCCAATATCAC 1364

QY 297 GluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaThrGlyPheLeuAlaVal 316

Db 1365 AACTATGCCATTGACTGGCAAACTGGGCGAGGCTGTGATGCTGCTGGCTTTTTCACCTGTC 1424

QY 317 LeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaValGln----- 332

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QY 351 SerValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuPro 370

Db 1530 GCTGCCAGTGTGATGGTGTGATGGGCTGGATT---TTTGCTTTTGACGCTGCCCTCTTTCCC 1586

QY 371 LeuAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGlu 390

Db 1587 ATCTTTGGCATCAGCAGCTACATGAAGGTGAGCATCTGCCTGCCCATG-----GATATT 1640

QY 391 GlyGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPhe 410

Db 1641 GACAGCCCTTTGTGCACAGTGTATGTCATGTCCTCTCTGTGTGCTCAATGTCCTGGCCTTT 1700
QY 411 LeuValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPhe--- 429
Db 1701 GTGGTCACTGTGGTGCTATATCCACATCTACCTCACAGTGGGAACCCCAACATCGTG 1760
QY 430 GluAlaValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGly 449
Db 1761 TCCTCCTCTAGTGACACAGGATCGCCAAGCGCATGGCCATGCTCATCTTCACTGACTTC 1820
QY 450 LeuLeuTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProVal 469
Db 1821 CTCTGCATGGCACCCATTCTTTCTTTGCCATTTCTGCCTCCCTCAAGGTGCCCTCATC 1880
QY 470 ThrProGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsn 489
Db 1881 ACTGTGTCCAAAGCAAGATTCTGTGTTCTGTTCACCCCATCAACTCCTGTGCCAAC 1940
QY 490 ProLeuLeuTyrLeuLeuPheAsnProHisPheArgAspLeuArgArgLeuArgPro 509
Db 1941 CCCTTCCTCTATGCCATCTTTACCAAAAACCTTTCGACAGAGATTCTTTCATTCTGCTGAGC 2000
QY 510 ArgAlaGlyAspSerGlyProLeuAlaTyrAlaAlaAlaGlyGluLeuGluLysSerSer 529
Db 2001 AAGTGTGGC-----TGCTATGAATGCAAGCCCAAAATTTATAGSACAGAA 2045
QY 530 CysAspSerThr 533
Db 2046 ACTTCATCCACT 2057

RESULT 11
US-08-531-070A-1
; Sequence 1, Application US/08531070A
; Patent No. 5851768
; GENERAL INFORMATION:
; APPLICANT: de la Chapelle, Albert
; APPLICANT: Aittomaki, Kristina
; APPLICANT: Huhtaniemi, Ilpo
; TITLE OF INVENTION: Method For Diagnosis Of Ovarian Dysgenesis
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS: 18
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,070A
; FILING DATE: 20-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28113/32879
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2179 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-531-070A-1

Alignment Scores: 2.08e-29 Length: 2179
Pred. No.: 414.50 Matches: 131
Score: 42.94% Conservative: 94
Percent Similarity: 25.00% Mismatches: 232
Best Local Similarity: 12.53% Indels: 67
Query Match: 2 Gaps: 13
DB: US-10-664-667-5 (1-633) x US-08-531-070A-1 (1-2179)
QY 55 LeuGlu***AspThrPheSerGlnLeuSer---SerLeuGlnAlaLeuAspLeuSerTrp 73
Db 552 ATTGAAAGAAATTCCTTCGTGGGGCTGAGCTTTGAAAAGTGTGATTCTATGGCTGAATAAG 611
QY 74 AsnAlaIleArgSerIleHisProGluAlaPhe----- 84
Db 612 AATGGGATTCAAGAAATACACAACCTGTGCATTCAAATGGAAACCAACTAGATGAGCTGAAT 671
QY 85 -----SerThrLeuHisSerLeu----- 90
Db 672 CTAAGCGATAATAATAATTAGAAAGATTGCCTAATGATGTTTTCCACGGAGCCTCTCGGA 731
QY 91 ---ValLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGly 109
Db 732 CCAGTCATTCTAGATATTCAAGAACAAGGATCCATTCCTGCCTAGCTATGGCTTAGAA 791
QY 110 GlyLeuMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAsp 129
Db 792 AATCTTAAGAAGCTGAGGGCCAGGTCGACTTACAACTTAAAAAGCTGCCTACTCTGGAA 851
QY 130 SerPheProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGly 149
Db 852 AAGCTTGTGCGCCCTCATGGAAGCCAGCCTCACCTATCCCAGCCATTGCTGTGCCCTTT--- 908
QY 150 MetCysAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHis----- 167
Db 909 -----GCAAACTGGAGCGGCAAAATCTCTGAGCTTCATCCAATT 947
QY 168 -----LeuAspAspGluGluSerSerLysArgProLeu 178
Db 948 TGCAACAAATCTATTTAAGGCAAGAGTTGATTATATGACTCAGACTAGGGGTCAGAGA 1007
QY 179 GlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspGlnAspLeuAspGlnLeuGlnLeu 198
Db 1008 TCCTCTCTGGCAGAGACAATGAGTCCAGCTACAGCAGAGGATTGTGACATGACGTACACT 1067
QY 199 GluMetGluAspSerLysProHisPro-----SerValGlnCysSerProThrProGly 216
Db 1068 GAGTTTGACTATGACTTATGCAATGAAGTGGTTGACGTGACCTGCTCCCTAAGCCAGAT 1127
QY 217 ProPheLysProCysGluTyrLeuPheGluSerTrpGlyIleArgLeuAlaValTrpAla 236
Db 1128 GCATTCAACCCCATGTGAAGATATCATGGGGTACAAACATCCTCAGAGTCTGTGATGGTTT 1187
QY 237 IleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuThrValPheAlaGlyGly 256
Db 1188 ATCAGCATCCTGGCCATCACTGGGAAC---ATCATAGTGTAGTGATCCTTAACCTACCAGC 1244
QY 257 ProAlaProLeuProValLysPheValValGlyAlaIleAlaGlyAlaAsnThrLeu 276
Db 1245 CAATATAAACTCACAGTCCCCAGGTTCTTATGTGCAACCTGGCCTTTGTGTGATCTCTGC 1304
QY 277 ThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuThrPheGlyGlnPheSer 296
Db 1305 ATTGGAATCTACCTGCTGCTCATTGCATCAGTTGATATCCATACCAAGAGCCCAATATCAC 1364
QY 297 GluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaThrGlyPheLeuAlaVal 316
Db 1365 AACTATGCCATTGACTGGCAAACTGGGGCAGGCTGTGATGCTGTGGCTTTTCTACTGTCTC 1424
QY 317 LeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaValGln----- 332

Db 1425 TTGCCAGTGAGCTGTCACTACACTCTGACAGCTATCACCTTGGAAGATGGCATAACC 1484
QY 333 -----CysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGly 350
Db 1485 ATCAGCATGCCATGCAGCTGGACTGC-----AAGGTGCAGCTCGCCAT 1529
QY 351 SerValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuPro 370
Db 1530 GCTGCCAGTGTCAATGGTATGGGCTGGATT---TTTGCTTTTGCAAGCTGCCCTCTTTCCC 1586
QY 371 LeuAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGlu 390
Db 1587 ATCTTTGGCATCAGCAGCTACATGAAGGTGAGCATCTGCCTGCCCATG-----GATATT 1640
QY 391 GlyGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPhe 410
Db 1641 GACAGCCCTTTGTACAGCTGTATGTATGTCATGTCCTCCTGTGTCTCAATGTCTGGCCTTT 1700
QY 411 LeuValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPhe--- 429
Db 1701 GTGGTCATCTGTGGCTGCTATATCCACATCTACCTCACAGTCGGGAACCCCAACATCGTG 1760
QY 430 GluAlaValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGly 449
Db 1761 TCCTCCTCTAGTGACACCAAGGATCGCAAGCGCATGCCCATGCTCATCTTCACTGACTTC 1820
QY 450 LeuLeuTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProVal 469
Db 1821 CTCTGCATGGCACCCATTCTTTCTTTGCCATTTCTGCCTCCCTCAAGGTGCCCTCATC 1880
QY 470 ThrProGluAlaValLysSerValLeuValValLeuProLeuProAlaCysLeuAsn 489
Db 1881 ACTGTGTCCAAAGCAAGATTCTGTGTTCTGTTCACCCCATCAACTCCTGTGCCAAC 1940
QY 490 ProLeuLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgArgLeuArgPro 509
Db 1941 CCCTTCCTCTATGCCATCTTTACCAAAACTTTCGAGAGATTTCCTTCATTCTGCTGAGC 2000
QY 510 ArgAlaGlyAspSerGlyProLeuAlaTyrAlaAlaAlaGlyGluLeuGluLysSerSer 529
Db 2001 AAGTGTGGC-----TGCTATGAATGCAAGCCCAAAATTTATAGCACAGAA 2045
QY 530 CysAspSerThr 533
Db 2046 ACTTCATCCACT 2057

RESULT 12

US-08-482-855-1
; Sequence 1, Application US/08482855
; Patent No. 6121016
; GENERAL INFORMATION:
; APPLICANT: Kelton, Christie Ann
; APPLICANT: Schweickhardt, Rene Lynn
; APPLICANT: Cheng, Shirley Vui Yen
; APPLICANT: Nugent, No. 6121016een Patrice
; TITLE OF INVENTION: Human Follicle Stimulating
; TITLE OF INVENTION: Hormone Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephan P. Williams,
; ADDRESSEE: Ares-Serono, Inc.
; STREET: Exchange Place, 37th floor
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
; COMPUTER: IBM PS/2, model 55 SX
; OPERATING SYSTEM: MS-DOS version 4.0
; SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,855

; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/670,085
; FILING DATE: 15-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Stephan P.
; REGISTRATION NUMBER: 28546
; REFERENCE/DOCKET NUMBER: US/252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 723-1300
; TELEFAX: (617) 723-8923
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2179
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Testis
; IMMEDIATE SOURCE:
; LIBRARY: lgt11 cDNA library, ClonTech #HL1010b
; CLONE: pFHSR11-11, pFHSR15-6
; FEATURE:
; NAME/KEY: protein coding region
; LOCATION: 75 to 2159
US-08-482-855-1

Alignment Scores:
Pred. No.: 2.08e-29 Length: 2179
Score: 414.50 Matches: 131
Percent Similarity: 42.94% Conservative: 94
Best Local Similarity: 25.00% Mismatches: 232
Query Match: 12.53% Indels: 67
DB: 3 Gaps: 13

US-10-664-667-5 (1-633) x US-08-482-855-1 (1-2179)
QY 55 LeuGlu***AspThrPheSerGlnLeuSer---SerLeuGlnAlaLeuAspLeuSerTrp 73
Db 552 ATTGAAGAAGAAATCTTTTCGTGGGCTGAGCTTTGAAAGTGTGATTCTATGGCTGAATAAG 611
QY 74 AsnAlaIleArgSerIleHisProGluAlaPhe----- 84
Db 612 AATGGGATTCAAGAAATACACAACCTGTGCATTCAATGGAAACCACTAGATGAGCTGAAT 671
QY 85 -----SerThrLeuHisSerLeu----- 90
Db 672 CTAAGCGATAATAATAATTAGAAAGATTGCCTAATGATGTTTTCCACGGAGCCTCTGGA 731
QY 91 ---ValLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGly 109
Db 732 CCAGTCATTCTAGATATTTCAAGAACAAAGGATCCATTCCTCGCCTAGCTATGGCTTAGAA 791
QY 110 GlyLeuMethHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAsp 129
Db 792 AATCTTAAGAAGCTGAGGGCCAGGTCGACTTACAACCTTAAAAAGCTGCTACTCTGGAA 851
QY 130 SerPheProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGly 149
Db 852 AAGCTTGTGCGCCTCATGGAAGCCAGCCTCACCTATCCCAGCCATTGCTGTCCTTT--- 908
QY 150 MetCysAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHis----- 167
Db 909 -----GCAAACTGGAGACGGCAAAATCTCTGAGCTTCATCCAATT 947
QY 168 -----LeuAspAspGluGluSerSerLysArgProLeu 178
Db 948 TGCAACAAATCTATTTTAAGGCAAGAAGTGTATTATATGACTCAGACTAGGGGTGAGAGA 1007
QY 179 GlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspGlnAspLeuAspGluLeuGlnLeu 198

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552 ATTGAAGAAATCTTTTCGTGGGCTGAGCTTTGAAAGTGTGATCTATGGCTGAATAAG 611


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; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G182770
US-09-016-434-1209

Alignment Scores:
Pred. No.:      2.4e-29      Length:      2393
Score:          414.50      Matches:      123
Percent Similarity: 44.20%      Conservative: 94
Best Local Similarity: 25.05%      Mismatches: 231
Query Match:      12.53%      Indels:      43
DB:              4          Gaps:      11

US-10-664-667-5 (1-633) x US-09-016-434-1209 (1-2393)

QY      64 SerSerLeuGlnAlaLeuAspLeuSer---TrpAsnAlaIleArgSerIleHisProGlu 82
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QY      83 AlaPheSerThrLeuHisSerLeuValLysLeuAspLeuThrAspAsnGlnLeuThrThr 102
Db      703 GTTTTCACGGAGCCTCTGGACCAGTCATTCTAGATATTCAAGAACCAAGGATCCATTCC 762

QY      103 LeuProLeuAlaGlyLeuGlyLeuMetHisLeuLysLeuLysGlyAsnLeuAlaLeu 122
Db      763 CTGCCTAGCTATGGCTTAGAAATCTTAAGAAAGCTGAGGCCAGGTCGACTTACAACCTTA 822

QY      123 SerGlnAlaPheSerLysAspSerPheProLysLeuArgIleLeuGluValProTyrAla 142
Db      823 AAAAAGCTGCCTACTCTGGAAAAGCTTGTGCCCCCTCATGGAAGCCAGCCTCACCTATCCC 882

QY      143 TyrGlnCysCysProTyrGlyMetCysAlaSerPhePheLysAlaSerGlyGlnTrpGlu 162
Db      883 AGCCATTGCTGTGCCTTT-----GCAAACTGGAGACGGCAA 918

QY      163 AlaGluAspLeuHis-----LeuAspAspGlu 171
Db      919 ATCTCTGAGCTTCATCCCAATTGCAACAAATCTATTTTAAGGCAAGAAGTTGATTATATG 978

QY      172 GluSerSerLysArgProLeuGlyLeuAlaArgGlnAlaGluAsnHisTyrAspGln 191
Db      979 ACTCAGGCTAGGGGTCAGAGATCCTCTCTGGCAGAAGACAATGAGTCCAGCTACAGCAGA 1038

QY      192 AspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisPro-----SerVal 209
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QY      210 GlnCysSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGly 229
Db      1099 ACCTGCTCCCCTAAGCCAGATGCATTCAACCCATGTGAAGATATCATGGGGTACAAACATC 1158

QY      230 IleArgLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeu 249
Db      1159 CTCAGAGTCCTGATATGGTTTATCAGCATCCTGGCCCATCACTGGGAAC--ATCATAGTG 1215

QY      250 LeuThrValPheAlaGlyGlyProAlaProLeuProValLysPheValValGlyAla 269
Db      1216 CTAGTGATCCTTAACACCAGCCAATATAAACTCACAGTCCCCAGGTTCTTATGTGCAAC 1275

QY      270 IleAlaGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAla 289
Db      1276 CTGGCCTTTGCTGATCTCTGCAATTGGAATCTACCTGTGCTCATTCATGCTGATATC 1335

QY      290 LeuThrPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArg 309
Db      1336 CATACCAAGAGCCCAATATACAACTATGCCATTGACCTGGCAAACTGGGGCAGGCTGTGAT 1395

QY      310 AlaThrGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAla 329
Db      1396 GCTGCTGGCTTTTTCACCTGTCTTTGCCAGTGAGCTGTGCTGCTACACTCTGACAGCTATC 1455
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QY      330 AlaValGln-----CysSerValSerValSerCysValArgAlaTyr 343
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QY      344 GlyLysSerProSerLeuGlySerValArgAlaGlyValLeuGlyCysLeuAlaLeuAla 363
Db      1504 ---AAGGTGCAGCTCCGCCATGCTGCCAGTGTGATGGTGGGCTGGATT---TTTGCT 1557

QY      364 GlyLeuAlaAlaLeuProLeuAlaSerValGlyGluTyrGlyAlaSerProLeuCys 383
Db      1558 TTTCAGCTGCCCTCTTCCCATCTTTGGCATCAGCAGCTACATGAAGGTGAGCATCTGC 1617

QY      384 LeuProTyrAlaProProGluGlyGlnProAlaAlaLeuGlyPheThrValAlaLeuVal 403
Db      1618 CTGCCCATG-----GATATTGACAGCCCTTTGTACAGCTGTATGTATGTCTCCCTCCTT 1671

QY      404 MetMetAsnSerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeuTyrCysAsp 423
Db      1672 GTGCTCAATGTCTTGCCCTTTGTGGTCATCTGTGGCTGTATATCCACATCTACCTCACA 1731

QY      424 LeuProArgGlyAspPhe---GluAlaValTrpAspCysAlaMetValArgHisValAla 442
Db      1732 GTGCGGAACCCCAACATCGTGTCTCTCTGTGATGGCACCAAGGATCGCCAAAGCGCATGGCC 1791

QY      443 TrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPheAlaSer 462
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QY      463 MetLeuGlyLeuPheProValThrProGluAlaValLysSerValLeuValValLeu 482
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QY      503 AspLeuArgArgLeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAlaAlaAla 522
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QY      523 GlyGluLeuGlyLysSerSerCysAspSerThr 533
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RESULT 15

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US-07-741-453A-57
; Sequence 57, Application US/07741453A
; Patent No. 6228597
; GENERAL INFORMATION:
; APPLICANT: PARMENTIER, MARC
; APPLICANT: LIBERT, FREDERIC
; APPLICANT: DUMONT, JACQUES
; APPLICANT: VASSART, GILBERT
; TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
; TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
; TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON, D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/741,453A
; FILING DATE: 19911015
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
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/ NAME: KOKULIS, PAUL N.
/ REGISTRATION NUMBER: 16773
/ REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 861-3000
/ TELEFAX: (202) 822-0944
/ TELEX: 6714627 CUSH
/ INFORMATION FOR SEQ ID NO: 57:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4417 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
US-07-741-453A-57

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US-10-664-667-5 (1-633) x US-07-741-453A-57 (1-4417)

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QY	85	SerThrLeuHisSer---LeuValLysLeuAspLeuThrAspAsnGlnLeuThrThrLeu	103
Db	726	GGAGGAGTGATACAGTGGACCAACCTTGTGGATGTCTCTTACACCAGTGTACTGCCCTG	785
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QY	144	GlnCysCysProTy-----GlyMetCysAlaSerPhe-----	154
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QY	160	GlnTrp-----GluAlaGluAsp	165
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QY	166	LeuHisLeuAspAspGluGluserSerLysArgProLeuGlyLeuLeuAlaArgGlnAla	185
Db	1146	GAGATCCTCGGTTTGGGCAGGAGCTTAAAAACCCACAGGAAGAGACCCCTCCAGGCCTTT	1205
QY	186	GluAsnHisTyAspGlnAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysPro	205
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QY	206	HisProSerValGlnCysSerProThrProGlyProPheLysProCysGluTyLeuPhe	225
Db	1239	AATGAAGACATGGTGTGTACTCCTAAGTCAGATGAGTTCAACCCCTGTGAAGACATAATG	1298
QY	226	GluSerTrpGlyIleArgLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsn	245
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QY	246	GlyLeuValLeuLeuThrValPheAlaGlyGlyProAlaProLeuProProValLysPhe	265
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QY	386	TyrAlaProProGluGlyGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMet	405
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Job time : 256 secs

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GenCore version 5.1.6
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Total number of hits satisfying chosen parameters: 11245082

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	3305	99.9	1899	17	US-10-664-667-6 Sequence 6, Appli
3	3305	99.9	2486	10	US-09-851-595-4 Sequence 4, Appli
4	3305	99.9	2486	17	US-10-664-667-4 Sequence 4, Appli
5	3045.5	92.1	2208	10	US-09-851-595-9 Sequence 9, Appli
6	3045.5	92.1	2208	17	US-10-664-667-9 Sequence 9, Appli
7	3045.5	92.1	2711	10	US-09-851-595-7 Sequence 7, Appli
8	3045.5	92.1	2711	17	US-10-664-667-7 Sequence 7, Appli
9	3045.5	92.1	2901	10	US-09-851-595-12 Sequence 12, Appl
10	3045.5	92.1	2901	17	US-10-664-667-12 Sequence 12, Appl
11	3045.5	92.1	3119	15	US-10-225-567A-580 Sequence 580, App
12	3045.5	92.1	3325	17	US-10-331-496A-52 Sequence 52, Appl
13	3045.5	92.1	3429	18	US-10-398-036-26 Sequence 26, Appl
14	3045.5	92.1	3438	14	US-10-176-847-89 Sequence 89, Appl
15	3045.5	92.1	3443	17	US-10-331-496A-94 Sequence 94, Appl
16	3045.5	92.1	3492	10	US-09-851-595-10 Sequence 10, Appl
17	3045.5	92.1	3492	17	US-10-664-667-10 Sequence 10, Appl
18	3045.5	92.1	3492	18	US-10-737-450-31 Sequence 31, Appl
19	3041.5	92.0	3273	17	US-10-295-027-1119 Sequence 1119, Ap
20	3041.5	92.0	3273	18	US-10-783-528-43 Sequence 43, Appl
21	3040.5	91.9	2487	14	US-10-270-336-1 Sequence 1, Appli
22	3040	91.9	2988	17	US-10-302-172-723 Sequence 723, App
23	3038.5	91.9	3349	14	US-10-270-336-4 Sequence 4, Appli
24	3016.5	91.2	3381	10	US-09-970-944-5 Sequence 5, Appli
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31	1275	38.6	2651	17	US-10-295-027-1113 Sequence 1113, Ap
32	1275	38.6	2651	17	US-10-173-999-27 Sequence 27, Appl
33	1275	38.6	2724	15	US-10-251-385-263 Sequence 263, App
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35	1275	38.6	2724	17	US-10-174-456-4 Sequence 4, Appli
36	1275	38.6	2724	18	US-10-751-736-21 Sequence 21, Appl
37	1275	38.6	2880	17	US-10-295-027-1114 Sequence 1114, Ap
38	1275	38.6	2880	19	US-10-482-029-157 Sequence 157, App
39	1275	38.6	2880	19	US-10-651-237-48 Sequence 48, Appl
40	1275	38.6	2880	19	US-10-782-413-48 Sequence 48, Appl
41	1275	38.6	3032	17	US-10-295-027-848 Sequence 848, App
42	1275	38.6	3032	17	US-10-295-027-945 Sequence 945, App
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45	1242.5	37.6	1173	17	US-10-343-650A-65 Sequence 65, Appl

ALIGNMENTS

RESULT 1
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; Sequence 6, Application US/09851595
; Publication No. US20030166047A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/09/851,595
; CURRENT FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:									
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QY	21	SerThrHisAlaSerValGluArgSerGlnGlyLeuSerLeuProAlaHisProAlaSer	40						
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Db	1141	CCACTCTGCCCTGCCCTACGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTG	1200
QY	401	AlaLeuValMetMetAsnSerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeu	420
Db	1201	GCCCTGGTGATGATGAACCTCCTTCTGTCTTCTGGTCTGTGGCCGTGCATCAAACTG	1260
QY	421	TyrCysAspLeuProArgGlyAspPheGluAlaValTrpAspCysAlaMetValArgHis	440
Db	1261	TACTGTGACCTGCCGCGGGCGACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGCAC	1320
QY	441	ValAlaTrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPhe	460
Db	1321	GTGGCCTGGCTCATCTTCGCAGACGGGCTCTCTACTGTCCCGTGGCCTTCTCAGCTTC	1380
QY	461	AlaSerMetLeuGlyLeuPheProValThrProGluAlaValLysSerValLeuLeuVal	480
Db	1381	GCCTCCATGTGGGCCTCTTCCCTGTACGCCCGAGGCCGTCAAAGTCTGTCTCTGTGCTG	1440
QY	481	ValLeuProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPhe	500
Db	1441	GTGCTGCCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCACTTC	1500
QY	501	ArgAspAspLeuArgArgLeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAla	520
Db	1501	CGGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT	1560
QY	521	AlaAlaGlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuValAlaPheSer	540
Db	1561	GCGGCCGGGAGCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT	1620
QY	541	AspValAspLeuIleLeuGluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyr	560
Db	1621	GATGTGGATCTCATTTGGAAGCTTCTGAAGCTGGCGGCCCTTGGCTGGAGACCTAT	1680
QY	561	GlyPheProSerValThrLeuIleSerCysGlnGlnProGlyAlaProArgLeuGluGly	580
Db	1681	GGCTTCCCCCTCAGTGACCCCTCATCTCTGTTCAGCAGCCAGGGGCCCCCAGGCTGGAGGC	1740
QY	581	SerHisCysValGluProGluGlyAsnHisPheGlyAsnProGlnProSerMetAspGly	600
Db	1741	AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGA	1800
QY	601	GluLeuLeuLeuArgAlaGluGlySerThrProAlaGlyGlyLeuSerGlyGlyGly	620
Db	1801	GAACCTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGC	1860
QY	621	GlyPheGlnProSerGlyLeuAlaPheAlaSerHisVal	633
Db	1861	GGCTTTCAGCCCTCTGGCTTGGCCTTGTGCTTGTGCTTACACCGTG	1899

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RESULT 2
US-10-664-667-6
; Sequence 6, Application US/10664667
; Publication No. US20040058377A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/10/664,667
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/851,595
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1899)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (171)
; OTHER INFORMATION: n = any nucleotide
US-10-664-667-6

Alignment Scores:
Pred. No.: 0 Length: 1899
Score: 3305.00 Matches: 632
Percent Similarity: 99.84% Conservative: 0
Best Local Similarity: 99.84% Mismatches: 1
Query Match: 99.94% Indels: 0
DB: 17 Gaps: 0

US-10-664-667-5 (1-633) x US-10-664-667-6 (1-1899)

QY 1 AsnThrThrHisTyrArgGluSerTrpTyrAlaCysArgTyrArgSerGlyIleProGly 20
D 1 AATACGACTCACTATAGGGAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATCCCGGG 60
QY 21 SerThrHisAlaSerValGluArgSerGlnGlyLeuSerLeuProAlaHisProAlaSer 40
D 61 TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGCTCATCCAGCCTCT 120
QY 41 LeuAlaAlaLeuAlaAlaSerAsnThrThrAlaSerGlyLysLeuGlu**AspThrPhe 60
D 121 CTGTGCTGCCCTAGCGGCCCTCCAAACACACCGCATCTTGGGAATTTGGAGCTNGACACCTTC 180
QY 61 SerGlnLeuSerSerLeuGlnAlaLeuAspLeuSerTrpAsnAlaIleArgSerIleHis 80
D 181 AGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCAC 240
QY 81 ProGluAlaPheSerThrLeuHisSerLeuValLysLeuAspLeuThrAspAsnGlnLeu 100
D 241 CCTGAGGCCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTG 300
QY 101 ThrThrLeuProLeuAlaGlyLeuGlyGlyLeuMetHisLeuLysLeuLysGlyAsnLeu 120
D 301 ACCACACTGCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 360
QY 121 AlaLeuSerGlnAlaPheSerLysAspSerPheProLysLeuArgIleLeuGluValPro 140
D 361 GCTCTCTCCAGGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCTCTGGAGGTGCCT 420
QY 141 TyrAlaTyrGlnCysCysProTyrGlyMetCysAlaSerPhePheLysAlaSerGlyGln 160
D 421 TATGCCCTACCAGTGTCTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTCTGGCAG 480
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QY 161 TrpGluAlaGluAspLeuHisLeuAspGluSerSerLysArgProLeuGlyLeu 180
D 481 TGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCTC 540
QY 181 LeuAlaArgGlnAlaGluAsnHisTyrAspGlnAspLeuAspGluLeuGlnLeuGluMet 200
D 541 CTTGCCAGACAAGCAGAGAACCACACTATGACCAGGACTGGATGAGCTCCAGCTGGAGATG 600
QY 201 GluAspSerLysProHisProSerValGlnCysSerProThrProGlyProPheLysPro 220
D 601 GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC 660
QY 221 CysGluTyrLeuPheGluSerTrpGlyIleArgLeuAlaValTrpAlaIleValLeuLeu 240
D 661 TGTGAGTACCTCTTTGAAAGCTGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTC 720
QY 241 SerValLeuCysAsnGlyLeuValLeuLeuThrValPheAlaGlyGlyProAlaProLeu 260
D 721 TCCGTGCTCTGCAATGAGTGGTGTGCTGTGACCGTGTTCGTGGCGGCCCTGCCCCCTG 780
QY 261 ProProValLysPheValValGlyAlaIleAlaGlyAlaAsnThrLeuThrGlyIleSer 280
D 781 CCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGCGCCCAACACCTTGACTGGCATTTC 840
QY 281 CysGlyLeuLeuAlaSerValAspAlaLeuThrPheGlyGlnPheSerGluTyrGlyAla 300
D 841 TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTGGTCAGTTCTCTGAGTACGAGCC 900
QY 301 ArgTrpGluThrGlyLeuGlyCysArgAlaThrGlyPheLeuAlaValLeuGlySerGlu 320
D 901 CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGTCCGAG 960
QY 321 AlaSerValLeuLeuLeuThrLeuAlaAlaValGlnCysSerValSerValSerCysVal 340
D 961 GCATCGGTGCTGTGCTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCTCTGTGTC 1020
QY 341 ArgAlaTyrGlyLysSerProSerLeuGlySerValArgAlaGlyValLeuGlyCysLeu 360
D 1021 CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCTTAGGCTGCC 1080
QY 361 AlaLeuAlaGlyLeuAlaAlaAlaLeuProLeuAlaSerValGlyGluTyrGlyAlaSer 380
D 1081 GCACCTGGCAGGGCTGSCCGCCGCACTGCCCTTGGCTCAGTGGGAGAAATACGGGGCTCC 1140
QY 381 ProLeuCysLeuProTyrAlaProProGluGlyGlnProAlaAlaLeuGlyPheThrVal 400
D 1141 CCACTCTGCCTGCCCTACGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTACCGTG 1200
QY 401 AlaLeuValMetMetAsnSerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeu 420
D 1201 GCCCTGGTGTGATGAATCCTTCTGTTTCCCTGGTGGCCGGTGCCTACATCAAACTG 1260
QY 421 TyrCysAspLeuProArgGlyAspPheGluAlaValTrpAspCysAlaMetValArgHis 440
D 1261 TACTGTGACCTGCCCGGGCGGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCAC 1320
QY 441 ValAlaTrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPhe 460
D 1321 GTGGCCTGGCTCATCTTCGAGACGGGCTCCTCTACTGTCCCGTGGCCTTCTCTAGCTTC 1380
QY 461 AlaSerMetLeuGlyLeuPheProValThrProGluAlaValLysSerValLeuLeuVal 480
D 1381 GCCTCCATGTGGGCCCTCTTCCCTGTACGCCCGGAGGCCGTCAAGTCTGTCTCTGCTGG 1440
QY 481 ValLeuProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPhe 500
D 1441 GTGCTGCCCTGCCCTGCCCTGCCCTCAACCCACTGCTGTACTGCTCTTCAACCCCACTTC 1500
QY 501 ArgAspAspLeuArgArgLeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAla 520
D 1501 CGGGATGACCTTCGGCGGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATG 1560
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QY 421 TyrCysAspLeuProArgGlyAspPheGluAlaValTrpAspCysAlaMetValArgHis 440
Db 1262 TACTGTGACCTGCCGGGGGACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGCAC 1321
QY 441 ValAlaTrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaPheLeuSerPhe 460
Db 1322 GTGGCCTGGCTCATCTTCGAGACGGGCTCCTCTACTGTCCGTGGCCTTCCTCAGCTTC 1381
QY 461 AlaSerMetLeuGlyLeuPheProValThrProGluAlaValLysSerValLeuVal 480
Db 1382 GCCTCCATGCTGGGCCTCTCCCTGTCAAGCCCGAGCGCTCAAGTCTGCTCCTGGTG 1441
QY 481 ValLeuProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPhe 500
Db 1442 GTGCTGCCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCACTTC 1501
QY 501 ArgAspAspLeuArgArgLeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAla 520
Db 1502 CGGGATGACCTTCGGCGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT 1561
QY 521 AlaAlaGlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuValAlaPheSer 540
Db 1562 GCGGCCGGGAGCTGGAGAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT 1621
QY 541 AspValAspLeuIleLeuGluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyr 560
Db 1622 GATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGCGGGCCCCCTGGGCTGGAGACCTAT 1681
QY 561 GlyPheProSerValThrLeuIleSerCysGlnGlnProGlyAlaProArgLeuGluGly 580
Db 1682 GGCTTCCCCTCAGTGACCTCATCTCCTGTACAGCAGCCAGGGGCCCCCAAGGCTGGAGGC 1741
QY 581 SerHisCysValGluProGluGlyAsnHisPheGlyAsnProGlnProSerMetAspGly 600
Db 1742 AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGA 1801
QY 601 GluLeuLeuLeuArgAlaGluGlySerThrProAlaGlyGlyLeuSerGlyGlyGly 620
Db 1802 GAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGTGGC 1861
QY 621 GlyPheGlnProSerGlyLeuAlaPheAlaSerHisVal 633
Db 1862 GGCTTTACGCCCTCTGGCTTGGCCTTTGCTTTCACACGTG 1900
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RESULT 4

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US-10-664-667-4
; Sequence 4, Application US/10664667
; Publication No. US20040058377A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/10/664,667
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/851,595
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2486
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1900)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (172)
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; OTHER INFORMATION: n = any nucleotide
US-10-664-667-4
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Alignment Scores:
Pred. No.: 0 Length: 2486
Score: 3305.00 Matches: 632
Percent Similarity: 99.84% Conservative: 0
Best Local Similarity: 99.84% Mismatches: 1
Query Match: 99.94% Indels: 0
DB: 17 Gaps: 0

US-10-664-667-5 (1-633) x US-10-664-667-4 (1-2486)

QY 1 AsnThrThrHisTyrArgGluSerTrpTyrAlaCysArgTyrArgSerGlyIleProGly 20
Db 2 AATACGACTCACTATAGGGAAGCTGGTACGCCCTGACGGTACCGGTCCGGAATTCGCGG 61
QY 21 SerThrHisAlaSerValGluArgSerGlnGlyLeuSerLeuProAlaHisProAlaSer 40
Db 62 TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCT 121
QY 41 LeuAlaAlaLeuAlaAlaSerAsnThrThrAlaSerGlyLysLeuGlu**AspThrPhe 60
Db 122 CTTGCTGCCCTAGCGSCTCCAACACACCGCATCTGGGAAATTGGAGCTNGACACCTTC 181
QY 61 SerGlnLeuSerSerLeuGlnAlaLeuAspLeuSerTrpAsnAlaIleArgSerIleHis 80
Db 182 AGCCAGCTGAGTCCCTGCAAGCCCTGGATCTTAGTGGAAACGCCATCCGGTCCATCCAC 241
QY 81 ProGluAlaPheSerThrLeuHisSerLeuValLysLeuAspLeuThrAspAsnGlnLeu 100
Db 242 CCTGAGGCCTTCTCCACCCCTGCATCCCTGGTCAAGCTGGACCTTGACAGAACACAGCTG 301
QY 101 ThrThrLeuProLeuAlaGlyLeuGlyGlyLeuMetHisLeuLysLeuLysGlyAsnLeu 120
Db 302 ACCACACTGCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 361
QY 121 AlaLeuSerGlnAlaPheSerLysAspSerPheProLysLeuArgIleLeuGluValPro 140
Db 362 GCTCTCTCCAGGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCT 421
QY 141 TyrAlaTyrGlnCysCysProTyrGlyMetCysAlaSerPhePheLysAlaSerGlyGln 160
Db 422 TATGCCTACCAGTGTCTCCCTATGGGATGTGTGCAGCTTCTTCAAGGCCTCTGSGCAG 481
QY 161 TrpGluAlaGluAspLeuHisLeuAspAspGluGluSerSerLysArgProLeuGlyLeu 180
Db 482 TGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCTC 541
QY 181 LeuAlaArgGlnAlaGluAsnHisTyrAspGlnAspLeuAspGluLeuGlnLeuGluMet 200
Db 542 CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG 601
QY 201 GluAspSerLysProHisProSerValGlnCysSerProThrProGlyProPheLysPro 220
Db 602 GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC 661
QY 221 CysGluTyrLeuPheGluSerTrpGlyIleArgLeuAlaValTrpAlaIleValLeuLeu 240
Db 662 TGTGAGTACCTCTTTGAAAGCTGGGCATCCGCCCTGGCCGTGTGGCCATCGTGTGCTC 721
QY 241 SerValLeuCysAsnGlyLeuValLeuLeuThrValPheAlaGlyGlyProAlaProLeu 260
Db 722 TCCGTGCTCTGCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 781
QY 261 ProProValLysPheValValGlyAlaIleAlaGlyAlaAsnThrLeuThrGlyIleSer 280
Db 782 CCCCCGGTCAAGTTTGTGGTAGGTGCGATTGACGGCGCAACACACCTTGACTGGCATTTCC 841
QY 281 CysGlyLeuLeuAlaSerValAspAlaLeuThrPheGlyGlnPheSerGluTyrGlyAla 300
Db 842 TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTTCAGTTTCTCTGAGTACGAGCC 901
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QY 301 ArgTrpGluThrGlyLeuGlyCysArgAlaThrGlyPheLeuAlaValLeuGlySerGlu 320
Db |||||||
902 CGCTGGAGACGGGGCTAGGCTGCGGGCCACTGGCTTCCTGGCAGTACTTGGGTGGAG 961

QY 321 AlaSerValLeuLeuLeuThrLeuAlaAlaValGlnCysSerValSerValSerCysVal 340
Db |||||||
962 GCATCGGTGCTGCTGCTCACTCTGGCCGAGTGTCAGTGCAGCGTCTCCGTCTCTGTGTC 1021

QY 341 ArgAlaTyrGlyLysSerProSerLeuGlySerValArgAlaGlyValLeuGlyCysLeu 360
Db |||||||
1022 CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCTTAGGCTGCCTG 1081

QY 361 AlaLeuAlaGlyLeuAlaAlaLeuProLeuAlaSerValGlyGluTyrGlyAlaSer 380
Db |||||||
1082 GCACTGGCAGGGCTGGCCCGCCGCACTGCCCTGGCCCTCAGTGGGAGAATACGGGGCTCC 1141

QY 381 ProLeuCysLeuProTyrAlaProProGluGlyGlnProAlaAlaLeuGlyPheThrVal 400
Db |||||||
1142 CCACTCTGCCCTACGGCCACCTGAGGGTCAGCCAGAGCCCTGGGCTTCACCGTG 1201

QY 401 AlaLeuValMetMetAsnSerPheCysPheLeuValValAlaGlyAlaTyrIleLysLeu 420
Db |||||||
1202 GGCCTGGTGATGATGAACCTCTCTGTTCTTGTCGTGGCCGGTGCCCTACATCAAACTG 1261

QY 421 TyrCysAspLeuProArgGlyAspPheGluAlaValTrpAspCysAlaMetValArgHis 440
Db |||||||
1262 TACTGTGACCTGCCCGGGCGGACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGCAC 1321

QY 441 ValAlaTrpLeuIlePheAlaAspGlyLeuLeuTyrCysProValAlaAlaPheLeuSerPhe 460
Db |||||||
1322 GTGGCCTGGCTCATCTTCGAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTC 1381

QY 461 AlaSerMetLeuGlyLeuPheProValThrProGluAlaValLysSerValLeuLeuVal 480
Db |||||||
1382 GCCTCCATGCTGGGCCCTCTCCCTGTCAAGCCGAGCCGCTCAAGTCTGTCTGTGGTG 1441

QY 481 ValLeuProLeuProAlaCysLeuAsnProLeuLeuTyrLeuLeuPheAsnProHisPhe 500
Db |||||||
1442 GTGCTGCCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCACTTC 1501

QY 501 ArgAspLeuArgArgLeuArgProArgAlaGlyAspSerGlyProLeuAlaTyrAla 520
Db |||||||
1502 CGGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGACTCAGGGCCCCCTAGCCTATGCT 1561

QY 521 AlaAlaGlyGluLeuGluLysSerSerCysAspSerThrGlnAlaLeuValAlaPheSer 540
Db |||||||
1562 GCGGCCGGGAGCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT 1621

QY 541 AspValAspLeuIleLeuGluAlaSerGluAlaGlyArgProProGlyLeuGluThrTyr 560
Db |||||||
1622 GATGTGGATCTCATTCTGGAAGCTTCTGAAGCTGGCGCGGCCCTGGGCTGGAGACCTAT 1681

QY 561 GlyPheProSerValThrLeuIleSerCysGlnGlnProGlyAlaProArgLeuGluGly 580
Db |||||||
1682 GGCCTCCCTCAGTGACCTCATCTCCTGTCAAGCCAGCGGGCCCCCAGGCTGGAGGCG 1741

QY 581 SerHisCysValGluProGluGlyAsnHisPheGlyAsnProGlnProSerMetAspGly 600
Db |||||||
1742 AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCCAACCTCCATGGATGGA 1801

QY 601 GluLeuLeuLeuArgAlaGluGlySerThrProAlaGlyGlyLeuSerGlyGlyGly 620
Db |||||||
1802 GAACTGCTGCTGAGGCGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGGTGGC 1861

QY 621 GlyPheGlnProSerGlyLeuAlaPheAlaSerHisVal 633
Db |||||||
1862 GGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTTCACACGTG 1900

RESULT 5

US-09-851-595-9

; Sequence 9, Application US/09851595

; Publication No. US20030166047A1

; GENERAL INFORMATION:

; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/09/851,595
; CURRENT FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2208)
US-09-851-595-9

Alignment Scores:

Pred. No.: 3.08e-308 Length: 2208
Score: 3045.50 Matches: 602
Percent Similarity: 92.61% Conservative: 12
Best Local Similarity: 90.80% Mismatches: 19
Query Match: 92.09% Indels: 32
DB: 10 Gaps: 4

US-10-664-667-5 (1-633) x US-09-851-595-9 (1-2208)

QY 1 AsnThrThrHisTyr----- 5
Db 224 AACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAG 283

QY 6 ---ArgGluSerTrpTyrAla-----CysArgTyrArg 15
Db 284 GCACCACCAGCCTGGAGATCCTGACCTGACCCGCGCAGGCATCCGGCTGCTCCCATCGG 343

QY 16 -----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---G1 31
Db 344 GGATGTGCCAAACAGCTGCCCAGGCTCCGAGTCTCGAACTGTCTCACAATCAAATTGAGG 403

QY 31 yLeuSerLeuProAlaHisProAlaSerLeuAlaAlaLeuAlaAlaSerAsnThrThrAl 51
Db 404 AGCTGCCCAAGCTGCACAGGTGTCAGAAATTGGAGGAAA-TCGGGCCTCCAACACACCGC 462

QY 51 aSerGlyLysLeuGlu**AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe 71
Db 463 ATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCT 521

QY 71 uSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa 91
Db 522 TAGCTGGAACCGCATCCGGTCCATCCACCTGAGGCCTTCTCCACCTGCACCTCCCTGGT 581

QY 91 lLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyLe 111
Db 582 CAAGCTGGACCTGACAGACAACCCAGCTGACCACACTGCCCTGGCTGGACTTGGGGCTT 641

QY 111 uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh 131
Db 642 GATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCAGGCCCTTCTCCAAGGACAGTTT 701

QY 131 eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy 151
Db 702 CCCAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCAAGTCTGCTCCCTATGGGATGTG 761

QY 151 sAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspG1 171
Db 762 TGCCAGCTTCTTCAAGGCCCTCTGGGAGTGGGAGGCTGAAGACCTTCACCTTGATGATGA 821

QY 171 uGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspG1 191
Db 822 GGAGTCTTCAAAAAGGCCCTCTGGGCCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCA 881

QY	191	nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy	211
Db	882	GGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCCAGTGTCCAGTG	941
QY	211	sSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGlyIleAr	231
Db	942	TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCG	1001
QY	231	gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh	251
Db	1002	CCTGGCCGTGTGGGCATCGTGTGTCTCCGTGCTGTGCAATGGACTGGTGTGCTGAC	1061
QY	251	rValPheAlaGlyGlyProAlaProLeuProProValLysPheValValGlyAlaIleAl	271
Db	1062	CGTGTTCGTGGGGCCCTGCCCCCTGCCCCCGTCAAGTTTGTGTAGGTGGATTGC	1121
QY	271	aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuTh	291
Db	1122	AGGCGCCAAACACTTGACTGGCATTTTCCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGAC	1181
QY	291	rPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaTh	311
Db	1182	CTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGGGCCAC	1241
QY	311	rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa	331
Db	1242	TGGCTTCCTGGCAGTACTTGGGTGGAGGCATCGGTGCTGCTGCTCACTCTGGCCGCAGT	1301
QY	331	lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe	351
Db	1302	GCAGTGCAGCGTCTCCGTCTCCTGTGTCGGGGCCTATGGGAAGTCCCCCTCCCTGGGCAG	1361
QY	351	rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe	371
Db	1362	CGTTCGAGCAGGGTCTTAGGTCCTGGCACTGGCAGGGCTGGCCGCCGCACTGCCCCCT	1421
QY	371	uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluGl	391
Db	1422	GGCCTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCCTGCCCTACGCGCCACTGAGGG	1481
QY	391	yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe	411
Db	1482	TCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACCTCCCTTCGTTCCT	1541
QY	411	uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluAl	431
Db	1542	GGTCGTGGCCGTGGCTTACATCAAACTGTACTGTGACCTGCCGCGGGCGACTTTGAGGC	1601
QY	431	aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe	451
Db	1602	CGTGTGGGACTGGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGCAGACGGGCTCCT	1661
QY	451	uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr	471
Db	1662	CTACTGTCCCGTGGCCTTCCTCAGCTTCGCCCTCCATGCTGGGCCCTCTTCCCTGTACAGCC	1721
QY	471	oGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe	491
Db	1722	CGAGGCCGTCAAGTCTGTCTGCTGGTGGTGTGCCCTGCCTGCCTCAACCCCACT	1781
QY	491	uLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgLeuArgProArgAl	511
Db	1782	GCTGTACCTGCTCTCAACCCCCACTTCGGGGATGACCTTCGGCGGCTTCGGCCCCCGCGC	1841
QY	511	aGlyAspSerGlyProLeuAlaTyrAlaAlaAlaGlyGluLeuGluLysSerSerCysAs	531
Db	1842	AGGGGACTCAGGGCCCTAGCCTATGCTGCGGCCGGGAGCTGGAGAAGAGCTCCTGTGA	1901
QY	531	pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl	551
Db	1902	TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGATCTCATTTCTGGAAGCTTCTGAAGC	1961

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Qy 551 aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysG1 571
    |||||
Db 1962 TGGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTCAGTGACCCCTCATCTCCTGTCA 2021

Qy 571 nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisPh 591
    |||||
Db 2022 GCAGCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTT 2081

Qy 591 eGlyAsnProGlnProSerMetAspGlyGluLeuLeuLeuArgAlaGluGlySerThrPr 611
    |||||
Db 2082 TGSGAACCCCAACCCCTCCATGGATGGAGAACTGTGTCTGAGGGCAGAGGGATCTACGCC 2141

Qy 611 oAlaGlyGlyLeuSerGlyGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSe 631
    |||||
Db 2142 AGCAGGTGAGGCTTGTACGGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTGTGCTTC 2201

Qy 631 rHisVal 633
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Db 2202 ACACGTG 2208

RESULT 6
US-10-664-667-9
; Sequence 9, Application US/10664667
; Publication No. US20040058377A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/10/664,667
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/851,595
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2208)
US-10-664-667-9

Alignment Scores:
Pred. No.: 3.08e-308 Length: 2208
Score: 3045.50 Matches: 602
Percent Similarity: 92.61% Conservative: 12
Best Local Similarity: 90.80% Mismatches: 19
Query Match: 92.09% Indels: 32
DB: 17 Gaps: 4

US-10-664-667-5 (1-633) x US-10-664-667-9 (1-2208)

Qy 1 AsnThrThrHisTyr-----CysArgTyrArg 15
    |||:::|||||
Db 224 AACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAG 283

Qy 6 ---ArgGluSerTrpTyrAla-----CysArgTyrArg 15
    ::::|:::
Db 284 GCACCACAGCCTGGAGATCCTGACCCCTGACCCGCGCAGGCATCCGGCTGCTCCCATCGG 343

Qy 16 -----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---G1 31
    ::: |||||:::
Db 344 GGATGTGCCAACAGCTGCCAGGCTCCGAGTCTCGGAAGTGTCTCACAATCAAAATTGAGG 403

Qy 31 yLeuSerLeuProAlaHisProAlaSerLeuAlaLeuAlaAlaSerAsnThrThrAl 51
    ::: |||||:::
Db 404 AGTGTCCCGAGCCTGCACAGGTGTGAGAAATTGGAGGAAA-TCGGCCTCCACACAAACCGC 462

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QY	51	aSerGlyLysLeuGlu**AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe	71
Db	463	ATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCT	521
QY	71	uSerTrpAsnAlaIleAArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa	91
Db	522	TAGCTGGAAACGCCATCCGGTCCATCCACCCCTGAGGCCCTTCTCCACCCCTGCACCTCCCTGGT	581
QY	91	lLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyGlyLe	111
Db	582	CAAGCTGGACCTGACAGACAACACAGCTGACCACACTGCCCTGGCTGGACTTGGGGGCTT	641
QY	111	uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh	131
Db	642	GATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCCCTTCTCCAAGGACAGTTT	701
QY	131	eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy	151
Db	702	CCCAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCAAGTGCTGCCCTATGGGATGTG	761
QY	151	sAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspAspGl	171
Db	762	TGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGCTGAAGACCTTCACCTTGATGATGA	821
QY	171	uGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspGl	191
Db	822	GGAGTCTTCAAAAAGGCCCTGGGCCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCA	881
QY	191	nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy	211
Db	882	GGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAGTGTCCAGTG	941
QY	211	sSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGlyLeAr	231
Db	942	TAGCCCTACTCCAGGCCCTTCAAGCCCTGTAGTACCTCTTTGAAAGCTGGGGCATCCG	1001
QY	231	gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh	251
Db	1002	CCTGGCCGTGTGGGCCATCGTGTGTCTCCGTGCTCTGCAATGGACTGGTGTGTGTGAC	1061
QY	251	rValPheAlaGlyGlyProAlaProLeuProProValLysPheValValGlyAlaIleAl	271
Db	1062	CGTGTTCGCTGGCGGGCTGCCCCCTGCCCCCGGTCAAAGTTTGTGGTAGGTCCGATGC	1121
QY	271	aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuTh	291
Db	1122	AGCGCCAACACCTTGACTGGCATTTCTGTGGCCCTTCTAGCCCTCAGTCGATGCCCTGAC	1181
QY	291	rPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaTh	311
Db	1182	CTTTGGTCAGTTCTCTGAGTACGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGGGCCAC	1241
QY	311	rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa	331
Db	1242	TGGCTTCTTGGCAGTACTTGGGTGGAGGCATCGGTGCTGTGCTCAGTCTGGCCCGAGT	1301
QY	331	lGlnCysSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe	351
Db	1302	GCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGCCCTATGGGAAGTCCCCCTCCCTGGGCGAG	1361
QY	351	rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe	371
Db	1362	CGTTTCGAGCAGGGGTCTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCCACTGCCCTT	1421
QY	371	uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluGl	391
Db	1422	GGCCTCAGTGGGAGATAACGGGGCCCTCCCCACTCTGCCTGCCCTACGGGCCACCTGAGGG	1481
QY	391	yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe	411
Db	1482	TCAGCCAGCAGCCCTTGGGCTTCACCGTGGCCCTGGTGATGATGAACCTCTTCTTCTCT	1541
QY	411	uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArqGlyAspPheGluAl	431

Db	1542	GGTCGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCTGCCGGGGGCGACCTTTGAGGC	1601
Qy	431	aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe	451
Db	1602	CGTGTGGGACTGCGCCCATGGTCAGGCACGTGGCCTGGCTCATCTTCGACAGCGGCTCCT	1661
Qy	451	uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr	471
Db	1662	CTACTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCATGCTGGGCTCTTCCCTGTCAAGCC	1721
Qy	471	oGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe	491
Db	1722	CGAGGCGGTCAAGTCTGTCTGCTGGTGGTGCTGCCCTGGCTGCCTCAACCCACT	1781
Qy	491	uLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgArgLeuArgProArgAl	511
Db	1782	GCTGTACCTGCTCTTCAACCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCCGCGC	1841
Qy	511	aGlyAspSerGlyProLeuAlaTyrAlaAlaAlaGlyGluLeuGluLysSerSerCysAs	531
Db	1842	AGGGGACTCAGGGCCCCCTAGCCTATGCTCGGCCGGGAGCTGGAGAAAGAGCTCCTGTGA	1901
Qy	531	pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl	551
Db	1902	TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTTCTGGAAGCTTCTGAAGC	1961
Qy	551	aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysGl	571
Db	1962	TGGCGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCCTCAGTGACCCCTCATCTCCTGTCA	2021
Qy	571	nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisPh	591
Db	2022	GCAGCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTT	2081
Qy	591	eGlyAsnProGlnProSerMetAspGlyGluLeuLeuLeuArgAlaGluGlySerThrPr	611
Db	2082	TGGGAACCCCAACCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGGATCTACGCC	2141
Qy	611	oAlaGlyGlyGlyLeuSerGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSe	631
Db	2142	AGCAGGTGGAGGCTTGTACGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTC	2201
Qy	631	rHisVal 633	
Db	2202	ACACGTG 2208	
RESULT 7			
US-09-851-595-7			
; Sequence 7, Application US/09851595			
; Publication No. US20030166047A1			
; GENERAL INFORMATION:			
; APPLICANT: Gu, Wei			
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR			
; FILE REFERENCE: MNI-080CP			
; CURRENT APPLICATION NUMBER: US/09/851,595			
; CURRENT FILING DATE: 2000-05-08			
; PRIOR APPLICATION NUMBER: 09/556,588			
; PRIOR FILING DATE: 2000-05-08			
; PRIOR APPLICATION NUMBER: 60/132,896			
; PRIOR FILING DATE: 1999-05-06			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 7			
; LENGTH: 2711			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)..(2208)			
US-09-851-595-7			
Alignment Scores:			

Pred. No.:	4.12e-308	Length:	2711
Score:	3045.50	Matches:	602
Percent Similarity:	92.61%	Conservative:	12
Best Local Similarity:	90.80%	Mismatches:	19
Query Match:	92.09%	Indels:	32
DB:	10	Gaps:	4
US-10-664-667-5 (1-633) x US-09-851-595-7 (1-2711)			
Qy	1	AsnThrThrHisTyr-----	----- 5
Db	224	AACTCCACACACTATCTCTGATGGTGCCATCCAGGAGTTTCCAGATCTCAAG	283
Qy	6	---ArgGluSerTrpTyrAla-----	-----CysArgTyrArg 15
Db	284	GCACCACGCGCTGGAGATCCTGACCCCTGACCCGGCAGGATCCGGCTGCTCCCATCGG	343
Qy	16	-----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---	Gln 31
Db	344	GGATGTGCCAACAGCTGCCCGAGGCTCCGAGTCTCTGGAACTGTCTACAATCAAATTGAGG	403
Qy	31	yLeuSerLeuProAlaHisProAlaSerLeuAlaAlaLeuAlaAlaSerAsnThrThrAl	51
Db	404	AGTGCCCGACCTGCACAGGTGTGAGAATTTGGAGGAAA-TCGGCCTCCAACAACCGC	462
Qy	51	aSerGlyLysLeuGlu**AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe	71
Db	463	ATCTGGGAATTGGAGCT-GACACCTTCAGCCAGCTGAGTCCCTGCAAGCCCTGGATCT	521
Qy	71	uSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa	91
Db	522	TAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCCTTCTCCACCCCTGCACCTCCCTGGT	581
Qy	91	lLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyGlyLe	111
Db	582	CAAGCTGGACCTGACAGACAACCAAGTGCACACACTGCCCTGGCTGGACTTGGGGGCTT	641
Qy	111	uMetHisLeuLysLeuLysGlyAenLeuAlaLeuSerGlnAlaPheSerLysAspSerPh	131
Db	642	GATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCTTCTCCAAGGACAGTTT	701
Qy	131	eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy	151
Db	702	CCCAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCACTGCTGCCCTATGGGATGTG	761
Qy	151	sAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspAspG1	171
Db	762	TGCCAGCTTCTTCAAGGCCCTCTGGGCAGTGGAGGCTGAAGACCTTCACCTTGATGATGA	821
Qy	171	uGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspG1	191
Db	822	GGAGTCTTCAAAAAGGCCCTTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCA	881
Qy	191	nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy	211
Db	882	GGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCAGTGTCAGTG	941
Qy	211	sSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGlyIleAr	231
Db	942	TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCCTTTTGAAAGCTGGGGCATCCG	1001
Qy	231	gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuth	251
Db	1002	CCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTGCAATGGAGCTGGTGTGCTGAC	1061
Qy	251	rValPheAlaGlyGlyProAlaProLeuProProValLysPheValValGlyAlaIleAl	271
Db	1062	CGTGTTCGCTGGCGGGCCTGCCCCCTGCCCGGTCAAGTTTGTGGTAGGTGCGATTGC	1121
Qy	271	aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuth	291
Db	1122	AGSCGCCAACACCTTGACTGGCATTTTCTGTGGCCCTTCTAGCCCTCAGTCGATGCCCTGAC	1181

Qy	291	rPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaTh	311
Db	1182	CTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGGGCCAC	1241
Qy	311	rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaVa	331
Db	1242	TGGCTTCTTGGCAGTACTTGGGTTCGAGGCATCGGTGCTGCTCACTCTGGCCGCAGT	1301
Qy	331	lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe	351
Db	1302	GCAGTGCAGCGTCTCCGTCCTCTGTGTCCGGGCCCTATGGGAAGTCCCCCTCCCTGGGCAG	1361
Qy	351	rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe	371
Db	1362	CGTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCCGCACTGCCCT	1421
Qy	371	uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluG1	391
Db	1422	GGCCTCAGTGGGAGATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGGG	1481
Qy	391	yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe	411
Db	1482	TCAGCCAGCAGCCCTGGGCTTCAACCTGGCCCTGGTGATGATGAACCTCCTTCTGTTTCT	1541
Qy	411	uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluA1	431
Db	1542	GGTCGTGGCCGTGCCTACATCAAACTGTACTGTGACCTGCCGGGGCGACTTTTGAGGC	1601
Qy	431	aValTrpAspCysAlaMetValArgHisValAlaTrpIlePheAlaAspGlyLeuLe	451
Db	1602	CGTGTGGACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGAGACGGGCTCCT	1661
Qy	451	uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr	471
Db	1662	CTACTGTCCCGTGGCCCTTCTCAGCTTCGCCTCCAATGTGGGCCCTTTCCTGTCAAGCC	1721
Qy	471	oGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe	491
Db	1722	CGAGGCCGTCAAGTCTGTCTGTGTGGTGTGCCCTGCCTGCCTCAACCCCACT	1781
Qy	491	uLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgArgLeuArgProArgAl	511
Db	1782	GCTGTACCTGTCTTCAACCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCCGGC	1841
Qy	511	aGlyAspSerGlyProLeuAlaTyrAlaAlaAlaGlyGluLeuGlyLysSerSerCysAs	531
Db	1842	AGGGACTCAGGGCCCTAGCCTATGCTCGGCCGGGAGCTGGAGAAGAGCTCCTGTGA	1901
Qy	531	pSerThrGlnAlaLeuValAlaPheSerAspValaAspLeuIleLeuGluAlaSerGluA1	551
Db	1902	TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTTCTGGAAGCTTCTGAAGC	1961
Qy	551	aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysG1	571
Db	1962	TGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCTCAGTGACCTCATCTCCTGTCA	2021
Qy	571	nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisPh	591
Db	2022	GCAGCCAGGGGCCCAAGCTCAGGTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTT	2081
Qy	591	eGlyAsnProGlnProSerMetAspGlyGluLeuLeuLeuArgAlaGluGlySerThrPr	611
Db	2082	TGGGAACCCCAACCTCCATGGATGGAGAACTGTGCTGAGGGCAGAGGGATCTACGCC	2141
Qy	611	oAlaGlyGlyLeuSerGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlase	631
Db	2142	AGCAGGTGAGGCTTGTACAGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTGTGCTTC	2201
Qy	631	rHisVal 633	
Db	2202	ACACGTG 2208	

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US-10-664-667-7
; Sequence 7, Application US/10664667
; Publication No. US20040058377A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/10/664,667
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/851,595
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 2711
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2208)
US-10-664-667-7

Alignment Scores:
Pred. No.:      4.12e-308      Length:      2711
Score:          3045.50      Matches:      602
Percent Similarity: 92.61%      Conservative: 12
Best Local Similarity: 90.80%      Mismatches:  19
Query Match:     92.09%      Indels:      32
DB:              17          Gaps:         4

US-10-664-667-5 (1-633) x US-10-664-667-7 (1-2711)

QY      1 AsnThrThrHisTyr----- 5
D      224 AACTCCACACACTATCTGTAATGGTGCATCCAGGAGTTTCCAGATCTCAAAG 283

QY      6 ---ArgGluSerTyrAla----- --CysArgTyrArg 15
D      284 GCACCACCAGCCTGGAGATCCTGACCCCGCAGGCATCCGGCTGCTCCCATCGG 343

QY      16 -----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---G1 31
D      344 GGATGTGCCAACAGCTGCCCAGGCTCCGAGTCTCGAACTGTCTCAAAATCAAAATTGAGG 403

QY      31 YLeuSerLeuProAlaHisProAlaSerLeuAlaLeuAlaLeuAlaSerAenThrThrAl 51
D      404 AGTGCCCGCAGCCTGCACAGGTGTACAGAAATTGGAGGAAA-TCGGCCTCCAAACACACCCGC 462

QY      51 aSerGlyLysLeuGlu**AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe 71
D      463 ATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCTGGATCT 521

QY      71 uSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa 91
D      522 TAGCTGGAACGCCATCCGGTCCATCCACCCTGAGCCTTCTCCACCCTGCACTCCCTGGT 581

QY      91 lLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyGlyLe 111
D      582 CAAGCTGGACCTGACAGACAACAGCTGACCACACTGCCCTGGCTGGACTTGGGGGCTT 641

QY      111 uMethHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh 131
D      642 GATGCATCTGAAGCTCAAAGGGGAACCTTGCTCTCTCCAGGCCTTCTCCAAGGACAGTTT 701

QY      131 eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy 151
D      702 CCCAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCAGTGCTGTCCTATGGGATGTG 761

QY      151 sAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspG1 171
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Db      762 TGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGCTGAAGACCTTTCACCTTGATGATGA 821
QY      171 uGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspG1 191
D      822 GGAGTCTTCAAAAAGGCCCTTGGGCCTCCTTGGCAGACAAGCAGAGAACCACTATGACCA 881

QY      191 nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy 211
D      882 GGACCTGGATGAGTCCAGCTGGAGATGGAGACTCAAAGCCACACCCCACTGTCCAGTG 941

QY      211 sSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGlyIleAr 231
D      942 TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCG 1001

QY      231 gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh 251
D      1002 CCTGGCCGTGTGGGCCATCGTGTTCCTCCGTGCTCTGCAATGGACTGGTGTGTGTGAC 1061

QY      251 rValPheAlaGlyGlyProAlaProLeuProProValLysPheValValGlyAlaIleAl 271
D      1062 CGTGTTCGTGGCGGGCCTTGCCCCCTTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGC 1121

QY      271 aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuTh 291
D      1122 AGGCGCCAACACCTTGACTGGCATTTCTGTGGCCTTCTAGCCTCAGTCGATGCCCTTGAC 1181

QY      291 rPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaTh 311
D      1182 CTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGGGCCAC 1241

QY      311 rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa 331
D      1242 TGGCTTCCCTGGCAGTACTTGGGTCCGAGGATCGGTGCTGCTGCTCAGTCGCGCCAGT 1301

QY      331 lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe 351
D      1302 GCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCCTATGGGAAGTCCCCCTCCCTGGGCAG 1361

QY      351 rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe 371
D      1362 CGTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGGGCTGGCGCGCAGCTGCCCT 1421

QY      371 uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluG1 391
D      1422 GGCCTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGGG 1481

QY      391 yGlnProAlaAlaLeuGlyPheThrValAlaAlaLeuValMetMetAsnSerPheCysPheLe 411
D      1482 TCAGCCAGAGCCCTGGGCTTCACCGTGGCCCTGGTGTATGATGAACCTCTTCTGTTTCT 1541

QY      411 uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluAl 431
D      1542 GGTCTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCCGGGGCGACTTTTGAGGC 1601

QY      431 aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe 451
D      1602 CGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGACAGACGGGCTCCT 1661

QY      451 uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr 471
D      1662 CTACTGTCCGTGGCCTTCTCTCAGCTTCGCCTCCATGTGGGCCTCTTCCCTGTACGCC 1721

QY      471 oGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe 491
D      1722 CGAGGCCGTCAAGTCTGTCTCTGTGGTGTGTCGCCCTGCCTGCCTCAACCCACT 1781

QY      491 uLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgArgLeuArgProArgAl 511
D      1782 GCTGTACTTGTCTTTCAAACCCCCACTTCGGGGATGACCTTCGGCGGGCTTCGGCCCCCGCG 1841

QY      511 aGlyAspSerGlyProLeuAlaTyrAlaAlaAlaGlyGluLeuGlyLysSerSerCysAs 531
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Db 1842 AGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGAGCTGGAGAAGAGCTCCTGTGA 1901

QY 531 pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl 551

Db 1902 TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTGGAAGCTTCTGAAGC 1961

QY 551 aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysG1 571

Db 1962 TGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCTCAGTGACCCCTCATCTCCTGTCA 2021

QY 571 nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisPh 591

Db 2022 GCAGCCAGGGCCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTT 2081

QY 591 eGlyAsnProGlnProSerMetAspGlyGluLeuLeuArgAlaGluGlySerThrPr 611

Db 2082 TGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCTGAGGCAGAGGGATCTAGGCC 2141

QY 611 oAlaGlyGlyGlyLeuSerGlyGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSe 631

Db 2142 AGCAGGTGGAGGCTTGTCAAGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTGGCTTC 2201

QY 631 rHisVal 633

Db 2202 ACACGTG 2208

RESULT 9

US-09-851-595-12

; Sequence 12, Application US/09851595

; Publication No. US20030166047A1

; GENERAL INFORMATION:

; APPLICANT: Gu, Wei

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR

; FILE REFERENCE: MNI-080CP

; CURRENT APPLICATION NUMBER: US/09/851,595

; CURRENT FILING DATE: 2000-05-08

; PRIOR APPLICATION NUMBER: 09/556,588

; PRIOR FILING DATE: 2000-05-08

; PRIOR APPLICATION NUMBER: 60/132,896

; PRIOR FILING DATE: 1999-05-06

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 12

; LENGTH: 2901

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2901)

US-09-851-595-12

Alignment Scores:

Pred. No.:	4.54e-308	Length:	2901
Score:	3045.50	Matches:	602
Percent Similarity:	92.61%	Conservative:	12
Best Local Similarity:	90.80%	Mismatches:	19
Query Match:	92.09%	Indels:	32
DB:	10	Gaps:	4

US-10-664-667-5 (1-633) x US-09-851-595-12 (1-2901)

QY 1 AsnThrThrHisTyr-----5

Db 917 AACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAG 976

QY 6 ---ArgGluSerTrpTyrAla-----CysArgTyrArg 15

Db 977 GCACCACCAGCTGGAGATCCTGACCCTTGACCCCGCGCAGGCATCCGGCTGCTCCCATCGG 1036

QY 16 -----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---G1 31

Db 1037 GGATGTGCCAACAGCTGCCAGGCTCCGAGTCTCGGAACTGTCTCACAATCAAATTGAGG 1096

QY 31 yLeuSerLeuProAlaHisProAlaSerLeuAlaAlaLeuAlaAlaSerAsnThrThrAl 51

Db 1097 ACCTGCCCAGCCTGCACAGGTGTGAGAAATTGGAGGAAA-TCGGCCTCCAACACACCCG 1155

QY 51 aserGlyLysLeuGlu**AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe 71

Db 1156 ATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCT 1214

QY 71 userTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa 91

Db 1215 TAGCTGGAACGCCATCCGCTCCATCCACCCTGAGGCCTTCTCCACCCTGCACCTCCCTGGT 1274

QY 91 lLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyGlyLe 111

Db 1275 CAAGCTGGACCTGACAGACAACCAGCTGACCACACTGCCCTTGGCTGGACTTGGGGGCTT 1334

QY 111 uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh 131

Db 1335 GATGCATCTGAAGCTCAAAGGAAACCTTGCTCTCTCCAGGCCTTCTCCAAGGACAGTTT 1394

QY 131 eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy 151

Db 1395 CCCAAAACCTGAGGATCCTGGAGGTGCCTTATGCCCTACAGTGCTGTCCCTATGGGATGTG 1454

QY 151 sAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspAspGl 171

Db 1455 TGCCAGCTTCTTCAAGGCTCTGGGCAGTGGGAGGCTGAAGACCTTCACCTTGATGATGA 1514

QY 171 uGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspGl 191

Db 1515 GGAGTCTTCAAAAAGGCCCTGGGCCTCCTTGCCGACACAAGCAGAGAACCACTATGACCA 1574

QY 191 nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy 211

Db 1575 GGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCACTGTCCAGTG 1634

QY 211 sSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGlyIleAr 231

Db 1635 TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCG 1694

QY 231 gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh 251

Db 1695 CCTGGCCGTGTGGCCATCGTGTGCTCTCCGTGCTCTGCAATGGACTGGTGTGCTGAC 1754

QY 251 rValPheAlaGlyGlyProAlaProLeuProProValLysPheValValGlyAlaIleAl 271

Db 1755 CGTGTTCGCTGGCGGCCTGCCCCCTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATGC 1814

QY 271 aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuTh 291

Db 1815 AGCGCCCAACACCTTGACTGGCATTTCTCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGAC 1874

QY 291 rPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaTh 311

Db 1875 CTTTGGTCAGTTCTCTGAGTACGGAGCCCCGCTGGAGACGGGGCTAGGCTGCCGGGCCAC 1934

QY 311 rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa 331

Db 1935 TGGCTTCTCTGGCAGTACTTGGGTCGGAGGCATCGTGCTGTGCTCAGTCTGGCGCAGT 1994

QY 331 lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe 351

Db 1995 GCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCTATGGGAAGTCCCCCTCCCTGGGCAG 2054

QY 351 rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe 371

Db 2055 CGTTCGAGCAGGGGTCTTAGGCTGCCCTGGCACTGGCAGGGCTGGCCCGCCGCACTGCCCT 2114

QY 371 uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluGl 391

Db 2115 GGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTTGCCTGCCCTACGGCCCACTGAGGG 2174

QY 391 yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe 411

Db 2175 TCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACCTCTTGTTCCT 2234
QY 411 uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluAl 431
Db 2235 GGTGTCGGCCGTGCCTACATCAAACTGTACTGTGACCTGCCGCGGGCGACTTTGAGGC 2294
QY 431 aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe 451
Db 2295 CGTGTGGACTGCGCCATGCTGAGGCACGTCGGCTGCCCTCATCTTCGCAGACGGGCTCCT 2354
QY 451 uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr 471
Db 2355 CTACTGTCCCGTGGCCTTCCTCAGCTTCGCCCTCCATGCTGGCCTCTTCCCTGTACGCC 2414
QY 471 oGluAlaValLysSerValLeuValValLeuProLeuProAlaCysLeuAsnProLe 491
Db 2415 CGAGGCCGTCAAGTCTGTCTGCTGGTGGTGCTGCCCTGCCTGCCTGCCCTCAACCCACT 2474
QY 491 uLeuTyrLeuLeuPheAsnProHisPheArgAspLeuArgArgLeuArgProArgAl 511
Db 2475 GCTGTACCTGCTCTTCAACCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCCGCG 2534
QY 511 aGlyAspSerGlyProLeuAlaTyrAlaAlaGlyGluLeuGluLysSerSerCysAs 531
Db 2535 AGGGGACTCAGGGCCCTAGCCTATGCTGCGCGCGGAGCTGGAGAAGAGCTCCTGTGA 2594
QY 531 pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl 551
Db 2595 TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGGATCTCATTTCTGGAAGCTTCTGAAGC 2654
QY 551 aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysG1 571
Db 2655 TGGCGGCCCCCTGGCTGGAGACCTATGGCTTCCCCTCAGTGACCCCTCATCTCCTGTCA 2714
QY 571 nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisPh 591
Db 2715 GCAGCCAGGGCCCCCAGGCTGGAGGCGAGCCATTGTGTAGAGCCAGAGGGAAACCACTT 2774
QY 591 eGlyAsnProGlnProSerMetAspGlyGluLeuLeuLeuArgAlaGluGlySerThrPr 611
Db 2775 TGGGAACCCCAACCCTCCATGGATGGAACTGTGCTGAGGGCAGAGGGATCTACGCC 2834
QY 611 oAlaGlyGlyGlyLeuSerGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSe 631
Db 2835 AGCAGGTGAGGCTTGTGAGGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTC 2894
QY 631 rHisVal 633
Db 2895 ACACGTG 2901

RESULT 10
US-10-664-667-12
; Sequence 12, Application US/10664667
; Publication No. US20040058377A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/10/664,667
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/851,595
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 12
; LENGTH: 2901
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2901)
US-10-664-667-12
Alignment Scores: 4.54e-308 Length: 2901
Pred. No.: 3045.50 Matches: 602
Score: 92.61% Conservative: 12
Percent Similarity: 90.80% Mismatches: 19
Best Local Similarity: 92.09% Indels: 32
Query Match: 17 Gaps: 4
DB: 17
US-10-664-667-5 (1-633) x US-10-664-667-12 (1-2901)
QY 1 AsnThrThrHisTyr----- 5
Db 917 AACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAG 976
QY 6 ---ArgGluSerTrpTyrAla-----CysArgTyrArg 15
Db 977 GCACCACAGCCTGGAGATCCTGACCCCTGACCCGCGCAGGCATCCGGCTGCTCCCATCGG 1036
QY 16 -----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---G1 31
Db 1037 GGATGTGCCAACACAGCTGCCAGGCTCCGAGTCCGAGTCTTGGAACTGTCTCACAATCAAATTGAGG 1096
QY 31 YLeuSerLeuProAlaHisProAlaSerLeuAlaAlaLeuAlaAlaSerAsnThrThrAl 51
Db 1097 AGCTGCCCCAGCTGCACAGGTGTCAGAAATGGAGGAAA-TCGSGCCTCCAACACACACCGC 1155
QY 51 aSerGlyLysLeuGlu**AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe 71
Db 1156 ATCTGGGAAATGGAGCT-GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCT 1214
QY 71 uSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa 91
Db 1215 TAGCTGGAAACCCATCCGGTCCATCCACCTGAGGCCTTCTCCACCTGCACTCCCTGGT 1274
QY 91 lLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyLe 111
Db 1275 CAAGCTGGACCTGACAGACAACCACTGACCACTGCCCTGGCTGGCTGGGGGCTT 1334
QY 111 uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh 131
Db 1335 GATGCATCTGAAGCTCAAAGGGAACCTTGTCTCTCCCAGGCCTTCTCCAGGCCTTCTCAAAGGACAGTTT 1394
QY 131 eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy 151
Db 1395 CCCAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCACTGCTGTCCCTATGGGATGTG 1454
QY 151 sAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspG1 171
Db 1455 TGCCAGCTTCTCAAGGCCTCTGGGCACTGGGAGGCTGAAGACCTTCACCTTGATGATGA 1514
QY 171 uGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspG1 191
Db 1515 GGAGTCTTCAAAAAGGCCCTTGGGCCTCTTGCCAGACAAGCAGAGAACCACTATGACCA 1574
QY 191 nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy 211
Db 1575 GGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCAGTGTCCAGTG 1634
QY 211 sSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGlyIleAr 231
Db 1635 TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCG 1694
QY 231 gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh 251
Db 1695 CCTGGCCGTGGGCCCATCGTGTGCTCTCCGTCTCTGCAATGGAGTGGTGTCTGAC 1754
QY 251 rValPheAlaGlyGlyProAlaProLeuProProValLysPheValGlyAlaIleAl 271

Db 1755 CGTGTTTCGCTGGCGGGCCTGCCCCCCTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGC 1814

Qy 271 aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuTh 291

Db 1815 AGCGCCAAACACCTTGACTGGCATTTCTGTGGCCTTTAGCCTCAGTCGATGCCCTGAC 1874

Qy 291 rPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaTh 311

Db 1875 CTTTGGTTCAGTTCTCTAGTACGGAGCCCGCTGGGAGACGGGGCTAGGTCGCCGGCCAC 1934

Qy 311 rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa 331

Db 1935 TGGCTTCCTGGCAGTACTTGGGTCGGAGGCATCGGTGCTGCTCACTCTGGCCGCAGT 1994

Qy 331 lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe 351

Db 1995 GCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGCCCTATGGGAAGTCCCCCTCCCTGGGCAG 2054

Qy 351 rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe 371

Db 2055 CGTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGGGTGGCCCGCACCTGCCCT 2114

Qy 371 uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluGl 391

Db 2115 GGCCTCAGTGGGAGATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGGG 2174

Qy 391 yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe 411

Db 2175 TCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACCTCTTCTGTTTCCT 2234

Qy 411 uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluAl 431

Db 2235 GGTCTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCCGGGCGACTTTGAGGC 2294

Qy 431 aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe 451

Db 2295 CGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGCAGACGGGGTCCT 2354

Qy 451 uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr 471

Db 2355 CTACTGTCCCGTGGCCTTCTCAGCTTCGCCTTCATGTGGGCCCTCTTCCCTGTACGCC 2414

Qy 471 oGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe 491

Db 2415 CGAGGCCGTCAAGTCTGTCTGCTGGTGGTGTGCTGCCCTGCCTGCCTGCCTCAACCCACT 2474

Qy 491 uLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgArgLeuArgProArgAl 511

Db 2475 GCTGTACCTGTCTCTTCAACCCCACTTCGGGATGACTTCGGCGGCTTCGGCCCCCGGC 2534

Qy 511 aGlyAspSerGlyProLeuAlaTyrAlaAlaAlaGlyGluLeuGluLysSerSerCysAs 531

Db 2535 AGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGAGCTGGAGAAGACTCTGTGA 2594

Qy 531 pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl 551

Db 2595 TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTTCTGGAAGCTTCTGAAGC 2654

Qy 551 aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysGl 571

Db 2655 TGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCCTCAGTGACCCCTCATCTCCTGTCA 2714

Qy 571 nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisph 591

Db 2715 GCAGCCAGGGCCCCCAGGTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTT 2774

Qy 591 eGlyAsnProGlnProSerMetAspGlyGluLeuLeuArgAlaGluGlySerThrPr 611

Db 2775 TGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGTGAGGGCAGAGGGATCTACGCC 2834

Qy 611 oAlaGlyGlyGlyLeuSerGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSe 631

Db 2835 AGCAGGTGAGGCTTGTcAGGGGGGTGGCGGCTTTTcAGCCCTCTGGCTTGGCCTTTGCTTC 2894

QY 631 rHisVal 633

Db 2895 ACACGTG 2901

RESULT 11

US-10-225-567A-580

; Sequence 580, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 580

; LENGTH: 3119

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-580

Alignment Scores:

Pred. No.: 5.03e-308 Length: 3119

Score: 3045.50 Matches: 602

Percent Similarity: 92.61% Conservative: 12

Best Local Similarity: 90.80% Mismatches: 19

Query Match: 92.09% Indels: 32

DB: 15 Gaps: 4

US-10-664-667-5 (1-633) x US-10-225-567A-580 (1-3119)

QY 1 AsnThrThrHisTyr----- 5

Db 802 AACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAG 861

QY 6 ---ArgGluSerTrpTyrAla-----CysArgTyrArg 15

Db 862 GCACCACCAGCCTGGAGATCCTGACCCCTGACCCCGCGCAGGCATCCGGCTGCTCCCATCGG 921

QY 16 -----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---Gl 31

Db 922 GGATGTGCCAACAGCTGCCAGGCTCCGAGTCTCGAACTGTCTCACAATCAAAATTGAGG 981

QY 31 yLeuSerLeuProAlaHisProAlaSerLeuAlaLeuAlaAlaSerAsnThrThrAl 51

Db 982 AGCTGCCCCAGCCTGCACAGGTGTcAGAAATTGGAGGAAA-TCGGCCTCCAACACACCGC 1040

QY 51 aSerGlyLysLeuGlu**AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe 71

Db 1041 ATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCT 1099

QY 71 uSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa 91

Db 1100 TAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCTTCTCCACCCTGCACCTCCCTGGT 1159

QY 91 lLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyGlyLe 111

Db 1160 CAAGCTGGACCTGCACAGACAAcCAGCTGACCACACTGCCCTGGCTGGACTTGGGGCTT 1219

QY 111 uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh 131

Db 1220 GATGCATCTGAAGCTCAAAGGGAAcCTTGCTCTCTCCAGGCCCTTCTCCAAGGACAGTTT 1279

QY 131 eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy 151

Db 1280 CCAAACACTGAGGATCCTGGAGGTGCCTTATGCCTACcAGTGTGTCCCTATGGGATGTG 1339

Qy	151	sAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspAspG1	171	Qy	511	aGlyAspSerGlyProLeuAlaTyrAlaAlaAGlyGluLeuGluLysSerSerCysAs	531
Db	1340	TGCCAGCTTCTTCAAGGCTCTGGGCAGTGGGAGGCTGAAGACCTTCACCTTGATGA	1399	Db	2420	AGGGGACTCAGGGCCCTAGCCTATGCTGCGGCGGGGAGCTGGAGAAGAGCTCTGTGA	2479
Qy	171	uGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspG1	191	Qy	531	pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl	551
Db	1400	GGAGTCTTCAAAAAGGCCCTTGGGCCTCCTTGCCAGACAAGCAGAACCACTATGACCA	1459	Db	2480	TTCTACCCAGGCCTGGTAGCCTTCTCTGATGTGGATCTCATTTCTGGAAGCTTCTGAAGC	2539
Qy	191	nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy	211	Qy	551	aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysG1	571
Db	1460	GGACCTGGATGAGCTCAGCTGGAGATGGAGGACTCAAAAGCCACACCCCAAGTGTCCAGTG	1519	Db	2540	TGGGGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTCAGTGACCCCTCATCTCCTGTCA	2599
Qy	211	sSerProThrProGlyPropPheLysProCysGluTyrLeuPheGluSerTrpGlyIleAr	231	Qy	571	nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisPh	591
Db	1520	TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGCATCCG	1579	Db	2600	GCAGCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGAACCACTT	2659
Qy	231	gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh	251	Qy	591	eGlyAsnProGlnProSerMetAspGlyGlyLeuLeuLeuArgAlaGlyGlySerThrPr	611
Db	1580	CCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCGAATGGACTGGTGTGCTGAC	1639	Db	2660	TGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTGTGAGGGCAGAGGATCTACGCC	2719
Qy	251	rValPheAlaGlyGlyProAlaProLeuProProValLysPheValValGlyAlaIleAl	271	Qy	611	oAlaGlyGlyGlyLeuSerGlyGlyGlyGlyGlnProSerGlyLeuAlaPheAlaSe	631
Db	1640	CGTGTTCGTGGCGGGCTGCCCCCTGCCCTGCGTCAAGTTTGTGGTAGGTGCGATTGC	1699	Db	2720	AGCAGGTGGAGCTTGTCAAGGGGTGGCGGCTTTTCAGCCCTCTGGCTTGGCCTTTGCTTC	2779
Qy	271	aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuTh	291	Qy	631	rHisVal	633
Db	1700	AGGCGCCAACACCTTGACTGGCATTTTCCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGAC	1759	Db	2780	ACACGTG	2786
Qy	291	rPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaTh	311	RESULT 12			
Db	1760	CTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGCTAGGCTGCGGGCCAC	1819	US-10-331-496A-52			
Qy	311	RGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa	331	; Sequence 52, Application US/10331496A			
Db	1820	TGGCTTCCTGGCAGTACTTGGTGGAGGCATCGGTGCTGTGCTCACTTGGCCGCAGT	1879	; Publication No. US20030228305A1			
Qy	331	lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe	351	; GENERAL INFORMATION:			
Db	1880	GCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCTATGGGAAGTCCCCCTCCCTGGGCAG	1939	; APPLICANT: FRANTZ,GRETCHEN			
Qy	351	rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe	371	; APPLICANT: HILLAN,KENNETH J.			
Db	1940	CGTTTCGAGCAGGGGTCTTAGGCTGCGTGGCACTGGCAGGGCTGGCCGCGCACTGCCCT	1999	; APPLICANT: PHILLIPS,HEIDI S.			
Qy	371	uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluG1	391	; APPLICANT: POLAKIS,PAUL			
Db	2000	GGCCTCAGTGGGAGAATACGGGGCTCCCCACTTCGCTGCCCTACGCGCACCTGAGGG	2059	; APPLICANT: SMITH,VICTORIA			
Qy	391	YGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe	411	; APPLICANT: SPENCER,SUSAN D.			
Db	2060	TCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACCTCTCTGTTTCCT	2119	; APPLICANT: WILLIAMS,P. MICKEY			
Qy	411	uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluAl	431	; APPLICANT: WU,THOMAS D.			
Db	2120	GGTCGTGGCCGTGGCTACATCAAACTGTACTGTGACCTGCCGGGGGCGCACTTTGAGGC	2179	; APPLICANT: ZHANG,ZEMIN			
Qy	431	aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe	451	; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND			
Db	2180	CGTGTGGACTGCGGCATGGTGGGCACGTGGCTGGCTCATCTTCGCAGACGGGCTCCT	2239	; TITLE OF INVENTION: TREATMENT OF TUMOR			
Qy	451	uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr	471	; FILE REFERENCE: P5014R1-PCT			
Db	2240	CTACTGTCCCGTGGCTTCTCTCAGCTTTGCCTTCCATGCTGGGCCTCTTCCCTGTCAAGCC	2299	; CURRENT APPLICATION NUMBER: US/10/331,496A			
Qy	471	oGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe	491	; CURRENT FILING DATE: 2002-12-30			
Db	2300	CGAGGGCCGTCAAGTCTGCTGCTGGTGTGTCCTGTCCTGTCCTGTCCTCAACCCACT	2359	; PRIOR APPLICATION NUMBER: US 60/345,444			
Qy	491	uLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgArgLeuArgProArgAl	511	; PRIOR FILING DATE: 2002-01-02			
Db	2360	GCTGTACCTGTCTTCAACCCCCACCTTCCGGGATGACCTTCCGGGGCTTCGGCCCCCGCGC	2419	; PRIOR APPLICATION NUMBER: US 60/351,885			
				; PRIOR FILING DATE: 2002-01-25			
				; PRIOR APPLICATION NUMBER: US 60/360,066			
				; PRIOR FILING DATE: 2002-02-25			
				; PRIOR APPLICATION NUMBER: US 60/362,004			
				; PRIOR FILING DATE: 2002-03-05			
				; PRIOR APPLICATION NUMBER: US 60/366,869			
				; PRIOR FILING DATE: 2002-03-20			
				; PRIOR APPLICATION NUMBER: US 60/366,284			
				; PRIOR FILING DATE: 2002-03-21			
				; PRIOR APPLICATION NUMBER: US 60/368,679			
				; PRIOR FILING DATE: 2002-03-28			
				; PRIOR APPLICATION NUMBER: US 60/404,809			
				; PRIOR FILING DATE: 2002-08-19			
				; PRIOR APPLICATION NUMBER: US 60/405,645			
				; PRIOR FILING DATE: 2002-08-21			
				; NUMBER OF SEQ ID NOS: 95			
				; SEQ ID NO 52			
				; LENGTH: 3325			
				; TYPE: DNA			
				; ORGANISM: Homo sapien			
				US-10-331-496A-52			
				Alignment Scores:			

Pred. No.:	5.51e-308	Length:	3325
Score:	3045.50	Matches:	602
Percent Similarity:	92.61%	Conservative:	12
Best Local Similarity:	90.80%	Mismatches:	19
Query Match:	92.09%	Indels:	32
DB:	17	Gaps:	4
US-10-664-667-5 (1-633) x US-10-331-496A-52 (1-3325)			
Qy	1	AanThrThrHisTyr-----	5
Db	845	AACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAG	904
Qy	6	---ArgGluSerTrpTyrAla-----	15
Db	905	GCACCACGAGCTGGAGATCCTGACCCTGACCCGGCAGGCATCCGGCTGCTCCCATCGG	964
Qy	16	-----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---	31
Db	965	GGATGTGCCAACACAGCTGCCAGGCTCCGAGTCTCTGGAACTGTCTCACAAATCAAAATTGAGG	1024
Qy	31	yLeuSerLeuProAlaHisProAlaSerLeuAlaAlaLeuAlaAlaSerAsnThrThrAl	51
Db	1025	AGTGCCCGAGCTGCACAGGTTGCAGAAATTGGAGGAAA-TCGGCCCTCCAACAACACCGC	1083
Qy	51	aSerGlyLysLeuGlu**AapThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe	71
Db	1084	ATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAGTCCCTGCAAGCCCTGGAATCT	1142
Qy	71	uSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa	91
Db	1143	TAGCTGGAAAGCCCATCCGGTCCATCCACCCCTGAGGCCCTTCTCCACCCCTGCACCTCCCTGGT	1202
Qy	91	lLysLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyLe	111
Db	1203	CAAGCTGGACCTGACAGACAACACAGCTGACCACACTGCCCTGGCTGGACTTGGGGGCTT	1262
Qy	111	uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh	131
Db	1263	GATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCCTTCTCCAAGGACAGTTT	1322
Qy	131	eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy	151
Db	1323	CCCAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCAGTGTGTCCTATGGGATGTG	1382
Qy	151	sAlaSerPheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspAspG1	171
Db	1383	TGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGAGGCTGAAGACCTTCACCTTGATGATGA	1442
Qy	171	uGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspG1	191
Db	1443	GGAGTCTTCAAAAAGGCCCTCGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCA	1502
Qy	191	nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy	211
Db	1503	GGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAAGTGTCCAGTG	1562
Qy	211	sSerProThrProGlyProPheLysProCysGluTyrIleuPheGluSerTipGlyIleAr	231
Db	1563	TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCG	1622
Qy	231	qLeuAlaValTrpAlaIleValIleuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh	251
Db	1623	CCTGGCCGTGTGGGCCATCGTGTGTCTCTCCGTGCTCTGCAATGGACTGGTGTGTGTGAC	1682
Qy	251	rValPheAlaGlyGlyProAlaProLeuProProValLysPheValValGlyAlaIleAl	271
Db	1683	CGTGTTCGTGGCGGCCCTGCCCCCTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGC	1742
Qy	271	aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuTh	291
Db	1743	AGGCCCAACACCTTGACTGSGCATTTCTGTGGCCCTTCTAGCCTCAGTCGATGCCCTGAC	1802

Qy	291	rPheGlyGlnPheSerGluTyrGlyAlaAArgTrpGluThrGlyLeuGlyCysArgAlaTh	311
Db	1803	CTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGAGACGGGGCTAGGCTGCCGGGCCAC	1862
Qy	311	rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa	331
Db	1863	TGGCTTCTGGCAGTACTTGGGTGGAGGCATCGGTGCTGTCTCACTCTGGCCGAGT	1922
Qy	331	lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe	351
Db	1923	GCAGTGCAGCGTCTCCGTCTCTGTGTCCGGGCTATGGAAAGTCCCCCTCCCTGGGCAG	1982
Qy	351	rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe	371
Db	1983	CGTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCCCACTGCCCT	2042
Qy	371	uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluG1	391
Db	2043	GGCCTCAGTGGAGAAATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGG	2102
Qy	391	yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe	411
Db	2103	TCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGAACCTCCTTCTGTTCCT	2162
Qy	411	uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluAl	431
Db	2163	GGTCGTGGCCGCTGCCTACATCAAACTGTACTGTACCTGCCGTGCCGGGGGACTTTGAGG	2222
Qy	431	aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeule	451
Db	2223	CGTGTGGACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGACAGACGGGCTCCT	2282
Qy	451	uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr	471
Db	2283	CTACTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCATGCTGGGCTCTTTCCTGTACGCC	2342
Qy	471	oGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe	491
Db	2343	CGAGGCCGTCAAGTCTGTCTGTGGTGGTGTGCTGCCCTGCCTGCCTCAACCCACT	2402
Qy	491	uLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgArgLeuArgProArgAl	511
Db	2403	GCTGTACCTGCTCTTCAACCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCGCGC	2462
Qy	511	aGlyAspSerGlyProLeuAlaTyrAlaAlaAlaGlyGluLeuGlyLysSerSerCysAs	531
Db	2463	AGGGGACTCAGGGCCCTAGCCTATGCTGCGCGCGGGAGCTGGAGAAGAGCTCCTGTGA	2522
Qy	531	pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl	551
Db	2523	TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTTCTGGAAGCTTCTGAAG	2582
Qy	551	aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysG1	571
Db	2583	TGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTCAGTGACCCCTCATCTCTGTCA	2642
Qy	571	nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisPh	591
Db	2643	GCAGCCAGGGGCCCCCAAGGCTGGAGGGCAGCCATGTGTAGAGCCAGAGGGGAACCACTT	2702
Qy	591	eGlyAsnProGlnProSerMetAspGlyGluLeuLeuLeuArgAlaGluGlySerThrPr	611
Db	2703	TGGGAACCCCAACCTCCATGGATGGAGAACTGTGTGAGGGCAGAGGGATCTACGCC	2762
Qy	611	oAlaGlyGlyLeuSerGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlase	631
Db	2763	AGCAGGTGGAGGCTTGTACAGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTCCTC	2822
Qy	631	rHisVal	633
Db	2823	ACACGTG	2829


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QY      311 rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa 331
      |||
Db      1987 TGGTTCCTGGCAGTACTTGGGTGGAGGCATCGGTGCTGCTCACTCTGGCCGCAGT 2046

QY      331 lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe 351
      |||
Db      2047 GCAGTGCAGCGTCTCCGTCTCTGTGTCCGGGCCTATGGGAAGTCCCCCTCCCTGGGCAG 2106

QY      351 rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe 371
      |||
Db      2107 CGTTCGAGCAGGGTCTTAGGCTGCCTGGCACGTGGCAGGGCTGGCCGCCGCACTGCCCT 2166

QY      371 uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluGl 391
      |||
Db      2167 GGCCTCAGTGGAGAAATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACTGAGGG 2226

QY      391 yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe 411
      |||
Db      2227 TCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACCTCTTCTGTTCCT 2286

QY      411 uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluAl 431
      |||
Db      2287 GGTGCTGGCCGTGCCTACATCAAACTGTACTGTGACCTGCCGCGGGCGACTTTGAGGC 2346

QY      431 aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe 451
      |||
Db      2347 CGTGTGGACTGCGCCATGTGTGAGGCACGTGGCCTGGCTGCATCTTCGCAGACGGGCTCCT 2406

QY      451 uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr 471
      |||
Db      2407 CTACTGTCCCGTGGCCTTCCTCAGCTTCGCCCTCCATGTGGCCTCTTCCCTGTACGCC 2466

QY      471 oGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe 491
      |||
Db      2467 CGAGGCCGTCAAGTCTGTCTGTGTGGTGTGCTGCCCTGCCTGCCTGCCTCAACCCACT 2526

QY      491 uLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgLeuArgProArgAl 511
      |||
Db      2527 GCTGTACCTGTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCCGCGC 2586

QY      511 aGlyAspSerGlyProLeuAlaTyrAlaAlaAlaGlyGluLeuGluLysSerSerCysAs 531
      |||
Db      2587 AGGGGACTCAGGGCCCTTAGCCTATGCTGCGCGCGGAGCTGGAGAAGAGCTCTGTGA 2646

QY      531 pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl 551
      |||
Db      2647 TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTTGGAAGCTTCTGAAGC 2706

QY      551 aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysGl 571
      |||
Db      2707 TGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCTCAGTGACCCCTCATCTCCTGTCA 2766

QY      571 nGlnProGlyAlaProArgLeuGluGlySerHisCysValGluProGluGlyAsnHisPh 591
      |||
Db      2767 GCAGCCAGGGGCCCCAGGCTGGAGGGCAGCCATTTGTGTAGAGCCAGAGGGGAACCACTT 2826

QY      591 eGlyAsnProGlnProSerMetAspGlyGluLeuLeuLeuArgAlaGluGlySerThrPr 611
      |||
Db      2827 TGGGAACCCCCAACCCCTCCATGGATGGAGAACTGTGCTGAGGGCAGAGGGATCTACGCC 2886

QY      611 oAlaGlyGlyLeuSerGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlase 631
      |||
Db      2887 AGCAGGTGAGGCTTTGTACGGGGGTGGCGGCTTTTCAGCCCTCTGGCTTGGCCTTTGCTTC 2946

QY      631 rHisVal 633
      |||
Db      2947 ACACGTG 2953

RESULT 15
US-10-331-496A-94
; Sequence 94, Application US/10331496A
; Publication No. US20030228305A1
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; GENERAL INFORMATION:
; APPLICANT: FRANTZ,GRETCHEN
; APPLICANT: HILLAN,KENNETH J.
; APPLICANT: PHILLIPS,HEIDI S.
; APPLICANT: POLAKIS,PAUL
; APPLICANT: SMITH,VICTORIA
; APPLICANT: SPENCER,SUSAN D.
; APPLICANT: WILLIAMS,P. MICKEY
; APPLICANT: WU,THOMAS D.
; APPLICANT: ZHANG,ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 94
; LENGTH: 3443
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-331-496A-94

Alignment Scores:
Pred. No.:      5.79e-308      Length:      3443
Score:          3045.50      Matches:      602
Percent Similarity: 92.61%      Conservative: 12
Best Local Similarity: 90.80%      Mismatches:  19
Query Match:      92.09%      Indels:       32
DB:              17          Gaps:         4

US-10-664-667-5 (1-633) x US-10-331-496A-94 (1-3443)

QY      1 AsnThrThrHisTyr-----
      |||:::|||||||
Db      971 AACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAG 1030

QY      6 ---ArgGluSerTrpTyrAla-----
      ::|||:::
Db      1031 GCACCACCAGCTGGAGATCCTGACCCCTGACCCCGCAGGCATCCGGCTGCTCCCATCGG 1090

QY      16 -----SerGlyIleProGlySer-ThrHisAlaSerValGluArgSerGln---G1 31
      ::|||:::
Db      1091 GGATGTGCCAACAGCTGCCAGGCTCCGAGTCTCGAACTGTCTCACAATCAAATTGAGG 1150

QY      31 yLeuSerLeuProAlaHisProAlaSerLeuAlaAlaLeuAlaAlaSerAsnThrThrAl 51
      ::|||:::
Db      1151 AGCTGCCCAGCCTGCACAGGTGTAGAAATTGGAGGAAA-TCGGCCTCCCAACACACCGC 1209

QY      51 aSerGlyLysLeuGlu***AspThrPheSerGlnLeuSerSerLeuGlnAlaLeuAspLe 71
      |||
Db      1210 ATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCT 1268

QY      71 uSerTrpAsnAlaIleArgSerIleHisProGluAlaPheSerThrLeuHisSerLeuVa 91
      |||
Db      1269 TAGCTGGAAAGCCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCACCTCCCTGGT 1328
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QY 91 llyLeuAspLeuThrAspAsnGlnLeuThrThrLeuProLeuAlaGlyLeuGlyGlyLe 111
Db 1329 CAAGCTGGACCTGACAGACAACAGACTGACCACACTGCCCTGGCTGGACTTGGGGGCTT 1388
QY 111 uMetHisLeuLysLeuLysGlyAsnLeuAlaLeuSerGlnAlaPheSerLysAspSerPh 131
Db 1389 GATGCATCTGAAGCTCAAAGGSAACCTTGCTCTCTCCAGGCCTTCTCCAAGGACAGTTT 1448
QY 131 eProLysLeuArgIleLeuGluValProTyrAlaTyrGlnCysCysProTyrGlyMetCy 151
Db 1449 CCCAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCACTGCTGTCCCTATGGGATGTG 1508
QY 151 sAlaSerPhePheLysAlaSerGlyGlnTrpGluAlaGluAspLeuHisLeuAspAspG1 171
Db 1509 TGCAGCTTCTTCAAGGCCCTTGGGCAGTGGAGGCTGAAGACCTTCACCTTGATGATGA 1568
QY 171 uGluSerSerLysArgProLeuGlyLeuLeuAlaArgGlnAlaGluAsnHisTyrAspG1 191
Db 1569 GGAGTCTTCAAAAAGGCCCTTGGGCCTCCTTGCCAGACAAGCAGAGAACCACCTATGACCA 1628
QY 191 nAspLeuAspGluLeuGlnLeuGluMetGluAspSerLysProHisProSerValGlnCy 211
Db 1629 GGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCACAGTGTCCAGTG 1688
QY 211 sSerProThrProGlyProPheLysProCysGluTyrLeuPheGluSerTrpGlyIleAr 231
Db 1689 TAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCG 1748
QY 231 gLeuAlaValTrpAlaIleValLeuLeuSerValLeuCysAsnGlyLeuValLeuLeuTh 251
Db 1749 CTTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTGCAATGGACTGGTGTCTGTGAC 1808
QY 251 rValPheAlaGlyGlyProAlaProLeuProProValLysPheValValGlyAlaIleAl 271
Db 1809 CGTGTTCGCTGGCGGGCCTTGCCCCCTGCCCCCGGTCAAGTTTGTGGTAGTGCGATTGC 1868
QY 271 aGlyAlaAsnThrLeuThrGlyIleSerCysGlyLeuLeuAlaSerValAspAlaLeuTh 291
Db 1869 AGCGCCAACACCTTGACTGGCATTTCTGTGGCCCTTAGCCCTCAGTCGATGCCCTGAC 1928
QY 291 rPheGlyGlnPheSerGluTyrGlyAlaArgTrpGluThrGlyLeuGlyCysArgAlaTh 311
Db 1929 CTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGGGCCAC 1988
QY 311 rGlyPheLeuAlaValLeuGlySerGluAlaSerValLeuLeuLeuThrLeuAlaAlaVa 331
Db 1989 TGGCTTCTTGGCAGTACTTGGGTGGAGGCATCGGTGCTGTGCTGCTCACTCTGGCCGCAGT 2048
QY 331 lGlnCysSerValSerValSerCysValArgAlaTyrGlyLysSerProSerLeuGlySe 351
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QY 351 rValArgAlaGlyValLeuGlyCysLeuAlaLeuAlaGlyLeuAlaAlaLeuProLe 371
Db 2109 CGTTCGAGCAGGGGTCCCTAGGCTGCCTGGCAGCTGGCAGGCTGGCCGCCGCACTGCCCT 2168
QY 371 uAlaSerValGlyGluTyrGlyAlaSerProLeuCysLeuProTyrAlaProProGluG1 391
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QY 391 yGlnProAlaAlaLeuGlyPheThrValAlaLeuValMetMetAsnSerPheCysPheLe 411
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QY 411 uValValAlaGlyAlaTyrIleLysLeuTyrCysAspLeuProArgGlyAspPheGluAl 431
Db 2289 GGTGTGGCCGGTGCCTACATCAAAACTGTACTGTGACCTGCGCGGGCGACTTTTGAGGC 2348
QY 431 aValTrpAspCysAlaMetValArgHisValAlaTrpLeuIlePheAlaAspGlyLeuLe 451
Db 2349 CGTGTGGGACTGCGCCATGGTGGGACACGTGGCCCTGGCTCATCTTCGCAGACGGGCTCCT 2408

QY 451 uTyrCysProValAlaPheLeuSerPheAlaSerMetLeuGlyLeuPheProValThrPr 471
Db 2409 CTACTGTCCCGTGGCCTTCCTCAGCTTCGCCCTCCATGCTGGGCCTCTTCCCTGTACGCC 2468
QY 471 oGluAlaValLysSerValLeuLeuValValLeuProLeuProAlaCysLeuAsnProLe 491
Db 2469 CGAGGCCGTCAAGTCTGTCTGCTGGTGGTGTGCCCTGCCTGCCTCAACCCACT 2528
QY 491 uLeuTyrLeuLeuPheAsnProHisPheArgAspAspLeuArgLeuArgProArgAl 511
Db 2529 GCTGTACCTGCTCTTCAACCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCGCGGC 2588
QY 511 aGlyAspSerGlyProLeuAlaTyrAlaAlaGlyGluLeuGluLysSerSerCysAs 531
Db 2589 AGGGGACTCAGGGCCCTAGCCTATGCTGCGGCCGGGAGCTGGAGAAGAGCTCCTGTGA 2648
QY 531 pSerThrGlnAlaLeuValAlaPheSerAspValAspLeuIleLeuGluAlaSerGluAl 551
Db 2649 TTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTTCTGGAAGCTTCTGAAGC 2708
QY 551 aGlyArgProProGlyLeuGluThrTyrGlyPheProSerValThrLeuIleSerCysG1 571
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Db 2769 GCAGCCAGGGGCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGATCTACGCC 2828
QY 591 eGlyAsnProGlnProSerMetAspGlyGluLeuLeuLeuArgAlaGluGlySerThrPr 611
Db 2829 TGGGAACCCCAACCTCCATGGATGGAGAACTGCTGTGAGGGCAGAGGGATCTACGCC 2888
QY 611 oAlaGlyGlyGlyLeuSerGlyGlyGlyPheGlnProSerGlyLeuAlaPheAlaSe 631
Db 2889 AGCAGGTGGAGGCTTGTCAAGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTC 2948
QY 631 rHisVal 633
Db 2949 ACACGTG 2955

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Job time : 694 secs

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 11:59:23 ; Search time 219.132 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1752.8	92.3	2988	4	US-09-799-451-723 Sequence 723, App
2	439.4	23.1	453	3	US-09-397-787-240 Sequence 240, App
3	355.6	18.7	2724	4	US-09-170-496D-263 Sequence 263, App
4	355.6	18.7	4570	4	US-09-976-594-201 Sequence 201, App
5	352.4	18.6	2724	4	US-09-170-496D-277 Sequence 277, App
6	194	10.2	2612	4	US-09-495-050A-214 Sequence 214, App
7	194	10.2	4203	2	US-08-866-757-1 Sequence 1, Appli
8	194	10.2	4203	3	US-09-153-593-1 Sequence 1, Appli
9	181.8	9.6	723	4	US-09-495-050A-220 Sequence 220, App
10	105	5.5	2703	4	US-09-482-273-75 Sequence 75, Appl
11	101.8	5.4	473	2	US-08-866-757-3 Sequence 3, Appli
12	101.8	5.4	473	3	US-09-153-593-3 Sequence 3, Appli
13	94.6	5.0	2709	4	US-09-482-273-101 Sequence 101, App
14	79.8	4.2	1898	4	US-09-589-510-7 Sequence 7, Appli
15	78.8	4.1	570	2	US-08-633-682-1 Sequence 1, Appli
16	78.8	4.1	570	3	US-08-936-772-1 Sequence 1, Appli
17	78.8	4.1	570	3	US-09-395-918-1 Sequence 1, Appli
18	78.4	4.1	1330	3	US-09-118-442-29, Sequence 29, Appl
19	78.4	4.1	1330	3	US-09-677-064-29, Sequence 29, Appl
20	77.8	4.1	1581	1	US-08-383-756-1 Sequence 1, Appli
21	77.8	4.1	1581	2	US-08-460-898-1 Sequence 1, Appli
22	77.6	4.1	1665	4	US-09-591-095-23 Sequence 23, Appl
23	77.4	4.1	1390	4	US-09-205-258-124 Sequence 124, App
24	77.4	4.1	4847	4	US-10-164-595-57 Sequence 57, Appl
25	77	4.1	223	4	US-09-016-434-597 Sequence 597, App
26	76	4.0	1297	4	US-09-800-729-80 Sequence 80, Appl
27	76	4.0	1790	4	US-09-118-637A-3 Sequence 3, Appli

28	75	3.9	3244	3	US-09-165-543-4	Sequence 4, Appli
29	73.8	3.9	1236	4	US-09-620-312D-1077	Sequence 1077, Ap
c 30	73.4	3.9	1236	4	US-09-620-312D-1077	Sequence 1077, Ap
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32	69.2	3.6	2019	3	US-09-063-950-3	Sequence 3, Appli
33	69.2	3.6	2852	3	US-09-063-950-1	Sequence 1, Appli
34	68	3.6	2765	4	US-09-620-312D-61	Sequence 61, Appl
35	66.8	3.5	2413	4	US-09-016-434-1469	Sequence 1469, Ap
36	66.8	3.5	3549	4	US-09-826-509-586	Sequence 586, App
37	65.8	3.5	1292	4	US-09-904-615-61	Sequence 61, Appl
38	65.6	3.5	538	1	US-08-890-572-1	Sequence 1, Appli
39	65.2	3.4	1597	3	US-09-038-832-3	Sequence 3, Appli
40	65.2	3.4	2292	4	US-09-826-509-394	Sequence 394, App
41	65.2	3.4	2292	4	US-09-826-509-418	Sequence 418, App
42	65.2	3.4	2292	4	US-09-826-509-422	Sequence 422, App
43	65	3.4	969	2	US-08-700-637-1	Sequence 1, Appli
44	64.8	3.4	831	4	US-09-904-615-25	Sequence 25, Appl
45	63.8	3.4	1262	4	US-09-489-847-69	Sequence 69, Appl

ALIGNMENTS

RESULT 1
US-09-799-451-723
; Sequence 723, Application US/09799451
; Patent No. 6783969

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yunging
APPLICANT: Yamazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids and
FILE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 723
LENGTH: 2988
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2484)
US-09-799-451-723

Query Match 92.3%; Score 1752.8; DB 4; Length 2988;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY	132	ACGGGCTCCAAACACACCGCATCTGGGAAATTCGAGCTNGACACCTTCAGCCAGCTGAG	191
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QY	192	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCTT	251
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QY	252	CTCCACCCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTGACCACACTGCC	311	QY	1332	CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCATGCT	1391
Db	837	CTCCACCCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTGACCACACTGCC	896	Db	1917	CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCATGCT	1976
QY	312	CCTGGCTGGACTTGGGGCTTGATGCACTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA	371	QY	1392	GGGCTCTTCCCTGTACGCCCGGAGGCCGTCAAGTCTGTCTGCTGGTGGTGTGCCCT	1451
Db	897	CCTGGCTGGACTTGGGGCTTGATGCACTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA	956	Db	1977	GGGCTCTTCCCTGTACGCCCGGAGGCCGTCAAGTCTGTCTGCTGGTGGTGTGCCCT	2036
QY	372	GGCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCA	431	QY	1452	GCCTGCCTGCCTCAACCCACTGCTGTACCTGCTTTCAACCCCCACTTCGGGATGACCT	1511
Db	957	GGCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCA	1016	Db	2037	GCCTGCCTGCCTCAACCCACTGCTGTACCTGCTTTCAACCCCCACTTCGGGATGACCT	2096
QY	432	GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGCTGA	491	QY	1512	TCGGCGGCTTCGGCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGA	1571
Db	1017	GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGCTGA	1076	Db	2097	TCGGCGGCTTCGGCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGA	2156
QY	492	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCTCCTTGCCAGACA	551	QY	1572	GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTTGGTAGCCTTCTCTGATGTGGATCT	1631
Db	1077	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCTCCTTGCCAGACA	1136	Db	2157	GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTTGGTAGCCTTCTCTGATGTGGATCT	2216
QY	552	AGCAGAGAACCACTATGACAGGACCTGGATGAGCTCCAGTCCAGCTGGAGATGGAGACTCAAA	611	QY	1632	CATTCTGGAAGCTTCTGAAGCTGGCGGCCCTTGGCTGGAGACCTATGGCTTCCCCTC	1691
Db	1137	AGCAGAGAACCACTATGACAGGACCTGGATGAGCTCCAGTGGAGATGGAGACTCAAA	1196	Db	2217	CATTCTGGAAGCTTCTGAAGCTGGCGGCCCTTGGCTGGAGACCTATGGCTTCCCCTC	2276
QY	612	GCCACACCCAGTGTCCAGGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	671	QY	1692	AGTGACCTCATCTCTGTTCAGCAGCCAGGGCCCCCAGGCTGGAGGGCAGCCATTGTGT	1751
Db	1197	GCCACACCCAGTGTCCAGGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	1256	Db	2277	AGTGACCTCATCTCTGTTCAGCAGCCAGGGCCCCCAGGCTGGAGGGCAGCCATTGTGT	2336
QY	672	CTTTGAAAGCTGGGGCATCCGCTTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG	731	QY	1752	AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTCCATGGATGGAGAACTGCTGCT	1811
Db	1257	CTTTGAAAGCTGGGGCATCCGCTTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG	1316	Db	2337	AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTCCATGGATGGAGAACTGCTGCT	2396
QY	732	CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGGCTGCCCTTCAAGCCCGGTCAA	791	QY	1812	GAGGCAGAGGGATCTACCCAGCAGGTGAGGCTTGTTCAGGGGTGGCGCTTTCAGCC	1871
Db	1317	CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGGCTGTCCCCCTGCCCGGTCAA	1376	Db	2397	GAGGCAGAGGGATCTACCCAGCAGGTGAGGCTTGTTCAGGGGTGGCGCTTTCAGCC	2456
QY	792	GTTTGTGGTAGGTGCGATTGACGGCGCCAAACACTTGACTGGCATTTCTGTGGCTTCT	851	QY	1872	CTCTGGCTTGSCCTTTGCTTCACACGTG	1899
Db	1377	GTTTGTGGTAGGTGCGATTGACGGCGCCAAACACTTGACTGGCATTTCTGTGGCTTCT	1436	Db	2457	CTCTGGCTTGSCCTTTGCTTCACACGTG	2484
QY	852	AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	911	RESULT 2			
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QY	912	GGGGCTAGGCTGCCGGCCACTGGCTTCCTGGCAGTACTGGGTGGAGGCATCGGTGCT	971	; Sequence 240, Application US/09397787			
Db	1497	GGGGCTAGGCTGCCGGCCACTGGCTTCCTGGCAGTACTGGGTGGAGGCATCGGTGCT	1556	; Patent No. 6468758			
QY	972	GCTGCTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGCCCTATGG	1031	; GENERAL INFORMATION:			
Db	1557	GCTGCTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGCCCTATGG	1616	; APPLICANT: Benson, Darin R.			
QY	1032	GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTAGGCTGCCTGGCACTGGCAGG	1091	; APPLICANT: Lodes, Michael J.			
Db	1617	GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTAGGCTGCCTGGCACTGGCAGG	1676	; APPLICANT: Mitcham, Jennifer L.			
QY	1092	GCTGGCCGCCGCACTGCCCTGGCCTCAGTGGGAGAATACGGGGCTTCCCACTCTGCCT	1151	; APPLICANT: King, Gordon E.			
Db	1677	GCTGGCCGCCGCACTGCCCTGGCCTCAGTGGGAGAATACGGGGCTTCCCACTCTGCCT	1736	; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN			
QY	1152	GCCCTACGCGCCACCTGAGGGTTCAGCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGAT	1211	; TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS			
Db	1737	GCCCTACGCGCCACCTGAGGGTTCAGCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGAT	1796	; FILE REFERENCE: 210121.466C2			
QY	1212	GATGAACCTCCTTCTGTTCCCTGGTCGTGGCCGCTGCCTACATCAAACTGTACTGTGACCT	1271	; CURRENT APPLICATION NUMBER: US/09/397,787			
Db	1797	GATGAACCTCCTTCTGTTCCCTGGTCGTGGCCGCTGCCTACATCAAACTGTACTGTGACCT	1856	; CURRENT FILING DATE: 1999-09-16			
QY	1272	GCCGCGGGGCGACTTTGAGGCCCGTGTGGGACTGCGCCCATGGTGAGGCACGTGGCCCTGGCT	1331	; NUMBER OF SEQ ID NOS: 334			
Db	1857	GCCGCGGGGCGACTTTGAGGCCCGTGTGGGACTGCGCCCATGGTGAGGCACGTGGCCCTGGCT	1916	; SOFTWARE: FastSeq for Windows Version 3.0			
				; SEQ ID NO 240			
				; LENGTH: 453			
				; TYPE: DNA			
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				Query Match 23.1%; Score 439.4; DB 3; Length 453;			
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				Matches 451; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			
QY	1328	GGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCA	1387	QY	1328	GGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCA	1387
Db	1	GGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCA	60	Db	1	GGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCA	60
QY	1388	TGCTGGGCTCTTCCCTGTTCAGCCCGAGGCCGTCAAGTCTGTCTCTGCTGGTGGTGTGC	1447	QY	1388	TGCTGGGCTCTTCCCTGTTCAGCCCGAGGCCGTCAAGTCTGTCTCTGCTGGTGGTGTGC	1447

Db	61	TGCTGGGCCTCTTCCCTGTACGCCCGAGGCCGTCAAGTCTGTCTCTGCTGGTGGTGTGCTGC	120
QY	1448	CCCTGCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCACTTCCGGGATG	1507
Db	121	CCCTGCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCACTTCCGGGATG	180
QY	1508	ACCTTCGGCGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGCTGCGGCCG	1567
Db	181	ACCTTCGGCGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGCTGCGGCCG	240
QY	1568	GGGAGCTGGAGAAGAGCTCCTGTGATTTACCCAGGCCCTGGTAGCCTTCTCTGTATGTG	1627
Db	241	GGGAGCTGGAGAAGAGCTCCCGTGATTTACCCAGGCCCTGGTAGCCTTCTCTGTATGTG	300
QY	1628	ATCTCATTTCTGGAAGCTTCTGAAGCTGGCGCGCCCTGGGCTGGAGACCTATGGCTTCC	1687
Db	301	ATCTCATTTCTGGAAGCTTCTGAAGCTGGCGCGCCCTGGGCTGGAGACCTATGGCTTCC	360
QY	1688	CCTCAGTGACCTCATCTCTCTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGC-AGCCAT	1746
Db	361	CCTCAGTGACCTCATCTCTCTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGCAAGCCAT	420
QY	1747	TGTGTAGAGCCAGAGGGGAACCACTTTGGGAAC	1779
Db	421	TGTGTAGAGCCAGAGGGGAACCACTTTGGGAAC	453
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; Sequence 263, Application US/09170496D			
; Patent No. 6555339			
; GENERAL INFORMATION:			
; APPLICANT: Behan, Dominic P.			
; APPLICANT: Chalmers, Derek T.			
; APPLICANT: Liaw, Chen W.			
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-			
; TITLE OF INVENTION: Receptors			
; FILE REFERENCE: AREN-0040			
; CURRENT APPLICATION NUMBER: US/09/170,496D			
; CURRENT FILING DATE: 1998-10-13			
; NUMBER OF SEQ ID NOS: 294			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 263			
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; TYPE: DNA			
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Best Local Similarity 56.2%; Pred. No. 2.1e-72;			
Matches 781; Conservative 0; Mismatches 580; Indels 28; Gaps 5;			
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QY	195	CCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTC	254
Db	1197	CCTCCGATCGTGAATTTGGCTTGGAAACAAAATTGCTATTATCACCCCAATGCATTTTC	1256
QY	255	CACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAAACAGCTGACACACTGCCCT	314
Db	1257	CACCTTGCCATCCCTTAATAAAGCTGGACCTATCGTCCAACTCTGTGCTCTTTCTAT	1316
QY	315	GGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGC	374
Db	1317	AACCTGGTTACATGGTTTAACTCACTTAAATTAAACAGGNAATCATGCCTTACAGAGCTT	1376
QY	375	CTTCTCCAAGGACAGTTTCCAAAACTGAGGATCCTGGAGGTGCCCTTATGCCCTACAGTG	434
Db	1377	GATATCATCTGAANAACCTTCCAGAACTCAAGGTTATAGAAATGCCTTATGCTTACCAGTG	1436
QY	435	CTGTCCCTATGGGATGTGTGCCAGCTTCTTCNAGGCCTCTGCGGAGCTGGGAGGCTGAAGA	494

Db	1437	CTGTGCATTTGGAGTGTGTGAGAAATGCCTATAAGATTTCTAATCAATGGAATAAAGGTGA	1496
QY	495	CCTTCACCTTGATGATGAGGAGTCTTTCAAAAAGGCCCTTGGCCTCCTTGGCAGACAAGC	554
Db	1497	CAACAGCAGTATGGACGACCTTCATAAGAAA-----GATGCTGGAATGTT	1541
QY	555	AGAGAACCACTATGACCAAGGACCTGGATGAGCTCCAGCTGGAGAT--GGAGGACTCAAA	611
Db	1542	TCAGGCTCAAGATGAACGTGACCTTGAAGATTTCTGCTTGACTTTGAGGAAGACCTGAA	1601
QY	612	GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	671
Db	1602	AGCCCTTCATTTCAGTGCAGTGTTCACCTTCCCAGGCCCTTCAAAACCTGTGAACACCT	1661
QY	672	CTTTGAAAGCTGGGCATCCGCCCTGGCCGTGTGGCCCATCGTTGCTCTCCGTGCTCTG	731
Db	1662	GCTTGATGGCTGGCTGATCAGAAATGGAGTGTGACCATAGCAGTTCTGGCACTTACTTG	1721
QY	732	CAATGGACTGGTGTGCTGACCGTGTTCGCTGGGGCCCTGCCCCCTGCCCCCGGTCAA	791
Db	1722	TAATGCTTTGGTGACTTCAACAGTTTTTCAGATCC--CCTCTGTACATTTCCCCCATTA	1778
QY	792	GTTTGTGGTAGTGCATTCAGGCGCCAAACACCTTGACTTGGCATTTCCTGTGGCCTTCT	851
Db	1779	ACTGTTAATTGGGGTCATCGCAGCAGTGAACATGTCCAGGGAGTCTCCAGTGCCGTGCT	1838
QY	852	AGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCCCGCTGGGAG	911
Db	1839	GGCTGGTGTGGATGCGTTCACTTTTGGCAGCTTTGCACGACATGGTGCTTGGGAGAA	1898
QY	912	GGGGCTAGGCTGCCGGCCACTGGCTTCTCTGGAGTACTTGGGTCGGAGGATCGGTGCT	971
Db	1899	TGGGGTTGGTTGCCATGTCAATGGTTTTTTTGTCAATTTTGTTCAGAAATCATCTGTTT	1958
QY	972	GCTGCTCACTCTGGCGCAGTGCAGTGCAGCGTCCGCTCTCTGTGTCCGGGCTATGG	1031
Db	1959	CCTGCTTACTCTGGCAGCCCTGGAGCGTGGGTTCTCTGTGAAATATTCTGCAAAATTGA	2018
QY	1032	GAAGTCCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCTTAGGTCCTGGCACTGGCAGG	1091
Db	2019	AACGAAAGCTCCATTTTCTAGCCTGAAAGTAATCATTTTGTCTGTGCCCTGTGSCCTT	2078
QY	1092	GCTGGCCGCCGACCTGCCCTGGCCTCAGTGGGAGAAATACGGGGCTCCCCCACTGTGCT	1151
Db	2079	GACCATGGCCGCGAGTTCCCTCTGCTGGGTGGCAGAAAGTATGGGCCCTCCCTCTCTGCT	2138
QY	1152	GCCCTACGCCCACTGAGGGTTCAGCCAGCAGCCCTGGGCTTTCACCGTGGCCCTGGTGAT	1211
Db	2139	GCCTT-----TGCCTTTTGGGGAGCCCAAGCACCATGGGCTACATGGTCGCTCATCTT	2192
QY	1212	GATGAACCTCCTTCTGTTCCTGGTCTGGTGGCCGGTGGCTTACATCAAACTGTACTGTGACCT	1271
Db	2193	GCTCAATTCCCTTTGCTTCTCTCATGATGACCATTTGCTTACACCAAGCTCTACTGCAATT	2252
QY	1272	GCCGGGGCGACTTTGAGGCCGTGTGGGACTGGGCCATGGTGAGGCACGTGGCCCTGGCT	1331
Db	2253	GGACAAGGGAGACCTGGAGAAATATTTGGGACTGCTCTATGGTAAACACATTTGCCCTGTT	2312
QY	1332	CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCTTCAGCTTTCGCCCTCCATGCT	1391
Db	2313	GCTCTTCACCAACTGCATCCTAAACCTGCCCTGTGGCTTCTTGTCTCTCTCTTTAAT	2372
QY	1392	GGGCCCTCTTCCCTGTACGCCCGGAGGCCGTCAAGTCTGTCTCTGTGGTGGTGTGCCCT	1451
Db	2373	AAACCTTACATTTATCAGTCTCTGAAGTAATTAAGTTTATCCTTCTGGTGGTAGTCCCACT	2432
QY	1452	GCCTGCCTGCCCTCAACCCACTGTGTACCTGCTCTTCAACCCCACTTCCGGGATGACCT	1511
Db	2433	TCCTGCATGTCTCAATCCCTTCTCTACATCTTGTGTCAATCCTCACCTTTAAGGAGGATCT	2492
QY	1512	TCGGCGGCT	1520

Db 2493 GGTGAGCCT 2501

RESULT 4
US-09-976-594-201
; Sequence 201, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 201
; LENGTH: 4570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 205542.2
; NAME/KEY: unsure
; LOCATION: 3900, 3919, 3934
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-201

Query Match 18.7%; Score 355.6; DB 4; Length 4570;
Best Local Similarity 56.2%; Pred. No. 2.4e-72;
Matches 781; Conservative 0; Mismatches 580; Indels 28; Gaps 5;

Qy 135 GGCCTCCAAACACAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAGCTC 194
Db 1399 GACCTAAGACATAATGAATCTACGAAATTAAAG-TTGACACTTCCAGCAGTTGCTTAG 1457

Qy 195 CTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCTTCTC 254
Db 1458 CCTCCGATCGTGAATTGGCTTGGAAACAAAATTGCTATTATTACCCCCAATGCATTTC 1517

Qy 255 CACCCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTGACCACACTGCCCT 314
Db 1518 CACTTTGCCATCCCTAATAAAGCTGGACCTATCGTCCAACCTCCTGTGCTCTTTCCAT 1577

Qy 315 GGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCCAGGC 374
Db 1578 AACTGGGTTACATGGTTTAACTCACTTAAATTAACAGGAAATCATGCCCTTACAGAGCTT 1637

Qy 375 CTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCCTTATGCCCTACCAGTG 434
Db 1638 GATATCATCTGAAAACCTTCCAGAACTCAAGGTTATAGAAATGCCCTTATGCTTACCAGTG 1697

Qy 435 CTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGCAGTGGGAGGCTGAAGA 494
Db 1698 CTGTGCATTTGGAGTGTGTGAGAATGCCTATAAGATTCTTAATCAATGGAATAAAGGTGA 1757

Qy 495 CCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGCCCTCCTTGGCAGACAAGC 554
Db 1758 CAACAGCAGTATGGACGACCTTCATAAGAA-----GATGCTGGAATGTT 1802

Qy 555 AGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGAT---GGAGCACTCAA 611
Db 1803 TCAGGCTCAAGATGAACGTGACCTTGAAGATTTCCTGCTTGACTTTGAGGAAGACCTGAA 1862

Qy 612 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTTGAGTACCT 671
Db 1863 AGCCCTTCATTCAGTGCAAGTGTTCACCTTCCCCAGGCCCTTCAAACCCCTGTGAACACCT 1922

Qy 672 CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTTGGGCCATCGTGTGTCTCTCGGTGCTCTG 731
Db 1923 GCTTGATGGCTGATCAGAAATTGGAGTGTGGACCATAGCAGTTCTGGCACTTACTTG 1982

Qy 732 CAATGGACTGGTGTGCTGCTGACCGTGTTCGCTGGCGGGCCTGCCCCCTGCCCGCGTCAA 791
Db 1983 TAATGCTTTGGTGACTTCAACAGTTTTTCAGATCC---CCTCTGTACATTTCCCCCAATA 2039

Qy 792 GTTTGTGGTAGGTGCGATTGCAGGCGCAACACACTTGACTGGCATTTCTCTGTGGCCTTCT 851
Db 2040 ACTGTTAAATTGGGTCATCGCAGCAGTGAAACATGCTCACGGAGTCTCCAGTGCCGTGCT 2099

Qy 852 AGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC 911
Db 2100 GGCTGGTGTGGATGCGTTCACTTTTGGCAGCTTTGACGACATGGTGCCTGGTGGGAGAA 2159

Qy 912 GGGGCTAGGCTGCCGGCCACTGGCTTCCCTGGCAGTACTTGGGTGCGAGGCATCGGTGCT 971
Db 2160 TGGGGTTGGTTGCCATGTCAATGGTTTTTTTGTCCATTTTGTCTTCAGAAATCATCTGTTT 2219

Qy 972 GCTGCTCACTCTGSCCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCTCCGGCCTATGG 1031
Db 2220 CCTGCTTACTCTGGCAGCCCTGGAGCGTGGTTCCTGTGAAATATTTCTGCAAAATTTGA 2279

Qy 1032 GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTAGGCTGCCTGGCACTGGCAGG 1091
Db 2280 AACGAAAGCTCCATTTTCTAGCCCTGAAAGTAATCATTTTGTCTGTGCCCTGCTGGCCTT 2339

Qy 1092 GCTGGCCCGCACTGCCCTGGCCTCAGTGGGAGAATAACGGGGCCTCCCACTCTGCCT 1151
Db 2340 GACCATGGCCGAGTTCCTCTGTGGTGGCAGCAAGTATGGCGCCTCCCTCTCTGCTGCT 2399

Qy 1152 GCCCTACGCGCCACCTGAGGGTTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT 1211
Db 2400 GCCTT-----TGCCTTTTGGGGAGCCCGCAGCACCATTGGGTACATGGTGTCTCATCTT 2453

Qy 1212 GATGAACTCCTTCTGTCTTCTGGTCTGTGGCCGTGCCTACATCAAACTGTACTGTGACCT 1271
Db 2454 GCTCAATTCCCTTGTCTTCTCATGATGACCATTTGCCCTACACCAAGCTCTACTGCAATTT 2513

Qy 1272 GCCGGGGGCGACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGACCGTGGCCTGGCT 1331
Db 2514 GGACAAGGGAGACCTGGAGAAATATTGGGACTGCTCTATGGTAAACACATTTGCCCTGTT 2573

Qy 1332 CATCTTCGACAGCGGCTCCTCTACTGTCCGTGGCCTTCTCTCAGCTTCGCTCCATGCT 1391
Db 2574 GCTCTTCACCAACTGCATCCTAAACTGCCCTGTGGCTTTCTTGTCTCTCTCTCTTTAAT 2633

Qy 1392 GGGCCTCTTCCCTGTACGCCCCGAGGCCCTCAAGTCTGTCTGTGTGGTGTGCTGCCCT 1451
Db 2634 AAACCTTACATTTATCAGTCTCTGAAGTAATAAGTTTATCCTTCTGTGGTAGTCCCCT 2693

Qy 1452 GCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCACTTCCGGGATGACCT 1511
Db 2694 TCCTGCATGTCTCAATCCCTTCTCTACATCTTGTTCATCCTCACTTTAAGGAGGATCT 2753

Qy 1512 TCGGCGGCT 1520
Db 2754 GGTGAGCCT 2762

RESULT 5
US-09-170-496D-277
; Sequence 277, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 277
; LENGTH: 2724
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-277

Query Match      18.6%; Score 352.4; DB 4; Length 2724;
Best Local Similarity 56.1%; Pred. No. 1.1e-71;
Matches 779; Conservative 0; Mismatches 582; Indels 28; Gaps 5;

QY 135 GGCCTCCAACACACCGCATCTGGGAAATTTGGAGCTNGACACCTTCAGCCAGCTGAGCTC 194
Db 1138 GACCTAAGACATAATGAAATCTACGAAATTAAG-TTGACACTTCCAGCAGTTGCTTAG 1196

QY 195 CTTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCCTTCTC 254
Db 1197 CTCCGATCGCTGAATTTGGCTTGGACAAAATTGCTATTATTACCCCAATGCATTTTC 1256

QY 255 CACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACACTGCCCT 314
Db 1257 CACTTGGCATCCCTAATAAAGTGGACCTATCGTCCAACCTCCTGTCTTTTCTAT 1316

QY 315 GGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGAACTTGTCTCTCTCCAGGC 374
Db 1317 AACTGGGTACATGGTTTAACCTACTTAAATTAACAGGAAATCATGCCTTACAGAGCTT 1376

QY 375 CTTCTCCAAGGACAGTTTCCAAAACCTGAGGATCCTGGAGTGCTTATGCCTACCAGTG 434
Db 1377 GATATCATCTGAAAACCTTCCAGAACTCAAGGTTATAGAAATGCCTTATGCTTACCAGTG 1436

QY 435 CTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGCTGAAGA 494
Db 1437 CTGTGCATTTGGAGTGTGTGAGATGCCTATAAGATTTCTAATCAATGAATAAAGTGA 1496

QY 495 CTTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCTCCTTGCCAGACAAGC 554
Db 1497 CAACAGCAGTATGGACGACCTTCATAAGAAA-----GATGCTGGAATGTT 1541

QY 555 AGAGAACCACTATGACCAAGACCTGGATGAGCTCCAGCTGGAGAT---GGAGGACTCAAA 611
Db 1542 TCAGGCTCAAGATGAACGTGACCTTGAAGATTTCTCTGCTTGACTTTGAGGAAGACCTGAA 1601

QY 612 GCACACCCAGTGTCAGTGTCCAGTGTAGCCTTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 671
Db 1602 AGCCCTTCATTTCAGTGCAGTGTTCACCTTCCCCAGGCCCTTCAAAACCTGTGAACACCT 1661

QY 672 CTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGGCCCATCGTGTGCTCTCCGTGCTGTG 731
Db 1662 GCTTGATGGCTGGCTGATCAGAATTGGAGTGTGGACCATAGCAGTTCTGGCACITACTTG 1721

QY 732 CAATGGACTGGTGTCTGCTGCTGCTGCTGGCGGGCTTCCCTGCCCCCCTGCCCCCGGTCAA 791
Db 1722 TAATGCTTTGGTGACTTCAACAGTTTTTCAGATCC---CCTCTGTACATTTCCCCCAATTAA 1778

QY 792 GTTTGTGGTAGGTGCGATTGACGGCGCCCAACACCTTGACTGGCATTTCTGTGGCCTTCT 851
Db 1779 ACTGTTAATTTGGGTCTATCGCAGCAGTGAACATGTCTACGGGAGTCTCCAGTGCCGTGCT 1838

QY 852 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGAGCCCGCTGGGAGAC 911
Db 1839 GGCTGGTGTGATGCGTTCACTTTTGGCAGCTTTGACGACATGTTGCCCTGTGGGAGAA 1898

QY 912 GGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTGGAGGCATCGGTGCT 971
Db 1899 TGGGTTGGTTGCCATGTCTATGGTTTTTTGTCCATTTTGTCTTCAGAAATCATCTGTTTT 1958

QY 972 GCTGCTCACTCTGGCCGCGAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCCTATGG 1031
Db 1959 CTTGCTTACTCTGGCAGCCCTGGAGCGTGGGTTCTCTGTGAAAATATTCTGCAAAATTGA 2018

QY 1032 GAAGTCCCCCTCCCTGGGACGGTTCGAGCAGGGGTCTTAGGCTGCCTGGCACCTGGCAGG 1091
Db 2019 AACGAAAGCTCCAATTTTCTAGCCTGAAAGTAATCATTTTGTCTGTGCCCTGTGGCCTT 2078
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QY 1092 GCTGGCCGCGCACTGCCCTGGCCTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCT 1151
Db 2079 GACCATGGCCGAGTTCCCTGCTGGGTGGCAGCAAGTATGGCGCCTCCCTCTCTGCCT 2138

QY 1152 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCGCCCTGGGCTTTCACCGTGGCCCTGGTGAT 1211
Db 2139 GCCTT-----TGCCTTTTGGGAGCCCGCAGCACCATGGGCTACATGGTCGCTCTCATCTT 2192

QY 1212 GATGAACCTCCTTCTGTTTCTTGGTCTGGCCGGTGCCTACATCAAACTGTACTGTGACCT 1271
Db 2193 GCTCAATTCCCTTTGCTTCCICATGATGACCATTGGCTACACCAAGCTCTACTGCAATTT 2252

QY 1272 GCCGCGGGCGCACTTTGAGGCCGTGTGGGACTGCGGCATGGTGAGGCACGTGGCCTGGCT 1331
Db 2253 GGACAAAGGAGACCTTGGAGAAATATTGGGACTGCTCTATGAAAAAACACATTGCCCTGTT 2312

QY 1332 CATCTTCGACAGCGGCTCCTCTACTGTCCCCTGGGCTTCTCAGCTTCGCCTCCATGCT 1391
Db 2313 GCTCTTCACCAACTGCATCCTAAACTGCCCTGTGGCTTCTTGTCTCTCTCTCTTAAT 2372

QY 1392 GGGCCTCTTCCCTGTCAAGCCCGGAGGCCGTCAAGTCTGTCTGTGGTGTGCTGCCCT 1451
Db 2373 AAACCTTACATTTATCAGTCTGAAGTAATTAAGTTTATCCTTCTGGTGTAGTCCACT 2432

QY 1452 GCCTGCCTGCCTCAACCCACTGTGTACCTGCTCTTCAACCCCACTTCCGGGATGACCT 1511
Db 2433 TCCTGCATGTCTCAATCCCTTCTCTACATCTTGTTCATCCTCACCTTAAAGGAGGATCT 2492

QY 1512 TCGGCGGCT 1520
Db 2493 GGTGAGCCT 2501
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RESULT 6

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US-09-495-050A-214
; Sequence 214, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 214
; LENGTH: 2612
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 2470285CT1
US-09-495-050A-214
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Query Match 10.2%; Score 194; DB 4; Length 2612;
Best Local Similarity 52.8%; Pred. No. 4e-35;
Matches 469; Conservative 0; Mismatches 410; Indels 9; Gaps 2;

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QY 622 AGTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGC 681
Db 1226 ATTATCCATTGTACACCTTCAACAGGTGCTTTTAAAGCCCTGTGAATATTTACTGGGAGC 1285

QY 682 TGGGGCATCCGCTGGCCGTGTGGCCCATCGTGTGCTCTCCGTGCTCTGCAATGGACTG 741
Db 1286 TGGATGATTGCTCTTACTGTGTGGTTCAATTTCTTGTGCTGATTTTTCACACCTGCTT 1345

QY 742 GTGCTGTGACCGTGTTCGCTGGCGGGCCTGCCCCCTGCCCGGTCAAGTTTGTGTA 801
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Db 1346 GTATATTTAAACAACATTTGCACTCTTG---TACATCACTGCGCTTCGTCCAAATTTGTTTATA 1402

Qy 802 GGTCGGAATTGCAGGCGCCAACACACTTGACTGGCAATTTCTGTGGCCTTCTAGCCTCAGTC 861

Db 1403 GGCCTGATTTCTGTGCTAACTATTATTCATGGGAATCTATACCTGGCATCCTAACTTTTCTT 1462

Qy 862 GATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGC 921

Db 1463 GATGCTGTCTCTGGGCGAGATTCTGCTGAATTTGGCAATTTGGTGGAAACTGGCGAGTGGC 1522

Qy 922 TGCCGGGCCACTGGCTTCTTGGCAGTACTTTGGGTCGGAGGCATCGGTGCTGCTCACT 981

Db 1523 TGCAAAAGTAGCTGGGTTTCTTGCAAGTTTCTCCTCAGAAAGTGCCATATTTTATTAATG 1582

Qy 982 CTGGCCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCGGGGCCTATGGGAAGTCCCCC 1041

Db 1583 CTAGCAACTGTCGAAAGAGCTTATCTGCAAAAGATATAATGAAAAATGGGAGAGCAAT 1642

Qy 1042 TCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCTGGCACTGGCAGGGCTGGCGGCC 1101

Db 1643 CATCTCAAAACAGTTCGGGTTGCTGCCCTTTTGCTTTCTTAGGTGCTACAGTAGCAGGC 1702

Qy 1102 GCACTGCCCTGGCCTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCCTGCCCTACGGC 1161

Db 1703 TGTTTCCCTTTTCCATAGAGGGAATATTCTGCATCACCCCTTTGTTGGCAT----- 1757

Qy 1162 CCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACCTCC 1221

Db 1758 -TTCCTACAGGTGAACCGCCATCATTAGGATTCACGTGAACGTTAGTGCTATTAACACTCA 1816

Qy 1222 TTCTGTTTCTGTGTCGGTGCCTACATCAAACTGTACTGTGACCTGCCCGGGGC 1281

Db 1817 CTAGCATTTTATTAATAGCGCGTTATCTACACTAAGCTATACTGCAACTTGGAAAAAGAG 1876

Qy 1282 GACTTTGAGGCCGTGTGGACTGCGCCATGGTAGGCACTGGCCTGGCTCAATCTTTCGCA 1341

Db 1877 GACCTCTCAGAAAACTCAAACTAGCATGATTAAGCATGTCGCTTGGCTAATCTTCACC 1936

Qy 1342 GACGGGCTCCTACTGTCCGTTGGCCTTCCCTCAGCTTCGCCCTCCATGCTGGGCTCTTC 1401

Db 1937 AATTGCATCTTTTCTGCCCTGTGGCGTTTTTTTTCATTTCACCATTTGATCACTGCAATC 1996

Qy 1402 CCTGTACGCCCGGAGGCCGCTCAAGTCTGTCTGTGTTGGTGTGCTGCCCTGCCTGCCTGC 1461

Db 1997 TCTATCAGCCCCGAAATAATGAAGTCTGTTACTCTGATATTTTTTCCATTTGCCCTGCTTG 2056

Qy 1462 CTCAACCCACTGCTGTACTCTCTTCAACCCCACTTCGGGGATGAC 1509

Db 2057 CTGAATCCAGTCTCTGTATGTTTCTTCAACCCCAAGTTTAAAGAAAGAC 2104

RESULT 7

US-08-866-757-1

; Sequence 1, Application US/08866757

; Patent No. 5858716

; GENERAL INFORMATION:

; APPLICANT: ELSHOURBAGY, NABIL A

; APPLICANT: LI, XIAOTONG

; APPLICANT: BERGSM, DEREK J

; TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/866,757

; FILING DATE: 30-MAY-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-70055

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4203 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-866-757-1

Query Match 10.2%; Score 194; DB 2; Length 4203;

Best Local Similarity 52.8%; Pred. No. 4.6e-35;

Matches 469; Conservative 0; Mismatches 410; Indels 9; Gaps 2;

Qy 622 AGTGTCAGTGTAGCCCTACTCCAGGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGC 681

Db 1117 ATTATCCATTGTACACCTTCAACAGGTGCTTTTAAGCCCTGTGAATATTTACTGGGAAGC 1176

Qy 682 TGGGCGATCCGCCTGGCCGTGTGGCCATCGTGTGCTCTCCGTGCTCTGCAATGGACTG 741

Db 1177 TGGATGATTCTGCTTACTGTGTGTTCAATTTCTTGGTTGCATTAATTTTCAACCTGCTT 1236

Qy 742 GTGCTGTGACCGTGTTCGTGGCGGCCCTGCCCCCTGCCCCCGTCAAGTTTGTGGTA 801

Db 1237 GTTATTTTAAACAACATTTGCATCTTG---TACATCACTGCCTTCGTCCAAATTTTATA 1293

Qy 802 GGTGCGATTGCAGGCGCCAAACACCTTGACTGGCAATTTCTGTGGCCTTCTAGCCTCAGTC 861

Db 1294 GGCTTGATTTCTGTGCTAACTTATTTCATGSGAATCTATACTGGCATCTCTAACTTTTCTT 1353

Qy 862 GATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGC 921

Db 1354 GATGCTGTGTCCTGGGGCAGATTCGCTGAATTTGGCATTTGGTGGGAAACTGGCAGTGGC 1413

Qy 922 TGCCGGGCCACTGGGCTTCTGGCAGTACTTGGGTGCGAGGCATCGGTGCTGCTCACT 981

Db 1414 TGCAAAAGTAACTGGGTTTCTTTCAGTTTTCTCCTCAGAAAAGTGCCATATTTTATTAATG 1473

Qy 982 CTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCCTCTGTGTCCGGGCCCTATGGGAAGTCCCCC 1041

Db 1474 CTAGCAACTGTCGAAAGAGCTTATCTGCAAAAGATATAATGAAAAATGGGAAAGCAAT 1533

Qy 1042 TCCCTGGSCAGCGTTTCGAGCAGGGGTCCCTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCC 1101

Db 1534 CATCTCAAACAGTTCCGGTTGCTGCCCTTTTGGCTTTTCCCTAGGTGTACAGTAACAGGC 1593

Qy 1102 GCACTGCCCTTGGCCCTCAGTGGGAGAATACGGGGCCCTCCCCACTCTGCTGCTGCCCTACGG 1161

Db 1594 TGTTTTCCTCTTCCATAGAGGGGAATATTCTGCATCACCCCTTTGTTGGCAT----- 1648

Qy 1162 CCACCTGAGGTCAGCCAGCAGCCCTGGGCTTACCGTGGCCCTGCTGATGATGAACCTCC 1221

Db 1649 -TTCCTACAGGTGAAACGCCATCATTAGGATTCATGTAACGTTAGTGCTATTAAACTCA 1707

Qy 1222 TTCTGTTTCTGTGTCGTGGCCGGTGCCTTACATCAAACTGTACTGTGACTGCCCGGGGC 1281

Db 1708 CTAGCATTTTATTAATGCGCGTTATCTACACTAAGCTATACTGCAACTTGGAAAAAGAG 1767

Qy 1282 GACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGCA 1341

Db	1768	GACCTCTCAGAAAACTCACAACTAGCATGATTAAAGCATGTGCGTTGGCTAATCTTCACC	1827
Qy	1342	GACGGGTCCTTACTACTGTCCCGTGGCCCTTCCTCAGCTTCGCCTCCATGCTGGGCGCTCTTC	1401
Dd	1828	AATTGCATCTTTTTCTGCCCTGTGGCGTTTTTTTCAATTTGCACCAATTGATCACTGCAATC	1887
Qy	1402	CCTGTACAGCCCGAGCCGTCAGTCTGTCTCTGTGTTGGTGCTGCCCTGCCCTGCCTGC	1461
Dd	1888	TCTATCAGCCCCGAAAATAATGAAGTCTGTTACTCTGATATTTTTTCCATTGCCCTGCTTC	1947
Qy	1462	CTCAACCCACTGCTGTACTCTGCTCTTTC AACCCCACTTCCGGGATGAC	1509
Dd	1948	CTGAATCCAGTCTGTATGTTTTCTTCAACCCAAAGTTTAAAGAAGAC	1995

RESULT. 8

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US-09-153-593-1
; Sequence 1, Application US/09153593A
; Patent No. 6174994
; GENERAL INFORMATION:
; APPLICANT: ELSHOURBAGY, NABIL A
; APPLICANT: LI, XIAOTONG
; APPLICANT: BERGSMAN, DERK J
; TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
; FILE REFERENCE: GH-70055-1
; CURRENT APPLICATION NUMBER: US/09/153,593A
; CURRENT FILING DATE: 1998-09-15
; EARLIER APPLICATION NUMBER: 08/866,757
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4203
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-153-593-1

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[illegible]

RESULT 9

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US-09-495-050A-220
; Sequence 220, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 220
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 2603450CT1
US-09-495-050A-220

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Query Match	9.6%;	Score 181.8;	DB 4;	Length 723;
Best Local Similarity	55.8%;	Pred. No. 1.8e-32;		
Matches 392;	Conservative	0;	Mismatches 302;	Indels 9;
			Gaps	2;
Qy	695	TGGCGGTGTGGCCCATCGTGTGCTCTCCGTGCTCTGCAATGGACTGGTGTGCTGTGACCG	754	
Db	1	TTGGAGTGTGGACCATAGCAGTCTCTGGCACTTACTTGTAACTGCTTGGTGACTTCAACAG	60	
Qy	755	TGTTCGCTGGCGGGCCTGCCCCCTGCCCCCGGTCAAGTTTGTGGTGGTGGATTCGATTGCAG	814	
Db	61	TTTTC---AGATCCCCCTCTGTACATTTCCCCCATTTAAACTGTTAAATGGGGGTCAATCGCAG	117	
Qy	815	GGGCCAACACCTTGACTGGCATTTCCCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCT	874	
Db	118	CAGTGAACATGCTCACGGGAGTCTCCAGTGCCGTGCTGGCTGGTGTGGATGCGTTCACTT	177	
Qy	875	TTGGTCAGTTCTCTGAGTACGGAGCCCCGCTGGGAGACGGGGCTAGGCTGCCGGGGCCACTG	934	

Db 178 TTGGCAGCTTTGACAGACATGGTGCCTGGTGGGAGAAATGGGGTTGGTTGCCATGTCAATTG 237
QY 935 GCTTCCTGGCAGTACTTGGGTGCGAGGCATCGGTGCTGCTCACTCTGCGCGCAGTGC 994
Db 238 GTTTTGTGCCATTTTGTCTCAGAAATCATCTGTTTTCTGCTTACTCTGCGAGCCCTGG 297
QY 995 AGTGCAGCGTCTCCGTCTCCTGTGTCCGGCCCTATGGGAAGTCCCCCTCCCTGGGCAGCG 1054
Db 298 AGCGTGGGTTCTCTGTGAAATATTCTGCAAAATTTGAAACGAAAGCTCCATTTTCTAGCC 357
QY 1055 TTCGAGCAGGGGTCCCTAGGTGCTGGCAGTGGCAGGGCTGGCCGCCGACACTGCCCCCTGG 1114
Db 358 TGAAAGTAATCATTTTGTCTGTGCCCTGTCTGGCCCTTGACCATGGCCGCGAGTTCCCTGTC 417
QY 1115 CCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCTGCCCTACGGCCACCTGAGGGTGC 1174
Db 418 TGGGTGGCAGCAAGTATGGCGCCTCCCTCTCTGCTGCTT-----TGCCTTTTGGGG 471
QY 1175 AGCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGATGATGAACCTCCTTCTGTTTCTTGG 1234
Db 472 AGCCAGCAGCACCATGGGTACATGGTGCCTCTCATCTGTGCTCAATTCCCTTTGCTTCTCA 531
QY 1235 TCGTGGCCGGTGCCATACATCAAACTGTACTGTGACTGCCGCGGGCGGACCTTTGAGGCCG 1294
Db 532 TGATGACCATTGCGCTACACCAAGCTCTACTGCAATTTGGACAAGGGAGACCTGGAGAATA 591
QY 1295 TGTGGGACTGCGCCCATGTTGAGGCACGTGGCCCTGCTCATCTTTCGCAGACGGGCTCCTCT 1354
Db 592 TTTGGGACTGCTCTATGGTAAACACATTTGCCCTGTGTGCTCTTCCACCAACTGCATCCTAA 651
QY 1355 ACTGTCCCGTGGCCTTCCCTCAGCTTCCCTCCATGCTGGGCCCT 1397
Db 652 ACTGCCCTGTGGCTTTCTTGTCTTCTCTCTCTTTAATAAACCT 694

RESULT 10
US-09-482-273-75
; Sequence 75, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: PZ030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; EARLIER FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-482-273-75

Query Match 5.5%; Score 105; DB 4; Length 2703;
Best Local Similarity 56.5%; Pred. No. 1.4e-14;
Matches 195; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
QY 1165 CCTGAGGGTACGCAGCAGCCCTGGGCTTCACGTGGCCCTGGTGATGATGAACCTCCTTC 1224
Db 13 CCTACAGGTGAAACGCCATCATTAGGATTCACTGTAACGTTAGTGTATTAAACTCACTA 72
QY 1225 TGTTTCCTGGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCGCGGGCGAC 1284
Db 73 GCATTTTATTAAATGGCCGTTATCTACACTAAGCTATACTGCAACTTACCACTTGGAAAAGAGGAC 132

QY 1285 TTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGACAGAC 1344
Db 133 CTCTCAGAAAACCTCACAATCTAGCATGATTAAGCATGTGCTTGGCTAATCTTCACCAAT 192
QY 1345 GGGCTCCTCTACTGTCCCGTGGCCTTCCCTCAGCTTCGCTCCATGCTGGGCCTCTTCCCT 1404
Db 193 TGCATCTTTTTCTGCCCTGTGGCGTTTTTTTTCATTTGCACCATTTGATCAGTGAATCTCT 252
QY 1405 GTCACGCCCGAGSCCGTCAAGTCTGTCTCTGCTGGTGGTGGTGGCTGCCCTGCCCTGCCTC 1464
Db 253 ATCAGCCCCCGAATAATGAAGTCTGTTACTCTGATATTTTTTCCATTGCTTGCCTG 312
QY 1465 AACCCTACTGCTGTACCTGCTCTTCAACCCCCACTTCCGGGATGAC 1509
Db 313 AATCCAGTCTGTATGTTTTTCTTCAACCCCAAAGTTTAAAGAAGAC 357

RESULT 11
US-08-866-757-3
; Sequence 3, Application US/08866757
; Patent No. 5858716
; GENERAL INFORMATION:
; APPLICANT: ELSHOURHAGY, NABIL A
; APPLICANT: LI, XIAOTONG
; APPLICANT: BERGSMAN, DERK J
; TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,757
; FILING DATE: 30-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-866-757-3

Query Match 5.4%; Score 101.8; DB 2; Length 473;
Best Local Similarity 56.8%; Pred. No. 4.7e-14;
Matches 187; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
QY 1181 CAGCCCTGGGCTTCAACCGTGGCCCTGGTGATGATGAACCTCCTTCTTCTTCTGGTGG 1240
Db 14 CATCATTAGGATTCACTGTAACGTTAGTGTCTATTAAACTCACTAGCATTTTATTATGG 73
QY 1241 CCGGTGCTTACATCAAACTGTACTGTGACCTGCCGCGGGCGGACTTTGAGGCCGTGTGG 1300

Db 74 CCGTTATCTACACTAAGCTATATACTGCAACTTGGAAAAAGGAGACCTCTCAGAAAACTCAC 133
Qy 1301 ACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTC 1360
Db 134 AATCTAGCATGATTAAGCATGTGCTTGGCTAATCTTCACCAATTGCATCTTTTCTGCC 193
Qy 1361 CCGTGGCCTTCCTCAGCTTCGCCCTCCATGTGGGCCTCTTCCTGTACGCCCGAGCGG 1420
Db 194 CTGTGGCGTTTTTTTCATTTGCACCATTTGATCACTGCAATCTCTATCAGCCCCGAAATAA 253
Qy 1421 TCAAGTCTGTCTGTGCTGGTGCTGCCCTGCCCTGCCTCAACCCACTGCTGTACC 1480
Db 254 TGAAGTCTGTACTCTGATATTTTTTCCATTGCCCTGCTTGCCTGAATCCAGTCCTGTATG 313
Qy 1481 TGCTCTTCAACCCCCACTTCCGGGATGAC 1509
Db 314 TTTTCTTCAACCCCAAAGTTTAAAGAGGAC 342

RESULT 12

US-09-153-593-3
; Sequence 3, Application US/09153593A
; Patent No. 6174994
; GENERAL INFORMATION:
; APPLICANT: ELSHOURBAGY, NABIL A
; APPLICANT: LI, XIAOTONG
; APPLICANT: BERGSM, DERK J
; TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
; FILE REFERENCE: GH-70055-1
; CURRENT APPLICATION NUMBER: US/09/153,593A
; EARLIER FILING DATE: 1998-09-15
; EARLIER APPLICATION NUMBER: 08/866,757
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 473
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (397) (400) (406) (432) (459)

US-09-153-593-3

Query Match 5.4%; Score 101.8; DB 3; Length 473;
Best Local Similarity 56.8%; Pred. No. 4.7e-14;
Matches 187; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
Qy 1181 CAGCCCTGGGCTTCACCGTGGCCTGGTGATGATGAACCTCCTTCTGTTTCCCTGGTCGTGG 1240
Db 14 CATCATTAGGATTCACTGTAACTTAGTGCTATTAAACTCACTAGCATTTTATTATATGG 73
Qy 1241 CCGGTGCCTACATCAAACTGTACTGTGACCTGCCGGGGCGGACCTTGAGGCCGTGTGGG 1300
Db 74 CCGTTATCTACACTAAGCTATATACTGCAACTTGGAAAAAGAGGACCTCTCAGAAAACTCAC 133
Qy 1301 ACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTC 1360
Db 134 AATCTAGCATGATTAAGCATGTGCTTGGCTAATCTTCACCAATTGCATCTTTTCTGCC 193
Qy 1361 CCGTGGCCTTCCTCAGCTTCGCCTCCATGTGGGCCTCTTCCTGTACGCCCGAGGCGG 1420
Db 194 CTGTGGCGTTTTTTTCATTTGCACCATTTGATCACTGCAATCTCTATCAGCCCCGAAATAA 253
Qy 1421 TCAAGTCTGTCTGTGCTGGTGCTGCCCTGCCCTGCCTCAACCCACTGCTGTACC 1480
Db 254 TGAAGTCTGTACTCTGATATTTTTTCCATTGCCCTGCTTGCTGAATCCAGTCCTGTATG 313
Qy 1481 TGCTCTTCAACCCCCACTTCCGGGATGAC 1509
Db 314 TTTTCTTCAACCCCAAAGTTTAAAGAGGAC 342

RESULT 13

US-09-482-273-101
; Sequence 101, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: PZ030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-482-273-101

Query Match 5.0%; Score 94.6; DB 4; Length 2709;
Best Local Similarity 56.5%; Pred. No. 3.5e-12;
Matches 195; Conservative 0; Mismatches 149; Indels 1; Gaps 1;
Qy 1165 CCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACCTCCTTC 1224
Db 13 CCTACAGGTGAAACGCCATCATTAGGATTCACTGTAAACGTTAGTGTATTAAACTCACTA 72
Qy 1225 TGTTTCCTGGTCGTGGCGGTGCCCTACATCAAACTGTACTGTGACCTGCCCGGGGGGAC 1284
Db 73 GCATTTTATTAAATGCGCGTTATCTACACTAAGCTATATACTGCAACTTGGAAAAAGAGGAC 132
Qy 1285 TTTGAGGCCGTGTGGACTGCGCCCATGGTGAGGACGTGGCCTGGCTCATCTTCGCAGAC 1344
Db 133 CTCTCAGAAAACTCACAATCTAGCATGATTAAGCATGTGCGTTGGCTAATCTTCACCAAT 192
Qy 1345 GGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCTCCATGTGGGCCCTCTTCCTCT 1404
Db 193 TGCATCTTTTCTGCCCTGTGGCGTTTTTTTTCATTTTGCACCATTTGATCACTGCAATCTCT 252
Qy 1405 GTCAGCCCGAGGCGGCTCAAGTCTGTCTGTGCTGGTGCTGCCCTGCCCTGCCCTGCCCTC 1464
Db 253 ATCAGCCCCGAAATAATGAAGTCTGTTACTCTGAT-ATTTTTCATGCTGCCCTGCTTGCCTG 311
Qy 1465 AACCCACTGCTGTACCTGCTCTTCAACCCCCACCTTCGGGGATGAC 1509
Db 312 AATCCAGTCCTGTATGTTTTCTTCAACCCCAAAGTTTAAAGAGAC 356

RESULT 14

US-09-589-510-7
; Sequence 7, Application US/09589510
; Patent No. 6706949
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; TITLE OF INVENTION: Maize Orthologues of Bacterial RuvB:
; TITLE OF INVENTION: cDNAs and Uses Thereof
; FILE REFERENCE: 1121
; CURRENT APPLICATION NUMBER: US/09/589,510
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: US 60/144,112
; PRIOR FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1898
; TYPE: DNA

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; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)...(1533)
US-09-589-510-7

Query Match      4.2%; Score 79.8; DB 4; Length 1898;
Best Local Similarity 80.9%; Pred. No. 8.2e-09;
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QY      1 AATACGACTCACTATAGGGAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATCCCCGGG 60
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Db      16 AATACGACTCACTATAGGGAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATCCCCGGG 75
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QY      61 TCGACCCACGCGTCCTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAG 115
      ||||||||||||||||||| || || || || || || || || || || || ||
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RESULT 15
US-08-633-682-1
; Sequence 1, Application US/08633682
; Patent No. 5840544
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL RANTES HOMOLOG FROM PROSTATE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,682
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0063 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 570 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: Prostrate
; CLONE: 836820
US-08-633-682-1

Query Match      4.1%; Score 78.8; DB 2; Length 570;
Best Local Similarity 73.2%; Pred. No. 1e-08;
Matches 101; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY      1 AATACGACTCACTATAGGGAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATCCCCGGG 60
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QY      61 TCGACCCACGCGTCCTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCT 120
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GenCore version 5.1.6
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QM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1898	99.9	2486	17	US-10-664-667-4
5	1754.4	92.4	2208	10	US-09-851-595-9
6	1754.4	92.4	2208	17	US-10-664-667-9
7	1754.4	92.4	2711	10	US-09-851-595-7
8	1754.4	92.4	2711	17	US-10-664-667-7
9	1754.4	92.4	2901	10	US-09-851-595-12
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					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 9, Appli
					Sequence 9, Appli
					Sequence 7, Appli
					Sequence 7, Appli
					Sequence 12, Appli
					Sequence 52, Appli

12	1754.4	92.4	3438	14	US-10-176-847-89	Sequence 89, Appli
13	1754.4	92.4	3443	17	US-10-331-496A-94	Sequence 94, Appli
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16	1754.4	92.4	3492	18	US-10-737-450-31	Sequence 31, Appli
17	1752.8	92.3	2988	17	US-10-302-172-723	Sequence 723, App
18	1752.8	92.3	3119	15	US-10-225-567A-580	Sequence 580, App
19	1751.2	92.2	3429	18	US-10-398-036-26	Sequence 26, Appli
20	1749.6	92.1	2487	14	US-10-270-336-1	Sequence 1, Appli
21	1748	92.0	3273	17	US-10-295-027-1119	Sequence 1119, Ap
22	1748	92.0	3273	18	US-10-783-528-43	Sequence 43, Appli
23	1746.4	92.0	3349	14	US-10-270-336-4	Sequence 4, Appli
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29	1254.8	66.1	119596	14	US-10-270-336-3	Sequence 3, Appli
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31	493.6	26.0	1078	17	US-10-264-049-395	Sequence 395, App
32	439.4	23.1	453	9	US-09-876-889-240	Sequence 240, App
33	416.2	21.9	422	10	US-09-918-995-34626	Sequence 34626, A
34	356.2	18.8	2082	19	US-10-851-470-3	Sequence 3, Appli
35	355.6	18.7	2651	17	US-10-295-027-483	Sequence 483, App
36	355.6	18.7	2651	17	US-10-295-027-1113	Sequence 1113, Ap
37	355.6	18.7	2651	17	US-10-173-999-27	Sequence 27, Appli
38	355.6	18.7	2724	15	US-10-251-385-263	Sequence 263, App
39	355.6	18.7	2724	15	US-10-225-567A-421	Sequence 421, App
40	355.6	18.7	2724	17	US-10-174-456-4	Sequence 4, Appli
41	355.6	18.7	2724	18	US-10-751-736-21	Sequence 21, Appli
42	355.6	18.7	2880	17	US-10-295-027-1114	Sequence 1114, Ap
43	355.6	18.7	2880	19	US-10-482-029-157	Sequence 157, App
44	355.6	18.7	2880	19	US-10-651-237-48	Sequence 48, Appli
45	355.6	18.7	2880	19	US-10-782-413-48	Sequence 48, Appli

ALIGNMENTS

RESULT 1

US-09-851-595-6
; Sequence 6, Application US/09851595
; Publication No. US20030166047A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/09/851,595
; CURRENT FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1899)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (171)
; OTHER INFORMATION: n = any nucleotide
US-09-851-595-6

Query Match 99.9%; Score 1898; DB 10; Length 1899;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1899; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATACGACTCACTATAGGAAAGCTGGTACGCTGAGGTACCGGTCCGGAATTCCTCCGGG 60

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1 AATACGACTCACTATAGGGAAGCTGGTACGCTGCAGGTACCGTCCGGAATTCCTCCGGG 60
QY
61 TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCT 120
Db
61 TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCT 120
QY
121 CTTGCTGCCCTAGCGGCCTTCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACTTC 180
Db
121 CTTGCTGCCCTAGCGGCCTTCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACTTC 180
QY
181 AGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCAC 240
Db
181 AGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCAC 240
QY
241 CTTGAGGCCCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTG 300
Db
241 CTTGAGGCCCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTG 300
QY
301 ACCACACTGCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 360
Db
301 ACCACACTGCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 360
QY
361 GCTCTCTCCAGGCCCTTCTCCAAAGGACAGTTTCCCAAAACTGAGGATCTCTGAGGTGCCT 420
Db
361 GCTCTCTCCAGGCCCTTCTCCAAAGGACAGTTTCCCAAAACTGAGGATCTCTGAGGTGCCT 420
QY
421 TATGCCCTACAGTGTCTCCCTATGGGATGTGTCCAGCTTCTTCAAGGCCTCTGGGCAG 480
Db
421 TATGCCCTACAGTGTCTCCCTATGGGATGTGTCCAGCTTCTTCAAGGCCTCTGGGCAG 480
QY
481 TGGGAGGCTGAAGACCTTACCTTGATGATGAGGAGTCTTCAAAAGGCCCTTGGGCCTC 540
Db
481 TGGGAGGCTGAAGACCTTACCTTGATGATGAGGAGTCTTCAAAAGGCCCTTGGGCCTC 540
QY
541 CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG 600
Db
541 CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG 600
QY
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Db
601 GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC 660
QY
661 TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTC 720
Db
661 TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTC 720
QY
721 TCCGTGCTCTGCAATGGAATGGTGCATGAGTGTAGCCCTGCGTGGCCGCTGAGTGTGCTC 780
Db
721 TCCGTGCTCTGCAATGGAATGGTGCATGAGTGTAGCCCTGCGTGGCCGCTGAGTGTGCTC 780
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781 CCCCCGGTCAAGTTTGTGTAGGTGCGATTGCAGSGCGCCAAACACCTTGACTGGCATTTCC 840
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841 TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCC 900
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841 TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCC 900
QY
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Db
901 CGCTGGGAGACGGGGCTAGGCTGCCGGCCACTGGGTTCTTGGCAGTACTTGGGTGCGAG 960
QY
961 GCATCGGTGCTGCTCACTCTGGCCGCACTGAGTGCAGTGCAGCGTCTCCGTCTCTGTGTC 1020
Db
961 GCATCGGTGCTGCTCACTCTGGCCGCACTGAGTGCAGTGCAGCGTCTCCGTCTCTGTGTC 1020
QY
1021 CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTAGGCTGCCTG 1080
Db
1021 CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTAGGCTGCCTG 1080
QY
1081 GCACTGGCAGGGCTGGCCGCGCACTGCCCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCC 1140
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Db 1081 GCACTGGCAGGGCTGGCCGCCGCACTGCCCTTGGCTCAGTGGGAGAAATACGGGGCCTCC 1140
QY 1141 CCACTCTGCCCTGCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCAACCGTG 1200
Db 1141 CCACTCTGCCCTGCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCAACCGTG 1200
QY 1201 GCCCTGGTGATGAGAACTCCTTCTGTGTTTCTGCTGCTGCGCGGTGCTACATCAAACTG 1260
Db 1201 GCCCTGGTGATGAGAACTCCTTCTGTGTTTCTGCTGCTGCGCGGTGCTACATCAAACTG 1260
QY 1261 TACTGTGACCTGCCGGGGCGACTTTTGAGGCGCGTGTGGGACTGCGCCCATGGTGAGGCAC 1320
Db 1261 TACTGTGACCTGCCGGGGCGACTTTTGAGGCGCGTGTGGGACTGCGCCCATGGTGAGGCAC 1320
QY 1321 GTGGCCTGGCTCATCTTTCGCAGACGGGCTCCTCTACTGTCCCCTGGCCTTCCCTCAGCTTC 1380
Db 1321 GTGGCCTGGCTCATCTTTCGCAGACGGGCTCCTCTACTGTCCCCTGGCCTTCCCTCAGCTTC 1380
QY 1381 GCCTCCATGTGGGCTCTTCCCCTGTACGCCGAGGCGCGTCAAGTCTGTCTGCTGGTG 1440
Db 1381 GCCTCCATGTGGGCTCTTCCCCTGTACGCCGAGGCGCGTCAAGTCTGTCTGCTGGTG 1440
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Db 1441 GTGCTGCCCTGCTGCTGCTCAACCCACTGTACCTGCTCTTCAACCCCACTTC 1500
QY 1501 CGGGATGACCTTCGGCGGCTTCGGCCCCCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT 1560
Db 1501 CGGGATGACCTTCGGCGGCTTCGGCCCCCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT 1560
QY 1561 GCGGCCGGGAGCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGTGAGCTTCTCT 1620
Db 1561 GCGGCCGGGAGCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGTGAGCTTCTCT 1620
QY 1621 GATGTGATCTCAATTCTGGAAGCTTCTGAAAGCTGGGCGGCCCTTGGGCTGGAGACCTAT 1680
Db 1621 GATGTGATCTCAATTCTGGAAGCTTCTGAAAGCTGGGCGGCCCTTGGGCTGGAGACCTAT 1680
QY 1681 GGCTTCCCCTCAGTGACCTCATCTCCTGTGAGCAGCCAGGGGCCCTCAGGCTGGAGGGC 1740
Db 1681 GGCTTCCCCTCAGTGACCTCATCTCCTGTGAGCAGCCAGGGGCCCTCAGGCTGGAGGGC 1740
QY 1741 AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGA 1800
Db 1741 AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGA 1800
QY 1801 GAACTGCTGTAGGGCAGAGGGATCTACCCAGCAGGTGGAGGCTTGTACAGGGGTGGC 1860
Db 1801 GAACTGCTGTAGGGCAGAGGGATCTACCCAGCAGGTGGAGGCTTGTACAGGGGTGGC 1860
QY 1861 GGCTTTACGCCCTCTGGCTTGGCCTTTGCTTACACAGTG 1899
Db 1861 GGCTTTACGCCCTCTGGCTTGGCCTTTGCTTACACAGTG 1899

RESULT 2
US-10-664-667-6
; Sequence 6, Application US/10664667
; Publication No. US20040058377A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/10/664,667
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/851,595
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 6
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1899)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (171)
; OTHER INFORMATION: n = any nucleotide
US-10-664-667-6

Query Match          99.9%; Score 1898; DB 17; Length 1899;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1899; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AATACGACTCACTATAGGGAAGCTGGTACGCGCTGCAGGTACCGGTCCGGAATTCCCGGG 60
Db      |||||||
QY      61 TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCTGCCGGCTCATCCAGCCTCT 120
Db      |||||||
QY      121 CTGTGCTGCCCTAGCGGCCCTTCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTC 180
Db      |||||||
QY      181 AGCCAGCTGAGCTCCCTGAAGCCCTTGGATCTTAGCTGGAAACGCCATCCGGTCCATCCAC 240
Db      |||||||
QY      241 CCTGAGGCCCTTCTCCACCCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTG 300
Db      |||||||
QY      301 ACCACACTGCCCCCTGGCTGGAAGCTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 360
Db      |||||||
QY      361 GCTCTCTCCCAGGCCCTTCTCAAGGACAGTCTTCCCAAACTGAGGATCCTGGAGGTGCCT 420
Db      |||||||
QY      421 TATGCCCTACCAAGTGTCTCCCTATGGGATGTGTGCCAGTCTTCAAGGCCTCTGGGCAG 480
Db      |||||||
QY      481 TGGGAGGCTGAAGACCTTCAAGGACAGTCTTCCCAAACTGAGGATCCTGGAGGTGCCT 540
Db      |||||||
QY      541 CTGTCCAGACAAGCAGAGAACCACTATGACCAAGGACCTGGATGAGCTCCAGCTGGAGATG 600
Db      |||||||
QY      601 GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC 660
Db      |||||||
QY      661 TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTC 720
Db      |||||||
QY      721 TCCGTGCTCTGCAATGGAATGGTGTGCTGACCGGTGTCGCTGGCGGCCCTGCCGCCCTG 780
Db      |||||||
QY      781 CCCCCTGTCGAGTTTGTGTAGGTGCGATTGACGGCGCAACACCTTGACTGGCAATTTC 840
Db      |||||||

QY      1 AATACGACTCACTATAGGGAAGCTGGTACGCGCTGCAGGTACCGGTCCGGAATTCCCGGG 60
Db      |||||||
QY      61 TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCTGCCGGCTCATCCAGCCTCT 120
Db      |||||||
QY      121 CTGTGCTGCCCTAGCGGCCCTTCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTC 180
Db      |||||||
QY      181 AGCCAGCTGAGCTCCCTGAAGCCCTTGGATCTTAGCTGGAAACGCCATCCGGTCCATCCAC 240
Db      |||||||
QY      241 CCTGAGGCCCTTCTCCACCCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTG 300
Db      |||||||
QY      301 ACCACACTGCCCCCTGGCTGGAAGCTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 360
Db      |||||||
QY      361 GCTCTCTCCCAGGCCCTTCTCAAGGACAGTCTTCCCAAACTGAGGATCCTGGAGGTGCCT 420
Db      |||||||
QY      421 TATGCCCTACCAAGTGTCTCCCTATGGGATGTGTGCCAGTCTTCAAGGCCTCTGGGCAG 480
Db      |||||||
QY      481 TGGGAGGCTGAAGACCTTCAAGGACAGTCTTCCCAAACTGAGGATCCTGGAGGTGCCT 540
Db      |||||||
QY      541 CTGTCCAGACAAGCAGAGAACCACTATGACCAAGGACCTGGATGAGCTCCAGCTGGAGATG 600
Db      |||||||
QY      601 GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC 660
Db      |||||||
QY      661 TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTC 720
Db      |||||||
QY      721 TCCGTGCTCTGCAATGGAATGGTGTGCTGACCGGTGTCGCTGGCGGCCCTGCCGCCCTG 780
Db      |||||||
QY      781 CCCCCTGTCGAGTTTGTGTAGGTGCGATTGACGGCGCAACACCTTGACTGGCAATTTC 840
Db      |||||||
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QY      841 TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTGGTCAGTTCTCTGAGTACGGAGCC 900
Db      |||||||
QY      901 CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTGGAG 960
Db      |||||||
QY      961 GCATCGGTGCTGCTGCTCACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCTGTGTC 1020
Db      |||||||
QY      1021 CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTCCGAGCAGGGGTCTTAGGCTGCTG 1080
Db      |||||||
QY      1081 GCACTGGCAGGGCTGSCCGCCGCACTGCCCTGSCCTCAGTGGGAGAAATACGGGSCCTCC 1140
Db      |||||||
QY      1141 CCACTCTGCCCTGCCCTAGCGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCAACCGTG 1200
Db      |||||||
QY      1201 GCCCTGGTGATGAATACTCTTCTGTCTTCTGTCGTGGCCGGTGCCCTACATCAAACTG 1260
Db      |||||||
QY      1261 TACTGTGACCTGCCGGGGCGACTTTGAGGCCCGTGTGGACTGCGCCATGGTGGAGCAC 1320
QY      1321 GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCCTGGCCCTTCTCTCAGCTTC 1380
Db      |||||||
QY      1381 GCCTCCATGTGGGCTCTTCCCTGTCAACGCCCGAGGGCCGTCAAGTCTGTCTGCTGGTG 1440
Db      |||||||
QY      1441 GTGCTGCCCTGCCCTGCTGCTCAACCCACTGTGTGTACTGTCTTCAACCCCACTTC 1500
Db      |||||||
QY      1501 CGGGATGACCTTCGGGGCTTCGGCCCCCGCGAGGGGACTCAGGGCCCCCTAGCCTATGCT 1560
Db      |||||||
QY      1561 GCGGCCGGGAGCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT 1620
Db      |||||||
QY      1621 GATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGGGGGCCCCCTGGGCTGGAGACCTAT 1680
Db      |||||||
QY      1681 GGCTTCCCCTCAGTGACCTCATCTCCTGTGACAGCCAGGGGCCCCCAAGGCTGGAGGGC 1740
Db      |||||||
QY      1741 AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTTGGGAACCCCAACCCCTCCATGGATGGA 1800
Db      |||||||
QY      1801 GAACTGCTGCTGAGGSCAGAGGGATCTACGCCACAGAGGTGGAGGCTTGTACGGGGGTGGC 1860
Db      |||||||
QY      1861 GGCTTTCAGCCCTCTGGCTTGGCCTTTTGGCTTTCACACGTG 1899
Db      |||||||
QY      1861 GGCTTTCAGCCCTCTGGCTTGGCCTTTTGGCTTTCACACGTG 1899
Db      |||||||
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Db      1682  |||||||TCCCTCAGTGACCCCTCATCTCCTGTGTCAGCAGCCAGGGGCCCCAGGCTGGAGGCG 1741
Qy      1741  AGCCATGTGTAGAGCCAGAGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGA 1800
Db      1742  |||||||TGTAGAGCCAGAGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGA 1801
Qy      1801  GAACTGCTGCTGAGGGCAGAGGGATCTAGCCAGCAGGTGAGAGGCTTGTGAGGGGTGCG 1860
Db      1802  GAACTGCTGCTGAGGGCAGAGGGATCTAGCCAGCAGGTGAGAGGCTTGTGAGGGGTGCG 1861
Qy      1861  GGCTTTTCAGCCCTCTGGCTTGGCTTTGCTTTCACACGTG 1899
Db      1862  GGCTTTTCAGCCCTCTGGCTTGGCTTTGCTTTCACACGTG 1900
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RESULT 4
US-10-664-667-4
; Sequence 4, Application US/10664667
; Publication No. US20040058377A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/10/664,667
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/851,595
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2486
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1900)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (172)}
; OTHER INFORMATION: n = any nucleotide
US-10-664-667-4
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Query Match      99.9%; Score 1898; DB 17; Length 2486;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1899; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AATACGACTCACTATAGGGAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATCCCGGG 60
Db      2  AATACGACTCACTATAGGGAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATCCCGGG 61

Qy      61  TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGTCCAGCCTCATCCAGCCTT 120
Db      62  TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGTCCATCCAGCCTCT 121

Qy      121  CTTGCTGCCCTAGCGGCCTCCAAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTC 180
Db      122  CTTGCTGCCCTAGCGGCCTCCAAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTC 181

Qy      181  AGCCAGCTGAGCTCCCTGCAAGCCCTTGGATCTTAGTGTGGAACGCCATCCGGTCCATCCAC 240
Db      182  AGCCAGCTGAGCTCCCTGCAAGCCCTTGGATCTTAGTGTGGAACGCCATCCGGTCCATCCAC 241

Qy      241  CCTGAGGCCCTTCTCCACCCCTGGACTCCCTGGTCAAGCTGGACCTGACAGACAAACAGCTG 300
Db      242  CCTGAGGCCCTTCTCCACCCCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAAACAGCTG 301

Qy      301  ACCACACTGCCCCCTGGCTGGACTTGGGGCTTGTATGCATCTGAAGCTCAAAGGGAACCTT 360
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Db      302  ACCACACTGCCCCCTGGCTGGACTTTGGGGCTTGTATGCATCTGAAGCTCAAAGGGGAACCTT 361
Qy      361  GCTCTCTCCAGGCCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCTT 420
Db      362  GCTCTCTCCAGGCCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCTT 421
Qy      421  TATGCCTACCAGTGTCTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGGAG 480
Db      422  TATGCCTACCAGTGTCTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGGAG 481
Qy      481  TGGGAGGCTGAAAGACCTTTCACCTTGTATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCTC 540
Db      482  TGGGAGGCTGAAAGACCTTTCACCTTGTATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCTC 541
Qy      541  CTTGCCAGACAAGCAGAGAACCACCTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG 600
Db      542  CTTGCCAGACAAGCAGAGAACCACCTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG 601
Qy      601  GAGGACTCAAAGCCACACCCCACTGTCCAGTGTAGCCCTACTTCCAGGCCCTTCAAGCCCC 660
Db      602  GAGGACTCAAAGCCACACCCCACTGTCCAGTGTAGCCCTACTTCCAGGCCCTTCAAGCCCC 661
Qy      661  TGTAGTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCGGTGTGGGCCATCGTGTGTGCTC 720
Db      662  TGTAGTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCGGTGTGGGCCATCGTGTGTGCTC 721
Qy      721  TCCGTGCTCTGCAATGGAATGGTGTGCTGTGACCCGTGTGCTGGGGGCTGCCCCCTG 780
Db      722  TCCGTGCTCTGCAATGGAATGGTGTGCTGTGACCCGTGTGCTGGGGGCTGCCCCCTG 781
Qy      781  CCCCCTGTCAGTTTGTGTAGGTGCGATTGCAGGCGCCAAACACCTTGACTGGCATTTCC 840
Db      782  CCCCCTGTCAGTTTGTGTAGGTGCGATTGCAGGCGCCAAACACCTTGACTGGCATTTCC 841
Qy      841  TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCC 900
Db      842  TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCC 901
Qy      901  CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTTGGGTGGAG 960
Db      902  CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTTGGGTGGAG 961
Qy      961  GCATCGGTGCTGTGCTCACTCTGGCCGCGAGTGCAGTCAGCGTCTCCGTCTCTCTGTGTC 1020
Db      962  GCATCGGTGCTGTGCTCACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCTCTGTGTC 1021
Qy      1021  CGGGCCTATGGGAAGTCCCCCTCCCTGGGCGAGCGTTCGAGCAGGGGTCTTAGGCTGCCTG 1080
Db      1022  CGGGCCTATGGGAAGTCCCCCTCCCTGGGCGAGCGTTCGAGCAGGGGTCTCTAGGCTGCCTG 1081
Qy      1081  GCACCTGGCAGGGCTGGCCCGCGCACTGCCCTTGGCTCAGTGGGAGAAATACGGGGCTCC 1140
Db      1082  GCACCTGGCAGGGCTGGCCCGCGCACTGCCCTTGGCTCAGTGGGAGAAATACGGGGCTCC 1141
Qy      1141  CCACTCTGCCTGCCCTACGGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCAACCGTG 1200
Db      1142  CCACTCTGCCTGCCCTACGGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCAACCGTG 1201
Qy      1201  GCCCTGGTGTATGAACTCCTTCTGTGTTTCTGTGCTGGCGGTGCCTACATCAAACTG 1260
Db      1202  GCCCTGGTGTATGAACTCCTTCTGTGTTTCTGTGCTGGCGGTGCCTACATCAAACTG 1261
Qy      1261  TACTGTGACCTGCCCGGGCGGACTTTGAGGCCGTGTGGGACTGCGCCATGTGAGGCAC 1320
Db      1262  TACTGTGACCTGCCCGGGCGGACTTTGAGGCCGTGTGGGACTGCGCCATGTGAGGCAC 1321
Qy      1321  GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTTACTGTCCCCTGGCCTTCTCAGCTTC 1380
Db      1322  GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTTACTGTCCCCTGGCCTTCTCAGCTTC 1381
Qy      1381  GCCTCCATGTGGGCTCTTCCCTGTACGCCGAGGCCGTCAAAGTCTGTCTGTGCTGGTG 1440
Db      1382  GCCTCCATGTGGGCTCTTCCCTGTACGCCGAGGCCGTCAAAGTCTGTCTGTGCTGGTG 1441
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QY 1441 GTGTCGCCCTGCCTGCCTCAACCCACTGCTGCTACCTGCTCTTCAACCCCACTTC 1500
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Db 1442 GTGTCGCCCTGCCTGCCTCAACCCACTGCTGCTACCTGCTCTTCAACCCCACTTC 1501
|||||
QY 1501 CGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT 1560
|||||
Db 1502 CGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT 1561
|||||
QY 1561 GCGCGCGGGAGCTGGAGAAGACTCCTGTGATTTACCCAGGCCCTTGGTAGCCTTCTCT 1620
|||||
Db 1562 GCGCGCGGGAGCTGGAGAAGACTCCTGTGATTTCTACCCAGGCCCTGGTAGCCTTCTCT 1621
|||||
QY 1621 GATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGCGGCCCCCTGGGCTGGAGACCTAT 1680
|||||
Db 1622 GATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGCGGCCCCCTGGGCTGGAGACCTAT 1681
|||||
QY 1681 GGCTTCCCCTCAGTGACCCCTCATCTCCTGTCAGCAGCCAGGGGGCCCCCAGGCTGGAGGGC 1740
|||||
Db 1682 GGCTTCCCCTCAGTGACCCCTCATCTCCTGTCAGCAGCCAGGGGGCCCCCAGGCTGGAGGGC 1741
|||||
QY 1741 AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCCAACCCCTCCATGGATGGA 1800
|||||
Db 1742 AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCCAACCCCTCCATGGATGGA 1801
|||||
QY 1801 GAACTGCTGTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGTGGC 1860
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Db 1802 GAACTGCTGTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGTGGC 1861
|||||
QY 1861 GGCTTTCAGCCCTCTGGCTTGGCCCTTTGCTTCACACGTG 1899
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Db 1862 GGCTTTCAGCCCTCTGGCTTGGCCCTTTGCTTCACACGTG 1900
|||||

RESULT 5

US-09-851-595-9
; Sequence 9, Application US/09851595
; Publication No. US20030166047A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/09/851,595
; CURRENT FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2208)
US-09-851-595-9

Query Match 92.4%; Score 1754.4; DB 10; Length 2208;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1766; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 132 AGCGGCCTCCAACACACACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG 191
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Db 442 ATCGGCCTCCAACACACACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG 500
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QY 192 CTCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCTT 251
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Db 501 CTCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCTT 560
|
QY 252 CTCACCCCTGCATCCCTGGTCAAGCTGGACCTGACAGACAACAGCTGACCACACTGCC 311
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QY 312 CCTGGCTGGACTTGGGGCTTGTATGCACTGAAGCTCAAAGGGAACCTTGTCTCTCCCCA 371
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Db 621 CCTGGCTGGACTTGGGGCTTGTATGCACTGAAGCTCAAAGGGAACCTTGTCTCTCCCCA 680
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QY 372 GGCCTTCTCCAAGGACAGTTTCCCCAAAACCTGAGGATCCTGGAGGTGCCCTTATGCCTACCA 431
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Db 681 GGCCTTCTCCAAGGACAGTTTCCCCAAAACCTGAGGATCCTGGAGGTGCCCTTATGCCTACCA 740
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QY 492 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTCTGGGCCCTCCTGTGCCAGACA 551
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Db 801 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTCTGGGCCCTCCTGTGCCAGACA 860
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QY 552 AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAA 611
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RESULT 6

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US-10-664-667-9
; Sequence 9, Application US/10664667
; Publication No. US20040058377A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/10/664,667
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/851,595
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2208
; TYPE: DNA
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2208)
US-10-664-667-9
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Query Match 92.4%; Score 1754.4; DB 17; Length 2208;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1766; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 132 AGCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG 191
Db 442 ATCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG 500
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QY 192 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCTT 251
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QY 252 CTCCACCCCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACTGCC 311
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QY 552 AGCAGAGAACCCTATGACACGAGCCTGGATGAGTCCAGCTGGAGATGGAGGACTCAAA 611
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RESULT 7
US-09-851-595-7
; Sequence 7, Application US/09851595
; Publication No. US20030166047A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/09/851,595
; CURRENT FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 2711
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2208)
US-09-851-595-7

Query Match 92.4%; Score 1754.4; DB 10; Length 2711;
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QY 132 AGCGGCTCCAAACAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG 191
Db 442 ATCGGCTCCAAACAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG 500
QY 192 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGSCATCCGGTCCATCCACCCCTGAGGCCTT 251
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QY 252 CTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTGACACACTGCC 311
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QY 312 CCTGGCTGGACTTGGGGGCTTGATGCACTGAAGCTCAAAGGAACTTGTCTCTCCCCA 371
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QY 672 CTTTGAAGCTGGGGCATCCGCCCTGGCCGTGGGGCCATCGTGTGCTCTCCGTGCTCTG 731
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Qy      1512  TCGGCGGCTTCGGCCCCCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGA 1571
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Qy      1572  GCTGGAGAAAGAGCTCCTGTGATTTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT 1631
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Qy      1872  CTCTGGCTTGGCCTTTGCTTCACACGTG 1899
Db      2181  CTCTGGCTTGGCCTTTGCTTCACACGTG 2208
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RESULT 8

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US-10-664-667-7
; Sequence 7, Application US/10664667
; Publication No. US20040058377A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/10/664,667
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/851,595
; PRIOR FILING DATE: 2000-05-08
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; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 2711
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2208)
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Query Match      92.4%; Score 1754.4; DB 17; Length 2711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1766; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy      132  ACGGGCCTCCAACACACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG 191
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Qy      492  AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGSCCCTGGGCCTCCTTGCCAGACA 551
Db      801  AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGSCCCTGGGCCTCCTTGCCAGACA 860
Qy      552  AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAA 611
Db      861  AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAA 920
Qy      612  GCCACACCCCAAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 671
Db      921  GCCACACCCCAAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 980
Qy      672  CTTTGAAGCTGGGCAATCCGCCTGGCCGTGTGGGCAATCGTGTGCTCTCCGTGCTCTG 731
Db      981  CTTTGAAGCTGGGCAATCCGCCTGGCCGTGTGGGCAATCGTGTGCTCTCCGTGCTCTG 1040
Qy      732  CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGCTGCCCCCTGCCCGGTCAA 791
Db      1041  CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGCTGCCCCCTGCCCGGTCAA 1100
Qy      792  GTTTGTGGTAGTCCGATTGACGGCGCCAAACACCTTGACTGGCATTTCCTGTGGCCTTCT 851
Db      1101  GTTTGTGGTAGTCCGATTGACGGCGCCAAACACCTTGACTGGCATTTCCTGTGGCCTTCT 1160
Qy      852  AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGAGAC 911
Db      1161  AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGAGAC 1220
Qy      912  GGGGCTAGGCTGCCGGSCACTGGCTTCCCTGGCAGTACTTGGGTCGGAGGCAATCGTGCT 971
Db      1221  GGGGCTAGGCTGCCGGSCACTGGCTTCCCTGGCAGTACTTGGGTCGGAGGCAATCGTGCT 1280
Qy      972  GCTGCTCACTCTGGCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCTATGG 1031
Db      1281  GCTGCTCACTCTGGCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCTATGG 1340
Qy      1032  GAAATCCCCCTCCCTGGGAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGG 1091
Db      1341  GAAATCCCCCTCCCTGGGAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGG 1400
Qy      1092  GCTGGCCGCCGCACTGCCCTTGGCCTCAGTGGAGAAATACGGGGCCTCCCCACTTGCCT 1151
Db      1401  GCTGGCCGCCGCACTGCCCTTGGCCTCAGTGGAGAAATACGGGGCCTCCCCACTTGCCT 1460
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QY 1152 GCCCTACGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT 1211
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Db 1461 GCCCTACGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT 1520
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QY 1212 GATGAACCTCCTTCTGTTCCTGGTCTGGCCGGTGCCTACATCAAACTGTACTGTGACCT 1271
|||||
Db 1521 GATGAACCTCCTTCTGTTCCTGGTCTGGCCGGTGCCTACATCAAACTGTACTGTGACCT 1580
|||||
QY 1272 GCCCGGGGCGACTTTGAGGCGGTGTGGGACTGCGGCATGGTGAGGCACGTGGCTGGCT 1331
|||||
Db 1581 GCCCGGGGCGACTTTGAGGCGGTGTGGGACTGCGGCATGGTGAGGCACGTGGCTGGCT 1640
|||||
QY 1332 CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGCGCTTCCTCAGCTTCGCTCCATGCT 1391
|||||
Db 1641 CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGCGCTTCCTCAGCTTCGCTCCATGCT 1700
|||||
QY 1392 GGGCCTCTCCCTGTACGCGCCGAGCCCGTCAAGTCTGTCTCTGCTGGTGGTGGCTGCCCT 1451
|||||
Db 1701 GGGCCTCTCCCTGTACGCGCCGAGCCCGTCAAGTCTGTCTCTGCTGGTGGTGGCTGCCCT 1760
|||||
QY 1452 GCCTGCCTGCCCTCAACCCACTGCTGTACTGCTCTTCAACCCCACTTCGCGGATGACCT 1511
|||||
Db 1761 GCCTGCCTGCCCTCAACCCACTGCTGTACTGCTCTTCAACCCCACTTCGCGGATGACCT 1820
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QY 1512 TCGGCGGCTTCGGCCCGGCGCAGGGGACTCAGGGCCCTAGCCCTATGCTGCGGCCGGGA 1571
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Db 1821 TCGGCGGCTTCGGCCCGGCGCAGGGGACTCAGGGCCCTAGCCCTATGCTGCGGCCGGGA 1880
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QY 1572 GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT 1631
|||||
Db 1881 GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT 1940
|||||
QY 1632 CATCTGGAAGCTTCTGNAAGCTGGCGGCCCTGGGCTGGAGACCTATGGCTTCCCCTC 1691
|||||
Db 1941 CATCTGGAAGCTTCTGAAAGCTGGCGGCCCTGGGCTGGAGACCTATGGCTTCCCCTC 2000
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QY 1692 AGTGACCTCATCTCTGTGACGAGCCAGGGGCCCTGGGCTGGAGGCGAGCCATTGTGT 1751
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Db 2001 AGTGACCTCATCTCTGTGACGAGCCAGGGGCCCTGGGCTGGAGGCGAGCCATTGTGT 2060
|||||
QY 1752 AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTTCATGGATGGAGAACTGCTGCT 1811
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Db 2061 AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTTCATGGATGGAGAACTGCTGCT 2120
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QY 1812 GAGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTTCAGGGGGTGGCGGCTTTCAGCC 1871
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Db 2121 GAGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTTCAGGGGGTGGCGGCTTTCAGCC 2180
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QY 1872 CTCTGGCTTGGCCTTTGCTTCACACGTG 1899
|||||
Db 2181 CTCTGGCTTGGCCTTTGCTTCACACGTG 2208
|||||

RESULT 9
US-09-851-595-12
; Sequence 12, Application US/09851595
; Publication No. US20030166047A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/09/851,595
; CURRENT FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 2901
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2901)
US-09-851-595-12

Query Match 92.4%; Score 1754.4; DB 10; Length 2901;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1766; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 132 AGCGGCTCCAAACACAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG 191
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Db 1135 ATCGGCTCCAAACACAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG 1193
|||
QY 192 CTCCCTGCAAGCCCTGGATCTTAGCTGGAAGCCCATCCGGTCCATCCACCTGAGGCCTT 251
|||
Db 1194 CTCCCTGCAAGCCCTGGATCTTAGCTGGAAGCCCATCCGGTCCATCCACCTGAGGCCTT 1253
|||
QY 252 CTCCACCCCTGCACTCCCTGGTCAAGCTGGAACCTGACAGACAAACCAGCTGACACACTGCC 311
|||
Db 1254 CTCCACCCCTGCACTCCCTGGTCAAGCTGGAACCTGACAGACAAACCAGCTGACACACTGCC 1313
|||
QY 312 CCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGTCTCTCTCCA 371
|||
Db 1314 CCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGTCTCTCTCCA 1373
|||
QY 372 GGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGTGCCCTTATGCCCTACCA 431
|||
Db 1374 GGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGTGCCCTTATGCCCTACCA 1433
|||
QY 432 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGAGTGGGAGGCTGA 491
|||
Db 1434 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGAGTGGGAGGCTGA 1493
|||
QY 492 AGACCTTACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCTCTCTGTCCTATCCA 551
|||
Db 1494 AGACCTTACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCTCTCTGTCAGACA 1553
|||
QY 552 AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 611
|||
Db 1554 AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 1613
|||
QY 612 GCCACACCCAGTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 671
|||
Db 1614 GCCACACCCAGTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 1673
|||
QY 672 CTTTGAAAGCTGGGGCATCCGCCTGGCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG 731
|||
Db 1674 CTTTGAAAGCTGGGGCATCCGCCTGGCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG 1733
|||
QY 732 CAATGGACTGGTGTGCTGACCGGTTCGCTGGCGGGCCTGCCCTGCCCCCCCCGGTCAA 791
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Db 1734 CAATGGACTGGTGTGCTGACCGGTTCGCTGGCGGGCCTGCCCTGCCCCCCCCGGTCAA 1793
|||
QY 792 GTTGTGTAGGTGCGGATTGCAAGCGGCCAACACACTTGACTGGCAATTCCTGTGGCCTTCT 851
|||
Db 1794 GTTGTGTAGGTGCGGATTGCAAGCGGCCAACACACTTGACTGGCAATTCCTGTGGCCTTCT 1853
|||
QY 852 AGCCTCAGTCGATGCCCTGACCTTTGGTTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC 911
|||
Db 1854 AGCCTCAGTCGATGCCCTGACCTTTGGTTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC 1913
|||
QY 912 GGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGGTCGAGGCGCATCGGTGCT 971
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Db 1914 GGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGGTCGAGGCGCATCGGTGCT 1973
|||
QY 972 GCTGCTCACTGTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCTGTGTCGGGGCCTATGG 1031
|||
Db 1974 GCTGCTCACTGTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCTGTGTCGGGGCCTATGG 2033
|||
QY 1032 GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGGCAGCTGGCAGG 1091
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Db 2034 GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGGCAGCTGGCAGG 2093
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|||||
Db 1974 GCTGCTCACTCTGGCCGAGTGCAGTGCAGGCTCTCGTCTCCTGTGTCGGGCTATGG 2033
QY 1032 GAAGTCCCCCTCCCTGGGAGCGTTTCGAGCAGGGGTCTAGGCTGCCTGGCACTGGCAGG 1091
Db 2034 GAAGTCCCCCTCCCTGGGAGCGTTTCGAGCAGGGGTCTAGGCTGCCTGGCACTGGCAGG 2093
QY 1092 GCTGGCCGCGCACTGCCCTGGCCTCAAGTGGGAGATACGGGCGCTCCCCACTCTGCCT 1151
Db 2094 GCTGGCCGCGCACTGCCCTGGCCTCAAGTGGGAGATACGGGCGCTCCCCACTCTGCCT 2153
QY 1152 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCAACGCTGGCCCTGGTGAT 1211
Db 2154 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCAACGCTGGCCCTGGTGAT 2213
QY 1212 GATGAACCTCTTCTGTTTCTGCTGGTCGTCGGCCGCTGCCTACATCAAACTGTACTGTGACCT 1271
Db 2214 GATGAACCTCTTCTGTTTCTGCTGGTCGTCGGCCGCTGCCTACATCAAACTGTACTGTGACCT 2273
QY 1272 GCCCGGGGGCGACTTTGAGCCCGTGTGGGACTGCGCATGGTGAGGCACGTGGCCTGGCT 1331
Db 2274 GCCCGGGGGCGACTTTGAGCCCGTGTGGGACTGCGCATGGTGAGGCACGTGGCCTGGCT 2333
QY 1332 CATCTTCGACACGGGCTCCTCTACTGTCCCGTGGCCTTCTCAGCTTCGCCTCCATGCT 1391
Db 2334 CATCTTCGACACGGGCTCCTCTACTGTCCCGTGGCCTTCTCAGCTTCGCCTCCATGCT 2393
QY 1392 GGGCCTCTTCCCTGTCAACGCCCGAGGCCGTCAAGTCTGCTCCTGCTGGTGCTGCCCT 1451
Db 2394 GGGCCTCTTCCCTGTCAACGCCCGAGGCCGTCAAGTCTGCTCCTGCTGGTGCTGCCCT 2453
QY 1452 GCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCACTTCCGGGATGACCT 1511
Db 2454 GCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCACTTCCGGGATGACCT 2513
QY 1512 TCGCGGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGCTGCGCCGGGGA 1571
Db 2514 TCGCGGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGCTGCGCCGGGGA 2573
QY 1572 GCTGGAGAAAGAGCTCCTGTGATTTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT 1631
Db 2574 GCTGGAGAAAGAGCTCCTGTGATTTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT 2633
QY 1632 CATCTGGAAGCTTCTGAAGCTGGCGGCCCTCCCTGGCTGGAGACCTATGGCTTCCCCCTC 1691
Db 2634 CATCTGGAAGCTTCTGAAGCTGGCGGCCCTCCCTGGCTGGAGACCTATGGCTTCCCCCTC 2693
QY 1692 AGTGACCCCTCATCTCTGTTCAGCAGCCAGGGGCCCGCCAGGCTGGAGGCGAGCCATTGTGT 1751
Db 2694 AGTGACCCCTCATCTCTGTTCAGCAGCCAGGGGCCCGCCAGGCTGGAGGCGAGCCATTGTGT 2753
QY 1752 AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT 1811
Db 2754 AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT 2813
QY 1812 GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTTCAGGGGTGGCGGCTTTCAGCC 1871
Db 2814 GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTTCAGGGGTGGCGGCTTTCAGCC 2873
QY 1872 CTCTGGCTTGGCCTTTGCTTTCACACGCTG 1899
Db 2874 CTCTGGCTTGGCCTTTGCTTTCACACGCTG 2901
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RESULT 11
US-10-331-496A-52
; Sequence 52, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL

; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 52
; LENGTH: 3325
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-331-496A-52

Query Match 92.4%; Score 1754.4; DB 17; Length 3325;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1766; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 132 AGCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG 191
Db 1063 ATCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG 1121
QY 192 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCTT 251
Db 1122 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTTCAGGCCTT 1181
QY 252 CTCCACCCCTGCACCTCCCTGGTCAAGCTGGAACCTGACAGACAACAGCTGACCACTGCC 311
Db 1182 CTCCACCCCTGCACCTCCCTGGTCAAGCTGGAACCTGACAGACAACAGCTGACCACTGCC 1241
QY 312 CTTGGCTGGAATTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTCTCTCCCA 371
Db 1242 CTTGGCTGGAATTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTCTCTCCCA 1301
QY 372 GGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCCCTACCA 431
Db 1302 GGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCCCTACCA 1361
QY 432 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGAGTGGGAGGCTGA 491
Db 1362 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGAGTGGGAGGCTGA 1421
QY 492 AGACCTTCACTTGTATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCTTCTTCCAGACA 551
Db 1422 AGACCTTCACTTGTATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCTTCTTCCAGACA 1481
QY 552 AGCAGAGAACCACTATGACCAGGACCTTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 611
Db 1482 AGCAGAGAACCACTATGACCAGGACCTTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 1541
QY 612 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGGCCCTGTGAGTACCT 671
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Db 1542 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGGCCCCCTTCAAGCCCTGTGAGTACCT 1601

Qy 672 CTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTGTG 731

Db 1602 CTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTGTG 1661

Qy 732 CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGGCTGCCCCCCTGCCCCCGGTCAA 791

Db 1662 CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGGCTGCCCCCCTGCCCCCGGTCAA 1721

Qy 792 GTTTGTGGTAGGTGCGATTGACGGCGCCAAACACCTTGACTGGCATTTCTGTGGCCTTCT 851

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Qy 852 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC 911

Db 1782 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC 1841

Qy 912 GGGGCTAGGCTGCCGGGCCACTGGGCTTCCTGGCAGTACTTTGGGTCGGAGGCATCGGTGCT 971

Db 1842 GGGGCTAGGCTGCCGGGCCACTGGGCTTCCTGGCAGTACTTTGGGTCGGAGGCATCGGTGCT 1901

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Db 1962 GAAATCCCCCTCCCTGGGAGCGTTCGAGCAGGGGTCCTAGGCTGCCTGGCACTGGCAGG 2021

Qy 1092 GCTGGCGCGCGCACTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCT 1151

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Qy 1152 GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT 1211

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Qy 1272 GCCGCGGGCGACTTTTAGGCGGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT 1331

Db 2202 GCCGCGGGCGACTTTTAGGCGGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT 2261

Qy 1332 CATCTTCGACAGCGGCTCCTCTACTGTCCCGTGGCCCTCCTCAGCTTCGCCCTCCATGCT 1391

Db 2262 CATCTTCGACAGCGGCTCCTCTACTGTCCCGTGGCCCTCCTCAGCTTCGCCCTCCATGCT 2321

Qy 1392 GGGCCTCTTCCCCTGCACGCGCGAGGCCGTCAAGTCTGTCTGCTGGTGGTGTGCCCT 1451

Db 2322 GGGCCTCTTCCCCTGCACGCGCGAGGCCGTCAAGTCTGTCTGCTGGTGGTGTGCCCT 2381

Qy 1452 GCCTGCCTGCCTCAACCCACTGTCTACCTGTCTTTCAACCCCCACTTCGGGGATGACCT 1511

Db 2382 GCCTGCCTGCCTCAACCCACTGTGTACCTGTCTTCAACCCCCACTTCGGGGATGACCT 2441

Qy 1512 TCGGCGGCTTCGGCCCCCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGA 1571

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Db 2562 CATTTGGAAGCTTCTGAAGCTGGGCGGCCCTCGGGCTGGAGACCTATGGCTTCCCCCTC 2621

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Db 2622 AGTGACCTCATCTCCTGTACGACGCCAGGGGCCCCAGGCTGGAGGGCAGCCATTGTGT 2681

Qy 1752 AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTGCT 1811

Db 2682 AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTGCT 2741

Qy 1812 GAGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGGCTTTTCAGCC 1871

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Qy 1872 CTCTGGCTTGGCCTTTGCTTCACACGTG 1899

Db 2802 CTCTGGCTTGGCCTTTGCTTCACACGTG 2829

RESULT 12

US-10-176-847-89

; Sequence 89, Application US/10176847

; Publication No. US20030068636A1

; GENERAL INFORMATION:

; APPLICANT: Veiby, Petter Ole

; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR

; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST

; TITLE OF INVENTION: AND OVARIAN CANCER

; FILE REFERENCE: MRI-039

; CURRENT APPLICATION NUMBER: US/10/176,847

; CURRENT FILING DATE: 2002-06-21

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 89

; LENGTH: 3438

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-176-847-89

Query Match 92.4%; Score 1754.4; DB 14; Length 3438;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1766; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 132 AGCGGCTCCAACACACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG 191

Db 1187 ATCGGCTCCAACACACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG 1245

Qy 192 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCCT 251

Db 1246 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCCT 1305

Qy 252 CTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTGACCACACTGCC 311

Db 1306 CTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTGACCACACTGCC 1365

Qy 312 CCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA 371

Db 1366 CCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA 1425

Qy 372 GGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCCCTACCA 431

Db 1426 GGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCCCTACCA 1485

Qy 432 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGTGA 491

Db 1486 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGTGA 1545

Qy 492 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGSCCCTGGGCCTCCTTGCCAGACA 551

Db 1546 AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGSCCCTGGGCCTCCTTGCCAGACA 1605

Qy 552 AGCAGAGAACCACCTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 611

Db 1606 AGCAGAGAACCACCTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 1665

Qy 612 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 671

Db 1666 GCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGGCCCTGTGAGTACCT 1725

QY 312 CCTGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGAAACCTTGCTCTCTCCA 371
Db 1368 CCTGGCTGGACTTGGGGCTTGATGCACTGAAGCTCAAAGGAAACCTTGCTCTCTCCA 1427
QY 372 GGCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCCCTACCA 431
Db 1428 GGCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCCCTACCA 1487
QY 432 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGCTGA 491
Db 1488 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGCTGA 1547
QY 492 AGACCTTCACTTGAATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCTCCTTGCCAGACA 551
Db 1548 AGACCTTCACTTGAATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCTCCTTGCCAGACA 1607
QY 552 AGCAGAGAAACCACTATGACCAAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 611
Db 1608 AGCAGAGAAACCACTATGACCAAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 1667
QY 612 GCCACACCCAGTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 671
Db 1668 GCCACACCCAGTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 1727
QY 672 CTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG 731
Db 1728 CTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG 1787
QY 732 CAATGGACTGGTGTGCTGCTGACCGTGTTCGCTGGCGGCTGCCCCCTGCCCCCGGTCAA 791
Db 1788 CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGCTGCCCCCTGCCCCCGGTCAA 1847
QY 792 GTTTGTGGTAGGTGCGATTGCAGGCGCCAAACACCTTGACTGGCATTTCCGTGSCCTTCT 851
Db 1848 GTTTGTGGTAGGTGCGATTGCAGGCGCCAAACACCTTGACTGGCATTTCCGTGSCCTTCT 1907
QY 852 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC 911
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QY 972 GCTGCTCACTCTGGCCGCAGTGCAGTGCAGCGTCTCCGTCTCTGTGTCGGGCCTATGG 1031
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QY 1032 GAAATCCCCCTCCCTGGGCGAGCGTTTCGAGCAGGGGTCTAGGCTGCCTGGCACTGSCAGG 1091
Db 2088 GAAATCCCCCTCCCTGGGCGAGCGTTTCGAGCAGGGGTCTAGGCTGCCTGGCACTGSCAGG 2147
QY 1092 GCTGGCCGCGCACTGCCCTGGCCCTCAGTGGGAGAATACGGGGCCCTCCCCACTCTGCCT 1151
Db 2148 GCTGGCCGCGCACTGCCCTGGCCCTCAGTGGGAGAATACGGGGCCCTCCCCACTCTGCCT 2207
QY 1152 GCCCTACGGCCCACTGAGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT 1211
Db 2208 GCCCTACGGCCCACTGAGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT 2267
QY 1212 GATGAACTCCTTCTGTTTCTGGTCTGTGGCCGGTGCCCTACATCAAACGTGACTGTGACCT 1271
Db 2268 GATGAACTCCTTCTGTTTCTGGTCTGTGGCCGGTGCCCTACATCAAACGTGACTGTGACCT 2327
QY 1272 GCCCGGGGCGACTTTGAGGCGGTGTGGGACTGCGGCCATGGTGAGGCACGTGGCCTGGCT 1331
Db 2328 GCCCGGGGCGACTTTGAGGCGGTGTGGGACTGCGGCCATGGTGAGGCACGTGGCCTGGCT 2387
QY 1332 CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCCTCCATGCT 1391
Db 2388 CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCCTCCATGCT 2447
QY 1392 GGGCCCTCTTCCCTGTACGCGCCGAGGCCGTCAAAGTCTGTCTCTCTGTGGTGTGCGCCCT 1451

Db 2448 GGGCCTCTTCCCTGTACGCGCCGAGGCCGTCAAGTCTGTCTGTGGTGTGCTGCCCT 2507
QY 1452 GCCTGCCTGCCTCAACCCACTGTGTACCTGTCTTCAACCCCCACACTTCCGGGATGACCT 1511
Db 2508 GCCTGCCTGCCTCAACCCACTGTGTACCTGTCTTCAACCCCCACACTTCCGGGATGACCT 2567
QY 1512 TCGGGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGCTGCGGCCGGGA 1571
Db 2568 TCGGGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGCTGCGGCCGGGA 2627
QY 1572 GCTGGAGAAAGACTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGATCT 1631
Db 2628 GCTGGAGAAAGACTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGATCT 2687
QY 1632 CATTCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCCTC 1691
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QY 1692 AGTGACCTCATCTCCTGTTCAGCAGCCAGGGGCCCCAGGCTGGAGGGCAGCCATGTGT 1751
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QY 1752 AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTCCATGGATGGAGAACTGCTGT 1811
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QY 1812 GAGGGCAGAGGGATCTACCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGGCTTTCAGCC 1871
Db 2868 GAGGGCAGAGGGATCTACCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGGCTTTCAGCC 2927
QY 1872 CTCTGGCTTGGCCTTTGCTTCACACGTG 1899
Db 2928 CTCTGGCTTGGCCTTTGCTTCACACGTG 2955

RESULT 14

US-09-851-595-10
; Sequence 10, Application US/09851595
; Publication No. US20030166047A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/09/851,595
; CURRENT FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 3492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)...(3004)
US-09-851-595-10

Query Match 92.4%; Score 1754.4; DB 10; Length 3492;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1766; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 132 AGCGGCCTCCAACAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG 191
Db 1238 ATCGGCCTCCAACAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG 1296
QY 192 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTCAGGCCTT 251
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QY 252 CTCCACCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACGACTGACCACACTGCC 311
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1357 CTCACCTTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACGACTGACCACACTGCC 1416
QY 312 CCTGGCTGGACTTGGGGCTTGATGCACTGAAGCTCAAAAGGGAACCTTGCTCTCTCCCA 371
Db |||||
1417 CCTGGCTGGACTTGGGGCTTGATGCACTGAAGCTCAAAAGGGAACCTTGCTCTCTCCCA 1476
QY 372 GGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCTTACCA 431
Db |||||
1477 GGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCTTACCA 1536
QY 432 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCAGTGGAGGCTGA 491
Db |||||
1537 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCAGTGGAGGCTGA 1596
QY 492 AGACCTTACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCCTCCTTGGCCAGACA 551
Db |||||
1597 AGACCTTACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCCTCCTTGGCCAGACA 1656
QY 552 AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGACTCAAA 611
Db |||||
1657 AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGACTCAAA 1716
QY 612 GCCACACCCCACTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCCTGTGAGTACCT 671
Db |||||
1717 GCCACACCCCACTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCCTGTGAGTACCT 1776
QY 672 CTTTGAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG 731
Db |||||
1777 CTTTGAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG 1836
QY 732 CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGCCCTGCCCCCCTGCCCGGTCAA 791
Db |||||
1837 CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGCCCTGCCCCCCTGCCCGGTCAA 1896
QY 792 GTTGTGTGATGCTGATGAGGCGCCAAACCTTGACTGGCATTTCTCTGTGGCCTTCT 851
Db |||||
1897 GTTGTGTGATGCTGATGAGGCGCCAAACCTTGACTGGCATTTCTCTGTGGCCTTCT 1956
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Db |||||
1957 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTTGAGTACGGAGCCCGCTGGGAGAC 2016
QY 912 GGGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGGTCGGAGGCATCGGTGCT 971
Db |||||
2017 GGGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGGTCGGAGGCATCGGTGCT 2076
QY 972 GCTGCTCACTCTGGCCGACGTGCAGTGCAGCGTCTCCGTCTCTCTGTGTCGGGCCCTATGG 1031
Db |||||
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QY 1032 GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCCTGGCACTGGCAGG 1091
Db |||||
2137 GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCCTGGCACTGGCAGG 2196
QY 1092 GCTGGCCCGCCACTGCCCCCTGGCCCTCAGTGGGAGAAATACGGGGCCCTCCCACCTCTGCCT 1151
Db |||||
2197 GCTGGCCCGCCACTGCCCCCTGGCCCTCAGTGGGAGAAATACGGGGCCCTCCCACCTCTGCCT 2256
QY 1152 GCCCTACGCCGCCACTGAGGGTCAGCCAGCAGCCCTGGGCTTCAACCGTGGCCCTGGTGAT 1211
Db |||||
2257 GCCCTACGCCGCCACTGAGGGTCAGCCAGCAGCCCTGGGCTTCAACCGTGGCCCTGGTGAT 2316
QY 1212 GATGAACCTCCTTCTGTTTCTGGTCTGGGCCGTGAGGACCTTACATCAAACTGTACTGTGACCT 1271
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2317 GATGAACCTCCTTCTGTTTCTGGTCTGGGCCGTGACCTTACATCAAACTGTACTGTGACCT 2376
QY 1272 GCCCGGGCGGACTTGTAGGCCCGTGTGGGACTGCGCCCATGGTGAGGCAGTGGCCCTGGCT 1331
Db |||||
2377 GCCCGGGCGGACTTGTAGGCCCGTGTGGGACTGCGCCCATGGTGAGGCAGTGGCCCTGGCT 2436
QY 1332 CATCTTCGACAGCGGGCTCCTCTACTGTCCCCGTGGCCCTTCCTCAGCTTCGCCCTCCATGCT 1391

Db |||||
2437 CATCTTCGACAGCGGGCTCCTCTACTGTCCGTGGCCTTCTCAGCTTCGCTCCATGCT 2496
QY 1392 GGGCCTCTTCCCTGTACGCCCGGAGGCCGTCAAGTCTGTCTGTGGTGGTGTGCCCT 1451
Db |||||
2497 GGGCCTCTTCCCTGTACGCCCGGAGGCCGTCAAGTCTGTCTGTGGTGGTGTGCCCT 2556
QY 1452 GCCTGCCTCCTCAACCCACTGCTGTACCTGTACCTGTCTTCAACCCCCACTTCCGGGATGACCT 1511
Db |||||
2557 GCCTGCCTGCCTCAACCCACTGCTGTACCTGTCTTCAACCCCCACTTCCGGGATGACCT 2616
QY 1512 TCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGA 1571
Db |||||
2617 TCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGA 2676
QY 1572 GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGATCT 1631
Db |||||
2677 GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGATCT 2736
QY 1632 CATTCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCCTC 1691
Db |||||
2737 CATTCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCCTC 2796
QY 1692 AGTGACCCCTCATCTCCTGTACAGCAGCCAGGGGCCCTCAGGCTGGAGGGCAGCCATTGTGT 1751
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QY 1812 GAGGCAGAGGGATCTAGCCAGCAGGTGAGGCTTGTCAAGGGGTGCGGCTTTCAGCC 1871
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RESULT 15

US-10-664-667-10
; Sequence 10, Application US/10664667
; Publication No. US20040058377A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: MNI-080CP
; CURRENT APPLICATION NUMBER: US/10/664,667
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/851,595
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 09/556,588
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: 60/132,896
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 3492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104) ... (3004)
US-10-664-667-10

Query Match 92.4%; Score 1754.4; DB 17; Length 3492;
Best local Similarity 99.9%; Pred. No. 0;
Matches 1766; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 132 AGCGGCTTCCAAACACACCGCATCTGGGAATTGGAGCTNGACACCTTCAGCCAGCTGAG 191
| |||||

Db	1238	ATCGGCCTCCAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG	1296
QY	192	CTCCCTGCAAGCCCTGGATCTTAGCTGGAAAGCCATCCGGTCCATCCACCCCTGAGCCCTT	251
Db	1297	CTCCCTGCAAGCCCTGGATCTTAGCTGGAAAGCCATCCGGTCCATCCACCCCTGAGGCCTT	1356
QY	252	CTCCACCCTGCACTCCCTGGTCAAGCTGGACCTGACAGAACACAGCTGACCACACTGCC	311
Db	1357	CTCCACCCTGCACTCCCTGGTCAAGCTGGACCTGACAGAACACAGCTGACCACACTGCC	1416
QY	312	CCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA	371
Db	1417	CCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA	1476
QY	372	GGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCA	431
Db	1477	GGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCA	1536
QY	432	GTGCTGTCCCTATGSGGATGTGTGCCAGCTTCTTCAAGSCCTCTGSGCAGTGGGAGCTGA	491
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QY	492	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTCTGGCCTCCTTGCCAGACA	551
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Db	2137	GAAGTCCCCCTCCCTGGGACGGTTTCGAGCAGGGGTCTAGGCTGCCCTGGCACTGGCAGG	2196
QY	1092	GCTGGCGCGCACTGCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCCT	1151
Db	2197	GCTGGCGCGCACTGCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCCT	2256
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QY	1272	GCCGCGGGCGACTTTGAGGCCGTGTGGACTGGSCATGGTGAGGCACGTGGCTGGCT	1331
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QY	1332	CATCTTCGCAGACGGGCTCCTTACTGTCCCGTGGCCTTCTCAGCTTCGCCCTCCATGCT	1391
Db	2437	CATCTTCGCAGACGGGCTCCTTACTGTCCCGTGGCCTTCTCAGCTTCGCCCTCCATGCT	2496
QY	1392	GGGCTCTTCCCTGTCAAGCCCGAGGGCCGTCAAGTCTGTCTGCTGGTGGTGTGCCCT	1451
Db	2497	GGGCTCTTCCCTGTCAAGCCCGAGGGCCGTCAAGTCTGTCTGCTGGTGGTGTGCCCT	2556
QY	1452	GCCTGCCTGCCTCAACCCACTGTGTACCTGTCTTCAACCCCCACTTCCCGGATGACCT	1511
Db	2557	GCCTGCCTGCCTCAACCCACTGTGTACCTGTCTTCAACCCCCACTTCCCGGATGACCT	2616
QY	1512	TCGGCGGCTTCGGCCCCCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTCGGCCGGGA	1571
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QY	1632	CATTCTGGAAGCTTCTGAAGCTGGCGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCTC	1691
Db	2737	CATTCTGGAAGCTTCTGAAGCTGGCGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCTC	2796
QY	1692	AGTGACCTCATCTCTGTCAAGCCAGGGGGCCCCAGGCTGGAGGGCAGCCATTGTGT	1751
Db	2797	AGTGACCTCATCTCTGTCAAGCCAGGGGGCCCCAGGCTGGAGGGCAGCCATTGTGT	2856
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Db	2857	AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCTCCATGGATGGAGAACTGCTGCT	2916
QY	1812	GAGGCGAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGGCTTTCAGCC	1871
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Job time : 724.624 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 11:17:08 ; Search time 5432.4 Seconds
(without alignments)
16938.466 Million cell updates

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Perfect score: 1899
Sequence: 1 aatacgactcactataggga.....tggcctttgcttcacacgtg 1899

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:★

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11: gb_sts:
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	%				
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2	1898	99.9	2486	6	AX301825	AX301825	Sequence
3	1820.4	95.9	2322	6	AX098217	AX098217	Sequence
4	1811.6	95.4	3451	6	QX840814	QX840814	Sequence
5	1754.4	92.4	2208	6	AX301830	AX301830	Sequence
6	1754.4	92.4	2711	6	AX301828	AX301828	Sequence
7	1754.4	92.4	2901	6	AX301833	AX301833	Sequence
8	1754.4	92.4	3325	9	AY358119	AY358119	Homo sapi
9	1754.4	92.4	3492	6	AX301831	AX301831	Sequence
10	1752.8	92.3	3119	6	AX549295	AX549295	Sequence
11	1752.8	92.3	3119	9	AB049405	AB049405	Homo sapi
12	1751.2	92.2	3429	6	AX451929	AX451929	Sequence
13	1749.6	92.1	2487	6	AX926297	AX926297	Sequence
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17	1746.4	92.0	3349	6	AX926300	AX926300	Sequence
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DEFINITION	Sequence 6 from Patent WO0185768.				
ACCESSION	AX301827				
VERSION	AX301827.1	GI:17382885			
KEYWORDS	.	-			
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1				
AUTHORS	Gu.W.				

Novel g-protein coupled receptors and uses therefor
Patent: WO 0185768-A 6 15-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)

Location/Qualifiers

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ORIGIN

Query Match 99.9%; Score 1898; DB 6; Length 1899;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1899;		Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Db	1	AATACGACTCACTATAGGGAAGCTGGTACGCCTGCAGGTACCGTCCGGAATTCCCGGG 60							
QY	61	TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCT 120							
Db	61	TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCT 120							
QY	121	CTTGCTGCCCTAGCGGCCTCCAAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTC 180							
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QY	241	CCTGAGGCCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTG 300							
Db	241	CCTGAGGCCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTG 300							
QY	301	ACCACACTGCCCCCTGGCTGGACTTGGGGCTTGATGCACTGAAGCTCAAAGSGGAACCTT 360							
Db	301	ACCACACTGCCCCCTGGCTGGACTTGGGGCTTGATGCACTGAAGCTCAAAGSGGAACCTT 360							
QY	361	GCTCTCTCCAGGCCCTTCTCCAAGGACAGTTTCCAAAACTGAGGATCCTGAGGTTGCCT 420							
Db	361	GCTCTCTCCAGGCCCTTCTCCAAGGACAGTTTCCAAAACTGAGGATCCTGAGGTTGCCT 420							
QY	421	TATGCCCTACAGTGTCTCCCTATGGGATGTGTCCAGCTTCTTCAAGGCCTCTGGGCAG 480							
Db	421	TATGCCCTACAGTGTCTCCCTATGGGATGTGTCCAGCTTCTTCAAGGCCTCTGGGCAG 480							
QY	481	TGGGAGGCTGAAGACCTTACCTTGATGATGAGGAGTCTTCAAAAGGCCCTTGGGCCCTC 540							
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QY	541	CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG 600							
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QY	661	TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTC 720							
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QY	721	TCCGTGCTCTGCAATGGAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTC 780							
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QY	781	CCCCCGGTCAAGTTTGTGTAGGTGCGATTGCAGSGCGCAACACCTTGACTGGCATTTCC 840							
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Db	841	TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCC 900							
QY	901	CGCTGGGAGACGGGGCTTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTCGGAG 960							
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QY	961	GCATCGGTGCTGCTCACTCTGGCCGCACTGCAAGTGCAGCGTCTCCGTCTCCTGTGTC 1020							
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QY	1021	CGGGCCTATGGGAAGTCCCCCTCCCTGGGACGCTTCGAGCAGGGGTCCCTAGGCTGCCTG 1080							
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QY	1081	GCACTGGCAGGGCTGGCCGCGCACTGCCCTGGCCCTCAGTGGGAGATACGGGGCCTCC										1140
Db	1081	GCACTGGCAGGGCTGGCCGCGCACTGCCCTGGCCCTCAGTGGGAGATACGGGGCCTCC										1140
QY	1141	CCACTCTGCCTGCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTACCCGTG										1200
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QY	1201	GCCCTGGTGATGATGAACCTCTTCTGTCTTCTGGTCTGTGGCCGTGCCTACATCAAACTG										1260
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QY	1261	TACTGTGACCTGCCCGGGGCGACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGCAC										1320
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QY	1321	GTGGCCTGGCTCATCTTCGCAGACGGGCTCTCTACTGTCCCCTGGCCCTTCTCAGCTTC										1380
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QY	1501	CGGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCTAGCCTATGCT										1560
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QY	1561	GCGGCCGGGAGCTGGAGAAGACTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT										1620
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QY	1621	GATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGCGGCCCTTGGCTGGAGACCTAT										1680
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QY	1681	GGCTTCCCTCAGTGACCTCATCTCCTGTCTCAGCAGCCAGGGGCCCCAGGCTGGAGGGC										1740
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QY	1741	AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTCCATGGATGGA										1800
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JOURNAL												
Patent: WO 0185768-A 4 15-NOV-2001;												

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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ORIGIN		
Query Match 99.9%; Score 1898; DB 6; Length 2486;		
Best Local Similarity 100.0%; Pred. No. 0;		
Matches 1899; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Db	2	AATACGACTCACTATAGGGAAGCTGGGTACGCTGCAGGTACCGGTCCGGAATTC
Qy	61	TCGACCCACGCTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGTCCATCCAGCCTT
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Qy	121	CTTGCTGCCCTAGCGGCCCTCCAAACACCGCATCTGGGAAATTGGAGCTNGACACCTTC
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Qy	181	AGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCAC
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Qy	241	CCTGAGGCCCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCATG
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Qy	301	ACCACACTGCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT
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Qy	541	CTTGCCAGACAAGCAGAGAACCCTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG
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Qy	1441	GTGCTGCCCTGCCCTGCCTCAACCCACTGTGTGTACCTGTCTTCAACCCCCACTTC
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Qy	1501	CGGGATGACCTTCGGCGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTTAGCCTATGCT
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Qy	1621	GATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGCGGGCCCCCTGGGCTGGAGACCTAT
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Qy	1681	GGCTTCCCCTCAGTGACCTCATCTCTGTGACGACGACGGGGCCCCCAGGCTGGAGGGC
Db	1682	GGCTTCCCCTCAGTGACCTCATCTCTGTGACGACGACGGGGCCCCCAGGCTGGAGGGC
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Db	1742																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														</
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Db	540	CTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCCCTTCAAGCCCTGTGA	599
QY	666	GTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGTCTCCGT	725
Db	600	GTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGTCTCCGT	659
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Db	720	GGTCAAAGTTTGTGTAGGTGCGATTGACGGCGCAACACCTTGACTGGCAFTTCTCTGTGG	779
QY	846	CCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTG	905
Db	780	CCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTG	839
QY	906	GGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGGTGGAGGCATC	965
Db	840	GGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGGTGGAGGCATC	899
QY	966	GGTGTGTGTGTCACTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCTGTGTCCGGGC	1025
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QY	1026	CTATGGGAAGTCCCTCCCTGGGCAGCGTTCGAGCAGGGTCCTAGGTCGCTGGCACT	1085
Db	960	CTATGGGAAGTCCCTCCCTGGGCAGCGTTCGAGCAGGGTCCTAGGTCGCTGGCACT	1019
QY	1086	GGCAGGGCTGGCCCGCCACTGCCCTGGCCTCAGTGGGAGAATACGGGGCCTTCCCCACT	1145
Db	1020	GGCAGGGCTGGCCCGCCACTGCCCTGGCCTCAGTGGGAGAATACGGGGCCTTCCCCACT	1079
QY	1146	CTGCTGCCCTACCGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTACCGTGGCCCT	1205
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QY	1206	GGTGATGATGAATCCTTCTGTTTCTGTGTCGTGGCCGTGCCCTACATCAAACCTGTA	1265
Db	1140	GGTGATGATGAATCCTTCTGTTTCTGTGTCGTGGCCGTGCCCTACATCAAACCTGTA	1199
QY	1266	TGACCTGCCCGCGGGCGACTTTAGGCCGTGTGGACTGCGCCATGTTGAGGCACGTGGC	1325
Db	1200	TGACCTGCCCGCGGGCGACTTTAGGCCGTGTGGACTGCGCCATGTTGAGGCACGTGGC	1259
QY	1326	CTGGCTCATCTTGCAGACGGGCTCCTTACTGTCCCCTGGGCTTCTCAGCTTGCCTC	1385
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QY	1386	CATGTGGGCTCTTCCCTGTCAACCCAGGCGCGTCAAGTCTGTCTGTGGTGGTGTCT	1445
Db	1320	CATGTGGGCTCTTCCCTGTCAACCCAGGCGCGTCAAGTCTGTCTGTGGTGGTGTCT	1379
QY	1446	GCCCCCTGCTGCTGCCCTCAACCCACTGCTGTACCTGTCTTCAACCCCACTTCCGGGA	1505
Db	1380	GCCCCCTGCTGCTGCCCTCAACCCACTGCTGTACCTGTCTTCAACCCCACTTCCGGGA	1439
QY	1506	TGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGACTCAGGGCCCCCTAGCCTATGTCGGC	1565
Db	1440	TGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGACTCAGGGCCCCCTAGCCTATGTCGGC	1499
QY	1566	CGGGAGCTGGAGAAAGACTCCTCTGTGATTTACCCAGGCCCTGGTAGCCTTCTCTGATGT	1625
Db	1500	CGGGAGCTGGAGAAAGACTCCTCTGTGATTTACCCAGGCCCTGGTAGCCTTCTCTGATGT	1559
QY	1626	GGATCTCATCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGGCTT	1685

Db	1560	GGATCTCATTTCTGGAAGCTTCTGAAGCTGGGGGGCCCCCTGGGCTGGAGACCTATGGCTT	1619
Qy	1686	CCCCCTAGTGACCCTCATCTCCTGTGAGCAGCCAGGGGCCCCCAGGCTGGAGGCAGCCA	1745
Db	1620	CCCCCTAGTGACCCTCATCTCCTGTGAGCAGCCAGGGGCCCCCAGGCTGGAGGCAGCCA	1679
Qy	1746	TTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACT	1805
Db	1680	TTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACT	1739
Qy	1806	GCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTGAGGGGTGGCGGCTT	1865
Db	1740	GCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTGAGGGGTGGCGGCTT	1799
Qy	1866	TCAGCCCTCTGGCTTGGCCCTTTGCTTCACACGTG	1899
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RESULT 4			
CQ840814			
LOCUS			
CQ840814			
DEFINITION			
Sequence 4 from Patent WO2004058818.			
ACCESSION			
CQ840814			
VERSION			
CQ840814.1 GI:50838404			
KEYWORDS			
Homo sapiens (human)			
SOURCE			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
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AUTHORS			
Muda,M.			
TITLE			
Spliced variants of lgr6			
JOURNAL			
Patent: WO 2004058818-A 4 15-JUL-2004;			
Applied Research Systems ARS Holding N.V. (AN)			
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ORIGIN			
Query Match			
Best Local Similarity			
Matches 1825; Conservative			
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4; Indels			
1; Gaps			
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Db	1066	GGGGGATGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCTCTTGCTGCC	1125
Qy	130	CTAGCGGCTCCAACACACACCACCTTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTG	189
Db	1126	CTAGCGGCTCCAACACACACCACCTTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTG	1184
Qy	190	AGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCC	249
Db	1185	AGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCC	1244
Qy	250	TTCTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACATG	309
Db	1245	TTCTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACATG	1304

Qy	310	CCCTGGCTGGACTTGGGGGTTGATGCACTGAAGCTCAAAGGGAACCTTGCTCTCTCC	369
Db	1305	CCCTGGCTGGACTTGGGGGTTGATGCACTGAAGCTCAAAGGGAACCTTGCTCTCTCC	1364
Qy	370	CAGGCCTTCTCCAAGGACAGTTTCCAAAACTGAGGATCTTGAGGTGCCTTATGCCTAC	429
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Qy	430	CAGTGTGTCCCTATGGGATGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGAGGCT	489
Db	1425	CAGTGTGTCCCTATGGGATGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGAGGCT	1484
Qy	490	GAAACCTTCACTTGATGAGGAGTCTTCAAAAAAGGCCCTTGGGCCCTCCTTGCCAGA	549
Db	1485	GAAACCTTCACTTGATGAGGAGTCTTCAAAAAAGGCCCTTGGGCCCTCCTTGCCAGA	1544
Qy	550	CAAGCAGAGAACCACTATGACCAGGACCTGGATGAGTCCAGCTGGAGATGGAGGACTCA	609
Db	1545	CAAGCAGAGAACCACTATGACCAGGACCTGGATGAGTCCAGCTGGAGATGGAGGACTCA	1604
Qy	610	AAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTAC	669
Db	1605	AAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTAC	1664
Qy	670	CTCTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGGCATCGTGTGCTCTCCGTGCTC	729
Db	1665	CTCTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGGCATCGTGTGCTCTCCGTGCTC	1724
Qy	730	TGCAATGGACTGGTGTGCTGACCCGTGTTTCGCTGGCGGGCCTGCCCCCTGCCCCGGTC	789
Db	1725	TGCAATGGACTGGTGTGCTGACCCGTGTTTCGCTGGCGGGCCTGCCCCCTGCCCCGGTC	1784
Qy	790	AAGTTTGTGGTAGGTGCGATTGCAGGGCGCCAAACACTTGACTGGCATTTCTGTGGCCTT	849
Db	1785	AAGTTTGTGGTAGGTGCGATTGCAGGGCGCCAAACACTTGACTGGCATTTCTGTGGCCTT	1844
Qy	850	CTAGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCCCTGGGAG	909
Db	1845	CTAGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCCCTGGGAG	1904
Qy	910	ACGGGCTAGGCTGCCGGGCACCTGGCTTCTTGGCAGTACTTGGTTCGGAGGCATCGGTG	969
Db	1905	ACGGGCTAGGCTGCCGGGCACCTGGCTTCTTGGCAGTACTTGGTTCGGAGGCATCGGTG	1964
Qy	970	CTGCTGCTCACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCTCTGTCTCCGGGCTAT	1029
Db	1965	CTGCTGCTCACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCTCTGTCTCCGGGCTAT	2024
Qy	1030	GGGAAGTCCCCCTCCCTGGGAGCGGTTTCGAGCAGGGGTCTTAGGTCCTGGCAGTGGCA	1089
Db	2025	GGGAAGTCCCCCTCCCTGGGAGCGGTTTCGAGCAGGGGTCTTAGGTCCTGGCAGTGGCA	2084
Qy	1090	GGGCTGGCCGCGCAGCTGCCCTGGCCTCAGTGGGAGAAATACGGGGCTCCCCACTTGC	1149
Db	2085	GGGCTGGCCGCGCAGCTGCCCTGGCCTCAGTGGGAGAAATACGGGGCTCCCCACTTGC	2144
Qy	1150	CTGCCCTACGCGCCACCTGAGGGTCAAGCCAGCAGCCCTTGGGCTTACCGTGGCCCTGGTG	1209
Db	2145	CTGCCCTACGCGCCACCTGAGGGTCAAGCCAGCAGCCCTTGGGCTTACCGTGGCCCTGGTG	2204
Qy	1210	ATGATGAACTCCTTCTGTTTCTTGGTCTGGTGGCCGGTGCCTACATCAAACTGTACTGTAC	1269
Db	2205	ATGATGAACTCCTTCTGTTTCTTGGTCTGGTGGCCGGTGCCTACATCAAACTGTACTGTAC	2264
Qy	1270	CTGCCGCGGGCGACTTTGAGGCCCGTGTGGGACTGCGCCATGTGTAGGACACGTGGCCTGG	1329
Db	2265	CTGCCGCGGGCGACTTTGAGGCCCGTGTGGGACTGCGCCATGTGTAGGACACGTGGCCTGG	2324
Qy	1330	CTCATCTTCGACAGCGGCTCCTCTACTGTCCCCTGGGCTTCTCAGCTTCGCCTCCATG	1389
Db	2325	CTCATCTTCGACAGCGGCTCCTCTACTGTCCCCTGGGCTTCTCAGCTTCGCCTCCATG	2384

Qy	1390	CTGGGCGCTCTTCCCTGTACAGCCCGAGGCGGTCAAGTCTGTCTCTGCTGGTGGTGTGCCCC	1449
Db	2385	CTGGGCGCTCTTCCCTGTACAGCCCGAGGCGGTCAAGTCTGTCTCTGCTGGTGGTGTGCCCC	2444
Qy	1450	CTGCGTGCCTGCCTCAACCCACTGTGTACTGCTCTTCAACCCCCCACTTCCGGGATGAC	1509
Db	2445	CTGCGTGCCTGCCTCAACCCACTGTGTACTGCTCTTCAACCCCCCACTTCCGGGATGAC	2504
Qy	1510	CTTCGGCGGCTTCGGCCCCCGGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGCGGCCGGG	1569
Db	2505	CTTCGGCGGCTTCGGCCCCCGGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGCGGCCGGG	2564
Qy	1570	GAGCTGGAGAAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGAT	1629
Db	2565	GAGCTGGAGAAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGAT	2624
Qy	1630	CTCATTTCTGGAAGCTTCTGAAGCTGGCGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCC	1689
Db	2625	CTCATTTCTGGAAGCTTCTGAAGCTGGCGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCC	2684
Qy	1690	TCAGTGACCCTCATCTCCTGTGAGCAGCCAGGGCCCCCAGGCTGGAGGGCAGCCATTGT	1749
Db	2685	TCAGTGACCCTCATCTCCTGTGAGCAGCCAGGGCCCCCAGGCTGGAGGGCAGCCATTGT	2744
Qy	1750	GTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTG	1809
Db	2745	GTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTG	2804
Qy	1810	CTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGTGGCGGCTTTCAG	1869
Db	2805	CTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGTGGCGGCTTTCAG	2864
Qy	1870	CCCTCTGGCTTGGCCTTTGCTTCACACGTG	1899
Db	2865	CCCTCTGGCTTGGCCTTTGCTTCACACGTG	2894

RESULT 5					
AX301830	AX301830	2208 bp	DNA	linear	PAT 30-NOV-2001
DEFINITION	Sequence 9 from Patent WO0185768.				
ACCESSION	AX301830				
VERSION	AX301830.1	GI:17382889			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Gu, W.				
TITLE	Novel g-protein coupled receptors and uses therefor				
JOURNAL	Patent: WO 0185768-A 9 15-NOV-2001;				
	Millennium Pharmaceuticals, Inc. (US)				
FEATURES	Location/Qualifiers				
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ORIGIN		Query Match	92.4%;	Score 1754.4;	DB 6;	Length 2208;
		Best Local Similarity	99.9%;	Pred. No. 0;		
		Matches 1766;	Conservative 0;	Mismatches 1;	Indels 1;	Gaps 1;
Qy	132	AGCGGCTCCACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG	191			
Db	442	ATCGGCTCCACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG	500			
Qy	192	CTCCCTGCAAGCCCTGGATCTTAGCTGGACGCCATCCGGTCCATCCACCTGAGGCCCTT	251			
Db	501	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCCTT	560			
Qy	252	CTCCACCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTGACCACTGCC	311			
Db	561	CTCCACCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTGACCACTGCC	620			
Qy	312	CCTGGCTGGACTTGGGGGCTTGATGCA TCTGAAGCTCAAAGGAACTTGTCTCTCTCCCA	371			
Db	621	CCTGGCTGGACTTGGGGGCTTGATGCA TCTGAAGCTCAAAGGAACTTGTCTCTCTCCCA	680			
Qy	372	GGCCTTCTCCAAAGACAGTTTCCCAAAACTGAGGATCCTGGAGTGCTTATGCCTACCA	431			
Db	681	GGCCTTCTCCAAAGACAGTTTCCCAAAACTGAGGATCCTGGAGTGCTTATGCCTACCA	740			
Qy	432	GTGCTGTCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGSCAGTGGGAGGCTGA	491			
Db	741	GTGCTGTCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGSCAGTGGGAGGCTGA	800			
Qy	492	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCCCTGGGCCCTCTTGCCAGACA	551			
Db	801	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCCCTGGGCCCTCTTGCCAGACA	860			
Qy	552	AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA	611			
Db	861	AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA	920			
Qy	612	GCCACACCCCACTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	671			
Db	921	GCCACACCCCACTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	980			
Qy	672	CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGGGCCCATCGTGTGCTCTCCGTCCTG	731			
Db	981	CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGGGCCCATCGTGTGCTCTCCGTCCTG	1040			
Qy	732	CAATGGACTGGTGTCTGACCCGTGTTCCGTGGCGGGCCCTGCCCCCTGCCCCCGGTCAA	791			
Db	1041	CAATGGACTGGTGTCTGACCCGTGTTCCGTGGCGGGCCCTGCCCCCTGCCCCCGGTCAA	1100			
Qy	792	GTTTGTGTTAGGTGCGATTGACGGCGCCAAACACCTTGACTGGCATTTCTGTGGCCTTCT	851			
Db	1101	GTTTGTGTTAGGTGCGATTGACGGCGCCAAACACCTTGACTGGCATTTCTGTGGCCTTCT	1160			
Qy	852	AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	911			
Db	1161	AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	1220			
Qy	912	GGGGCTAGGCTGCCGGGCCACTGGCTTCTGGCAGTACTTGGGTCGAGGCGCATCGGTGCT	971			
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Qy	1032	GAAGTCCCCCTCCCTGGGCAGCGTTCCAGCAGGGGTCCCTAGGCTGCCTGGCACTGGCAGG	1091			
Db	1341	GAAGTCCCCCTCCCTGGGCAGCGTTCCAGCAGGGGTCCCTAGGCTGCCTGGCACTGGCAGG	1400			

QY	1092	GCTGGCCGCGCACTGCCCTGGCCTCAGTGGGAGAAATACGGGGGCTCCCCACTCTGCCT	1151
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QY	1152	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTACCCGTGGCCCTGGTGAT	1211
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QY	1212	GATGAACCTCTTCTGTTTCTGTGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGACCT	1271
Db	1521	GATGAACCTCTTCTGTTTCTGTGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGACCT	1580
QY	1272	GCCGGGGCGGACCTTTAGGGCCGTGTGGGACTGCGCCATGTTGAGGCACGTGGCCTGGCT	1331
Db	1581	GCCGGGGCGGACCTTTAGGGCCGTGTGGGACTGCGCCATGTTGAGGCACGTGGCCTGGCT	1640
QY	1332	CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCCTCCATGCT	1391
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QY	1392	GGGCTCTTCCCTGTTCACGCCCGAGSCCGTCAAGTCTGTCTCTGTTGGTGGTGTGCCCT	1451
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QY	1452	GCCTGCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCACTTCCGGGATGACCT	1511
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QY	1512	TCGGCGGCTTCGGCCCCCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTCGGCCCGGGA	1571
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QY	1572	GCTGGAGAAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT	1631
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QY	1632	CATTCTGGAAGCTTCTGAAGCTGGCGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCCTC	1691
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QY	1692	AGTGACCTCATCTCCTGTTCAGCAGCCAGGGGCCCCAGGCTGGAGGGCAGCCATTGTGT	1751
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QY	1752	AGAGCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT	1811
Db	2061	AGAGCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT	2120
QY	1812	GAGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGTGGCGGCTTTCAGCC	1871
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QY	1872	CTCTGGCTTGGCCTTTGCTTTCACACGTG	1899
Db	2181	CTCTGGCTTGGCCTTTGCTTTCACACGTG	2208

RESULT 6					
AX301828					
LOCUS	AX301828	2711 bp	DNA	linear	PAT 30-NOV-2001
DEFINITION	Sequence 7 from Patent WO0185768.				
ACCESSION	AX301828				
VERSION	AX301828.1	GI:17382887			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1				
AUTHORS	Gu, W.				
TITLE	Novel g-protein coupled receptors and uses therefor				
JOURNAL	Patent: WO 0185768-A 7 15-NOV-2001;				
	Millennium Pharmaceuticals, Inc. (US)				

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ORIGIN

Query Match	92.4%;	Score 1754.4;	DB 6;	Length 2711;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1766;	Conservative 0;	Mismatches 1;	Indels 1;	Gaps 1;
QY	132	AGCGGCTTCCAAACACACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG	191	
Db	442	ATCGGCTTCCAAACACACACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG	500	
QY	192	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCTT	251	
Db	501	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCTT	560	
QY	252	CTCCACCTTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTGACCACTGCC	311	
Db	561	CTCCACCTTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTGACCACTGCC	620	
QY	312	CCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA	371	
Db	621	CCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA	680	
QY	372	GGCCTTCTCCAAGGACAGTTTCCCAAAACCTGAGGATCCTGGAGGTGCCTTATGCCTACCA	431	
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ACCESSION AX301833
VERSION AX301833.1 GI:17382893
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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ORIGIN

Query Match 92.4%; Score 1754.4; DB 6; Length 2901;
Best local Similarity 99.9%; Pred. No. 0;
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VERSION AY358119.1 GI:37181343
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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3325)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
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Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
12975309
REFERENCE 2 (bases 1 to 3325)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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ORIGIN

Query Match		92.4%;	Score 1754.4;	DB 9;	Length 3325;
Best Local Similarity		99.9%;	Pred. No. 0;		
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Burner,G.C., Roush,C.L. and Brown,J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 580 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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AB049405

LOCUS

DEFINITION

AB049405

AB049405.1 GI:13447609

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

Okaze,H., Hayashi,A., Kozuma,S. and Saito,T.

AUTHORS

TITLE

a member of g-protein coupled receptor family

JOURNAL

Published Only in Database (2001)

REFERENCE

2 (bases 1 to 3119)

Okaze,H., Hayashi,A., Kozuma,S. and Saito,T.

AUTHORS

TITLE

Direct Submission

JOURNAL

Submitted (27-SEP-2000) Toshiyuki Saito, National Institute of Radiological Sciences, Genome Research Group; Anagawa 4-9-1, Chiba,Inage-ku, Chiba 263-8555, Japan (E-mail:t_saito@nirs.go.jp, Tel:81-43-206-3135, Fax:81-43-251-9818)

FEATURES

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VERSION AX451929.1 GI:21698752
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Baughn,M.R., Graul,R.C., Walia,N.K., Gandhi,A.R., Hafalia,A.J.,
Ramkumar,J., Tribouley,C.M., Thornton,M., Kallick,D.A., Yao,M.G.,
Elliott,V.S., Burford,N., Khan,F.A., Yue,H., Lu,Y., Arvizu,C.,
Roopa,R., Nguyen,D.B., Lee,E.A., Lu,D.A., Ison,C.H., Walsh,R.T. and
Policky,J.L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 0226825-A 26 04-APR-2002;
Incyte Genomics, Inc. (US)
FEATURES
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VERSION AX926297.1 GI:40245651
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1
REFERENCE
AUTHORS Zhu,S.C., Chaturvedi,K.C., Ketchum,K.C., di Francesco,V.C. and
Beasley,E.M.
TITLE Isolated human g-protein coupled receptors, nucleic acid molecules
encoding human gpcr proteins, and uses thereof
JOURNAL Patent: WO 02068651-A 1 06-SEP-2002;
PE Corporation (NY) (US)
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ORIGIN

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VERSION CQ870634.1 GI:52000145
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1
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AUTHORS Aziz,N., Gish,K.C., Wilson,K.E. and Zlotnik,A.
TITLE Methods of diagnosis of cancer, composition and methods of
screening for modulators of cancer
JOURNAL Patent: WO 2004073657-A 43 02-SEP-2004;
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ACCESSION BC047905
VERSION BC047905.1 GI:29126870

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REFERENCE 1 (bases 1 to 3286)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skaleka,U., Smalilus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932

REFERENCE 2 (bases 1 to 3286)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (03-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cdNA Library Preparation: Life Technologies, Inc.
cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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GenCore version 5.1.6
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 - 11: Geneseqn2003ds:*
 - 12: Geneseqn2004as:*
 - 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1898	99.9	1899	6	AAI67923 Human LGR
2	1898	99.9	1899	11	Adn02244 Human par
3	1898	99.9	1899	12	Adk19409 ORF of CD
4	1898	99.9	2486	6	AAI67922 Human LGR
5	1898	99.9	2486	11	Adn02242 Human par
6	1898	99.9	2486	12	Adk19407 cDNA enco
7	1820.4	95.9	2322	5	Aaf98722 Human lat
8	1811.6	95.4	3451	12	ADQ76775 Human LGR
9	1754.4	92.4	2208	6	AAI67925 Human LGR
10	1754.4	92.4	2208	11	Adn02247 Human par
11	1754.4	92.4	2208	12	ADK19412 ORF of pa
12	1754.4	92.4	2711	6	AAI67924 Partial c
13	1754.4	92.4	2711	11	Adn02245 Human par
14	1754.4	92.4	2711	12	ADK19410 Partial c
15	1754.4	92.4	2901	6	AAI67927 Human LGR
16	1754.4	92.4	2901	10	ADK16692 cDNA enco
17	1754.4	92.4	2901	11	Adn02250 Human ful
18	1754.4	92.4	2901	12	ADK19415 ORF of fu
19	1754.4	92.4	3042	10	ADK16698 cDNA enco
20	1754.4	92.4	3325	10	ADD89048 Encoding

21	1754.4	92.4	3438	10	ABT31938 Human bre
22	1754.4	92.4	3443	10	ADD89090 Encoding
23	1754.4	92.4	3492	6	AAI67926 Human LGR
24	1754.4	92.4	3492	11	ADN02248 Human ful
25	1754.4	92.4	3492	12	ADK19413 Full leng
26	1754.4	92.4	3492	12	ADQ15073 Human can
27	1752.8	92.3	2786	10	ADK16710 Human G-p
28	1752.8	92.3	2964	10	ADI21981 Novel hum
29	1752.8	92.3	2988	6	ABZ11841 Human pol
30	1752.8	92.3	2988	12	ADM44359 Novel hum
31	1752.8	92.3	3000	6	AAS98067 Human DNA
32	1752.8	92.3	3042	10	ADC16700 cDNA enco
33	1752.8	92.3	3119	8	ABZ42549 Human G p
34	1751.2	92.2	3429	6	AAD37674 Human G-p
35	1749.6	92.1	2487	6	ADH50804 Human G-p
36	1749.6	92.1	2901	10	ADC16695 cDNA with
37	1749.6	92.1	3042	10	ADC16701 cDNA with
38	1748	92.0	2901	10	ADC16694 cDNA enco
39	1748	92.0	2901	10	ADC16696 cDNA enco
40	1748	92.0	3042	10	ADC16702 cDNA with
41	1748	92.0	3273	11	ADN39801 Cancer/an
42	1748	92.0	3273	13	ADR46630 Cancer-as
43	1748	92.0	3306	12	ADQ76773 Human LGR
44	1748	92.0	3618	10	ADF70543 Orphan re
45	1746.4	92.0	3349	6	ADH50807 Human G-p

ALIGNMENTS

RESULT 1
AAI67923
ID AAI67923 standard; cDNA; 1899 BP.
XX
AC AAI67923;
XX

DT 13-MAR-2002 (first entry)
XX

DE Human LGR6 polypeptide coding sequence (clone fahr).
XX

KW Large G-protein coupled receptor 6; LGR6; GPCR; immunomodulator;
KW anti-HIV; cytostatic; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; neuroleptic; antidepressant; tranquilizer; antimigraine;
KW osteopathic; antiarteriosclerotic; vasotropic; hypotensive; cardiant;
KW antiarrhythmic; anorectic; gene therapy; human; ss.
XX Homo sapiens.

OS Location/Qualifiers
XX
FH 1. .1899
FT /*tag= a
FT /product= "LGR6 polypeptide"
FT /transl_except= (pos: 169. .171, aa: Xaa)
FT /note= "Xaa = unknown"

XX WO200185768-A2.
PN

XX 15-NOV-2001.
PD

XX 08-MAY-2001; 2001WO-US015002.
PF

XX 08-MAY-2000; 2000US-00566588.
PR

XX (MILL-) MILLENNIUM PHARM INC.
PA

XX Gu W;
PI

XX WPI; 2002-055584/07.
DR

XX P-PSDB; AAG66139.
DR

XX Novel isolated large G-protein coupled receptor 6 polypeptide, useful for
diagnosing and treating weight disorder, metabolic disorder, central
nervous system disorder, endocrine disorder and cardiovascular disorder.
PT

XX Example 1; Fig 4; 198pp; English.

PS The invention provides isolated large G-protein coupled receptor 6 (LGR6)

XX polypeptides and polynucleotides encoding them. The LGR6 polypeptides and

CC polynucleotides are useful as targets for developing modulating agents

CC that regulate a variety of cellular process, e.g. neural and endocrine

CC processes, as well as thermogenesis. They are useful for developing novel

CC diagnostic and therapeutic agents for LGR6 associated disorders such as

CC weight disorders (anorexia, obesity), eating disorders, acquired

CC immunodeficiency syndrome (AIDS)-related wasting, cancer-related wasting,

CC metabolic disorders, central nervous system disorders (e.g. Alzheimer's

CC disease, Parkinson's disease, Huntington's disease, Gilles de la

CC Tourette's syndrome, multiple sclerosis, amyotrophic lateral sclerosis,

CC epilepsy, Jakob-Creutzfeldt disease, depression, schizophrenia,

CC obsessive-compulsive disorder, anxiety, panic disorder, migraine),

CC endocrine disorders (hypo and hyperthyroidism, dwarfism, gigantism,

CC acromegaly), and cardiovascular disorders (atherosclerosis, restenosis,

CC hypertension, myocardial infarction, arrhythmia). The LGR6 polypeptides,

CC polynucleotides and antibodies are useful in screening assays, detection

CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),

CC predictive medicine (e.g. diagnostic assays, prognostic assays,

CC monitoring clinical trials and pharmacogenomics), and in methods of

CC treatment (e.g. therapeutic and prophylactic). The present sequence

CC represents a human LGR6 polypeptide coding sequence

XX

SQ Sequence 1899 BP; 302 A; 624 C; 563 G; 409 T; 0 U; 1 Other;

Query Match 99.9%; Score 1898; DB 6; Length 1899;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1899; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATACGACTCACTATAGGGAAGCTGGTACGCCTGCAGGPACCGGTCCGGAATTCOCGGG 60

DB 1 AATACGACTCACTATAGGGAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATTCOCGGG 60

QY 61 TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCTGCCGGTCCATCCAGCCTCT 120

DB 61 TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCTGCCGGTCCATCCAGCCTCT 120

QY 121 CTGTGTCCTAGCGGCCTCCAACACACCGCATCTGSGAAATTGGAGCTNGACACCTTC 180

DB 121 CTGTGTCCTAGCGGCCTCCAACACACCGCATCTGSGAAATTGGAGCTNGACACCTTC 180

QY 181 AGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCAC 240

DB 181 AGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCAC 240

QY 241 CTTGAGGCCTTCTCCACCCCTGCACTCCCTGGTCAAGTGGACCTGACAGAACAGCTG 300

DB 241 CTTGAGGCCTTCTCCACCCCTGCACTCCCTGGTCAAGTGGACCTGACAGAACAGCTG 300

QY 301 ACCACACTGCCCTGGCTGGAATGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 360

DB 301 ACCACACTGCCCTGGCTGGAATGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 360

QY 361 GCTCTCTCCAGGCCTTCTCCAAGGACAGTTTCCCAAAGCTGAGGATCCTGGAGTGCCT 420

DB 361 GCTCTCTCCAGGCCTTCTCCAAGGACAGTTTCCCAAAGCTGAGGATCCTGGAGTGCCT 420

QY 421 TATGCCTACCACTGCTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTTGGGCAG 480

DB 421 TATGCCTACCACTGCTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTTGGGCAG 480

QY 481 TGGGAGGCTGAAGACCTTACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCTC 540

DB 481 TGGGAGGCTGAAGACCTTACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCTC 540

QY 541 CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACTGGATGAGCTCCAGCTGGAGATG 600

DB 541 CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACTGGATGAGCTCCAGCTGGAGATG 600

QY 601 GAGGACTCAAAGCCACACCCCACTGCTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC 660

DB 601 GAGGACTCAAAGCCACACCCCACTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC 660

QY 661 TGTGAGTACCTCTTTGAAAAGCTGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCTC 720

DB 661 TGTGAGTACCTCTTTGAAAAGCTGGGCATCCGCTGGCCGTGTGGGCCATCGTGTGCTC 720

QY 721 TCCGTGCTCTGCAATGGACTGGTGTGCTGTGCTGACCGTGTTCGCTGGCGGCCCTGCCCTG 780

DB 721 TCCGTGCTCTGCAATGGACTGGTGTGCTGTGCTGACCGTGTTCGCTGGCGGCCCTGCCCTG 780

QY 781 CCCCCGGTCAAGTTTGTGTAGGTGCGATTGACGGCGCCAAACACCTTGACTGGCATTTCC 840

DB 781 CCCCCGGTCAAGTTTGTGTAGGTGCGATTGACGGCGCCAAACACCTTGACTGGCATTTCC 840

QY 841 TGTGGCCTTCTAGCCTCAGTCGATGCCCTTGCTTTGGTCAGTTTCTCTGAGTACGGAGCC 900

DB 841 TGTGGCCTTCTAGCCTCAGTCGATGCCCTTGCTTTGGTCAGTTTCTCTGAGTACGGAGCC 900

QY 901 CGCTGGGAGACGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTCCGAG 960

DB 901 CGCTGGGAGACGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTCCGAG 960

QY 961 GCATCGGTGCTGCTGTCTCACTCTGGCCGACGTGCGAGTGCAGCGTCTCCGTCTCTGTGTC 1020

DB 961 GCATCGGTGCTGCTGTCTCACTCTGGCCGACGTGCGAGTGCAGCGTCTCCGTCTCTGTGTC 1020

QY 1021 CGGGCCTATGGGAAGTCCCCCTCCCTGGGACAGCGTTGAGCAGGGGTCTTAGGCTGCCTG 1080

DB 1021 CGGGCCTATGGGAAGTCCCCCTCCCTGGGACAGCGTTGAGCAGGGGTCTTAGGCTGCCTG 1080

QY 1081 GCACCTGGCAGGGCTGGCCCGCACCTGCCCTGGCCCTCAGTGGGAGATACGGGGCCTCC 1140

DB 1081 GCACCTGGCAGGGCTGGCCCGCACCTGCCCTGGCCCTCAGTGGGAGATACGGGGCCTCC 1140

QY 1141 CCACTCTGCTGCCCTACGCGCCACCTGAGGGTCAAGCAGCCCTGGGTTTCAACCTG 1200

DB 1141 CCACTCTGCTGCCCTACGCGCCACCTGAGGGTCAAGCAGCCCTGGGTTTCAACCTG 1200

QY 1201 GCCCTGGTGAATGAATCCTTCTGTCTTCTGGTCTGTGGCCGTGCTTCAATCAAACTG 1260

DB 1201 GCCCTGGTGAATGAATCCTTCTGTCTTCTGGTCTGTGGCCGTGCTTCAATCAAACTG 1260

QY 1261 TACTGTGACCTGCGCGGGCGACTTTGAGSCCGTGTGGACTCGCCCATGGTGAGGCAC 1320

DB 1261 TACTGTGACCTGCGCGGGCGACTTTGAGSCCGTGTGGACTCGCCCATGGTGAGGCAC 1320

QY 1321 GTGGCCTGGCTCATCTTTCGAGACGGGCTCTCTACTGTCCCCTGGCCTTCTCAGCTTC 1380

DB 1321 GTGGCCTGGCTCATCTTTCGAGACGGGCTCTCTACTGTCCCCTGGCCTTCTCAGCTTC 1380

QY 1381 GCCTCCATGCTGGGCCTCTTCCCTGTACGCCCGAGGCCGTCAAAGTCTGTCTGTGGTG 1440

DB 1381 GCCTCCATGCTGGGCCTCTTCCCTGTACGCCCGAGGCCGTCAAAGTCTGTCTGTGGTG 1440

QY 1441 GTGCTGCCCTGCTGCTGCTCCCTCAACCCACTGTGTACCTGTCTTCAACCCCACTTC 1500

DB 1441 GTGCTGCCCTGCTGCTGCTCCCTCAACCCACTGTGTACCTGTCTTCAACCCCACTTC 1500

QY 1501 CGGGATGACCTTCCGGGGCTTCGGCCCGAGGGGACTCAGGGCCCTAGCCTATGCT 1560

DB 1501 CGGGATGACCTTCCGGGGCTTCGGCCCGAGGGGACTCAGGGCCCTAGCCTATGCT 1560

QY 1561 GCGGCCGGGAGCTGGAGAAGAGCTCTGTGATTTACCCAGGCCCTGGTGTGCTCTCT 1620

DB 1561 GCGGCCGGGAGCTGGAGAAGAGCTCTGTGATTTACCCAGGCCCTGGTGTGCTCTCT 1620

QY 1621 GATGTGGATCTATTCTGGAAGCTTCTGAAGCTGGCGGCCCTGGGTGGAGACCTAT 1680

DB 1621 GATGTGGATCTATTCTGGAAGCTTCTGAAGCTGGCGGCCCTGGGTGGAGACCTAT 1680

QY 1681 GGCTTCCCTCAGTGACCTCATCTCTGTGACGAGCCAGGGGCCCTCAGGCTGGAGGGC 1740

Db 1681 GGCTTCCCCTCAGTGACCCCTCATCTCCTGTGTGTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGC 1740

Qy 1741 AGCCATTGTGTAGAGCCAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGA 1800
|||||

Db 1741 AGCCATTGTGTAGAGCCAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGA 1800
|||||

Qy 1801 GAACTGCTGTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGGTGGC 1860
|||||

Db 1801 GAACTGCTGTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGGTGGC 1860
|||||

Qy 1861 GGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTTCACACGTG 1899
|||||

Db 1861 GGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTTCACACGTG 1899
|||||

RESULT 2
ADN02244

ID ADN02244 standard; cDNA; 1899 BP.

XX

AC ADN02244;

XX

DT 17-JUN-2004 (first entry)

XX

DE Human partial large G protein-coupled receptor, LGR6, CDS #1.

XX

Kw Human; ss; large G protein-coupled receptor 6; LGR6; heart failure;
Kw ischaemic heart disease; myocardial infarction; hypertension;
Kw pericarditis; atherosclerosis; hepatic failure; viral hepatitis; cancer;
Kw intracerebral haemorrhage; brain abscess; Alzheimer's disease;
Kw Pick disease; Parkinson's disease; Huntington's disease;
Kw amyotrophic lateral sclerosis; inflammatory bowel disease;
Kw Crohn's disease; benign prostatic hypertrophy;
Kw systemic lupus erythematosus.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .1899

FT /*tag= a

FT /partial

FT /note= "No start or stop codon shown"

FT /product= "Partial LGR6"

XX

PN US2003166047-A1.

XX

PD 04-SEP-2003.

XX

PF 08-MAY-2001; 2001US-00851595.

XX

PR 06-MAY-1999; 99US-0132896P.

PR 08-MAY-2000; 2000US-00566588.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Gu W;

XX

DR WPI; 2003-898067/82.

XX

PT New isolated LGR6 nucleic acids and polypeptides, useful for diagnosing
PT and treating LGR6-mediated disorders, such as myocardial infarction,
PT hypertension, atherosclerosis, viral hepatitis, cancer and/or Alzheimer's
PT disease.

XX

PS Claim 1; SEQ ID NO 6; 145pp; English.

XX

CC The invention relates to an isolated LGR6 (large G protein-coupled
CC receptor) nucleic acid molecule comprising the mouse and human cDNA
CC sequences appearing as ADN02239, ADN02241, ADN02242, ADN02244, ADN02245,
CC ADN02247, ADN02248 and ADN02250. Also included are a host cell or a non-
CC human mammalian host cell containing an LGR6 nucleic acid (and producing
CC LGR6), an isolated LGR6 polypeptide appearing as ADN02240, ADN02243,
CC ADN02246 and ADN02249, an antibody which selectively binds to LGR6, a
CC method for detecting the presence of LGR6 in a sample, a kit (comprising

CC a compound which selectively binds to LGR6, or hybridises to LGR6 nucleic
CC acid, and instructions for use), a method for detecting LGR6 nucleic acid
CC in a sample, a method for identifying a compound which binds to LGR6, a
CC method for modulating the activity of LGR6 and a method for identifying a
CC compound that modulates the activity of LGR6. The methods and
CC compositions of the present invention are useful for diagnosing and
CC treating large G-protein coupled receptor 6 (LGR6)-mediated or -related
CC disorders, such as heart failure, ischaemic heart disease, myocardial
CC infarction, hypertension, pericarditis, atherosclerosis, hepatic failure,
CC viral hepatitis, cancer, intracerebral haemorrhage, brain abscess,
CC Alzheimer's disease, Pick disease, Parkinson's disease, Huntington's
CC disease, amyotrophic lateral sclerosis, inflammatory bowel disease,
CC Crohn's disease, benign prostatic hypertrophy and systemic lupus
CC erythematosus. The present sequence is a partial human CDS for LGR6.

XX

SQ Sequence 1899 BP; 302 A; 624 C; 563 G; 409 T; 0 U; 1 Other;

Query Match 99.9%; Score 1898; DB 11; Length 1899;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1899; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATACGACTCATTATAGGAAAGCTGGTACGCCCTGCAGGTACCGGTCCGGAATCCCGGG 60
|||||

Db 1 AATACGACTCATTATAGGAAAGCTGGTACGCCCTGCAGGTACCGGTCCGGAATCCCGGG 60
|||||

Qy 61 TCGACCCACGGCTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGTCCATCCAGCCTCT 120
|||||

Db 61 TCGACCCACGGCTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGTCCATCCAGCCTCT 120
|||||

Qy 121 CTTGCTGCCCTAGCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTC 180
|||||

Db 121 CTTGCTGCCCTAGCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTC 180
|||||

Qy 181 AGCCAGCTGAGTCTCCCTGCAAGCCCTGGATCTTAGTGGAAACGCCATCCGGTCCATCCAC 240
|||||

Db 181 AGCCAGCTGAGTCTCCCTGCAAGCCCTGGATCTTAGTGGAAACGCCATCCGGTCCATCCAC 240
|||||

Qy 241 CCTGAGGCCCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTTGACAGACAACCAAGCTG 300
|||||

Db 241 CCTGAGGCCCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTTGACAGACAACCAAGCTG 300
|||||

Qy 301 ACCACACTGCCCCCTGGCTGGACTTGGGGCTTGATGTCATCTGAAGCTCAAAGGGAAACCTT 360
|||||

Db 301 ACCACACTGCCCCCTGGCTGGACTTGGGGCTTGATGTCATCTGAAGCTCAAAGGGAAACCTT 360
|||||

Qy 361 GCTCTCTCCCAGGCCCTTCTCCAAGGACAGTTTCCAAAAAAGTGGAGTCTCTGGAGGTGCCT 420
|||||

Db 361 GCTCTCTCCCAGGCCCTTCTCCAAGGACAGTTTCCAAAAAAGTGGAGTCTCTGGAGGTGCCT 420
|||||

Qy 421 TATGCTTACCAGTGTGTCTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCAG 480
|||||

Db 421 TATGCTTACCAGTGTGTCTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCAG 480
|||||

Qy 481 TGGGAGGCTGAAGACCTTCACTTGTATGATGAGGAGTCTTCAAAAAGGCCCTCTGGGCCTC 540
|||||

Db 481 TGGGAGGCTGAAGACCTTCACTTGTATGATGAGGAGTCTTCAAAAAGGCCCTCTGGGCCTC 540
|||||

Qy 541 CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG 600
|||||

Db 541 CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG 600
|||||

Qy 601 GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGGCCCCCTTCAAGCCC 660
|||||

Db 601 GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGGCCCCCTTCAAGCCC 660
|||||

Qy 661 TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGCCCATCGTGTGCTC 720
|||||

Db 661 TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGCCCATCGTGTGCTC 720
|||||

Qy 721 TCCGTGCTCTGCAATGGACTGGTGTGCTGTGACCGTGTTCGCTGGCGGGCCTGCCCCCTG 780
|||||

Db 721 TCCGTGCTCTGCAATGGACTGGTGTGCTGTGACCGTGTTCGCTGGCGGGCCTGCCCCCTG 780
|||||

QY 781 CCCCCGGTCAAGTTTGTGTAGGTGCGATTG CAGGGCCAAACACCTTGACTGGCATTTCC 840
Db |||||||
QY 841 TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCC 900
Db |||||||
QY 901 CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGGTGGAG 960
Db |||||||
QY 961 GCATCGGTGCTGCTCACTCTGGCCGCGCAGTGCAGTCAGCGTCTCCGTCTCCTGTGTC 1020
Db |||||||
QY 1021 CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTGAGCAGGGGTCTTAGGGTGCCTG 1080
Db |||||||
QY 1081 GCACTGGCAGGGCTGGCCGCGCACTGCCCTGGCTCAGTGGAGAATACGGGCTCTCC 1140
Db |||||||
QY 1141 CCACTCTGCCCTAGCCGCCACCTGAGGGTACGCCAGCAGCCCTGGGCTTCACCGTG 1200
Db |||||||
QY 1201 GCCCTGGTGATGATGAACCTCTTCTGTCTTCTGTGTCGTGGCCGGTGCCTACATCAAAC 1260
Db |||||||
QY 1261 TACTGTGACCTGCCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGFTGAGGCAC 1320
Db |||||||
QY 1321 GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTC 1380
Db |||||||
QY 1381 GCCTCCATGCTGGGCTCTTCCCTGTCAAGCCGAGCCCGTCAAGTCTGTCTGCTGGTG 1440
Db |||||||
QY 1441 GTGCTGCCCCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTCAACCCCCACTTC 1500
Db |||||||
QY 1501 CGGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT 1560
Db |||||||
QY 1561 GCGGCCGGGAGCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGTAGCCTTCTCT 1620
Db |||||||
QY 1621 GATGTGGATCTCATTCTGGAAGCTTCTGAAGCTGGCGGGCCCCCTGGGCTGGAGACCTAT 1680
Db |||||||
QY 1681 GGCTTCCCCCTCAGTGACCCTCATCTCCTGTTCAGCAGCCAGGGCCCCCAGGCTGGAGGC 1740
Db |||||||
QY 1741 AGCCATTGTGTAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGA 1800
Db |||||||
QY 1801 GAACTGCTGTAGGGCAGAGGGATCTACGCCAGAGGTGGAGGCTTGTGAGGGGGTGGC 1860
Db |||||||
QY 1861 GGCCTTCAGCCCTCTGGCTTGGCCTTTGCTTCACACGTG 1899

Db 1861 GGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACACGTG 1899
|||
RESULT 3
ADK19409
ID ADK19409 standard; cDNA; 1899 BP.
XX
AC ADK19409;
XX
DT 17-JUN-2004 (first entry)
XX
DE ORF of cDNA encoding human LGR6 polypeptide #1.
XX
KW G-protein coupled receptor; GPCR; large G-protein coupled receptor 6;
KW LGR6; weight disorder; neural disorder; endocrine disorder;
KW cardiovascular disorder; anorectic; anabolic; immunomodulator;
KW neuroprotective; nootropic; antiparkinsonian; anti-HIV; anticonvulsant;
KW antithyroid; osteopathic; cardiant; vasotropic; hypotensive;
KW antiarteriosclerotic; antiarrhythmic; human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..1899
/*tag= a
/partial
/product= "LGR6 polypeptide #1"
/note= "This sequence lacks both start and stop codons"
/transl_except= (pos:169..171,aa:Xaa)
/note= "Xaa= Unknown"
XX
PN US2004058377-A1.
XX
PD 25-MAR-2004.
XX
PF 18-SEP-2003; 2003US-00664667.
XX
PR 06-MAY-1999; 99US-0132896P.
PR 08-MAY-2000; 2000US-00566588.
PR 08-MAY-2001; 2001US-00851595.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gu W;
XX
DR WPI; 2004-268789/25.
DR P-PSDB; ADK19408.
XX
PT New large G-protein coupled receptor 6 nucleic acid molecules and
PT polypeptides, useful for diagnosing, preventing or treating diseases
PT associated with aberrant nucleic acid or protein activity, e.g. obesity,
PT anorexia or cachexia.
XX
PS Claim 2; SEQ ID NO 6; 145pp; English.
XX
CC The present invention relates to the isolation of novel members of the G-
CC protein coupled receptor (GPCR) family designated as large G-protein
CC coupled receptor 6 (LGR6), and the polynucleotide sequences encoding
CC them. The invention also discloses LGR6 fusion proteins, antigenic
CC peptides, anti-LGR6 antibodies, recombinant expression vectors, host
CC cells, and non-human transgenic animals in which an LGR6 gene has been
CC introduced or disrupted. The LGR6 polynucleotide sequences, polypeptide
CC sequences, and antibodies are useful for diagnosing, treating or
CC preventing diseases associated with aberrant LGR6 expression or activity,
CC such as weight disorders (e.g. obesity, anorexia nervosa or cachexia),
CC neural disorders (e.g. central nervous system disorder, including
CC Alzheimer's disease, Parkinson's disease), endocrine disorders (e.g.
CC sclerosis and Huntington's disease), immunomodulators (e.g.
CC hypothyroidism, hyperthyroidism or acromegaly), or cardiovascular
CC disorders (e.g. ischaemia-reperfusion injury, coronary artery disease,
CC myocardial infarction, arrhythmia, atherosclerosis, hypertension or
CC congestive heart failure). The LGR6 polynucleotide and polypeptide

CC sequences are also useful as targets for developing modulating agents
CC that regulate a variety of cellular processes, e.g. neural and endocrine
CC processes and thermogenesis. They can be used in screening assays (e.g.
CC chromosome mapping, tissue typing or in forensic biology), or in
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials or pharmacogenomics). The present sequence
CC encodes a human LGR6 polypeptide.
xx
SQ Sequence 1899 BP; 302 A; 624 C; 563 G; 409 T; 0 U; 1 Other;

Query Match 99.9%; Score 1898; DB 12; Length 1899;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1899; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AATACGACTCACTATAGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATTC	CGG 60
Dd	1	AATACGACTCACTATAGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATTC	CGG 60
QY	61	TCGACCCACGCGTCCGTTGGAGCGGAGCCAGGGTCTGAGCCCTGCCGGCTCAT	CCAGCCTCT 120
Dd	61	TCGACCCACGCGTCCGTTGGAGCGGAGCCAGGGTCTGAGCCCTGCCGGCTCAT	CCAGCCTCT 120
QY	121	CTTGCTGCCCTAGCGGCCTCCAAACAAACCGCATCTGGGAAATTGGAGCTNG	ACACCTTC 180
Dd	121	CTTGCTGCCCTAGCGGCCTCCAAACAAACCGCATCTGGGAAATTGGAGCTNG	ACACCTTC 180
QY	181	AGCAGACTGAGCTCCCTGCAAGCCCTGGTCAAGCTGGACCTGACAGACAAC	CCAGCTC 240
Dd	181	AGCAGACTGAGCTCCCTGCAAGCCCTGGTCAAGCTGGACCTGACAGACAAC	CCAGCTC 240
QY	241	CCTGAGGCCTTCTCCACCCCTGCCTCCCTGGTCAAGCTGGACCTGACAGACA	CCAGCTC 300
Dd	241	CCTGAGGCCTTCTCCACCCCTGCCTCCCTGGTCAAGCTGGACCTGACAGACA	CCAGCTC 300
QY	301	ACCACACTGCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGG	GAACCTT 360
Dd	301	ACCACACTGCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGG	GAACCTT 360
QY	361	GCTCTCTCCAGGCCTTCTCCAAAGGACAGTTTCCCAAACTGAGGATCCTGG	AGGTGCTT 420
Dd	361	GCTCTCTCCAGGCCTTCTCCAAAGGACAGTTTCCCAAACTGAGGATCCTGG	AGGTGCTT 420
QY	421	TATGCTACCAAGTGTCTCCATAGGGATGTGTCCAGCTTCTTCAAGGCCTCTG	GGGAG 480
Dd	421	TATGCTACCAAGTGTCTCCATAGGGATGTGTCCAGCTTCTTCAAGGCCTCTG	GGGAG 480
QY	481	TGGAGGCTGAAGACCTTACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTC	GGGCCTC 540
Dd	481	TGGAGGCTGAAGACCTTACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTC	GGGCCTC 540
QY	541	CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAG	CTGGAGATG 600
Dd	541	CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAG	CTGGAGATG 600
QY	601	GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTT	CAAGCCC 660
Dd	601	GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTT	CAAGCCC 660
QY	661	TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCTGGCCGTGGGGCCATCGT	GTGTGCTC 720
Dd	661	TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCTGGCCGTGGGGCCATCGT	GTGTGCTC 720
QY	721	TCCGTGCTCTGCAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGCCCTG	CCCCCCTG 780
Dd	721	TCCGTGCTCTGCAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGCCCTG	CCCCCCTG 780
QY	781	CCCCCGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCAAACACCTTGACT	GGCATTTCC 840
Dd	781	CCCCCGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCAAACACCTTGACT	GGCATTTCC 840
QY	841	TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAG	TACGGAGCC 900
Dd	841	TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAG	TACGGAGCC 900

QY	901	CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGT	CGGAG 960
Dd	901	CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGT	CGGAG 960
QY	961	GCATCGGTGCTGCTCACTCTTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTG	TGTC 1020
Dd	961	GCATCGGTGCTGCTCACTCTTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTG	TGTC 1020
QY	1021	CGGGCCTATGGGAAGTCCCTCCCTGGGCAGCGTTCGAGCAGGGTCTTAGGCTG	CCCTG 1080
Dd	1021	CGGGCCTATGGGAAGTCCCTCCCTGGGCAGCGTTCGAGCAGGGTCTTAGGCTG	CCCTG 1080
QY	1081	GCATGGCAGGGCTGGCCCGCGCACTGCCCTGAGGTGAGGTGAGGTGAGGTGAG	GTGTC 1140
Dd	1081	GCATGGCAGGGCTGGCCCGCGCACTGCCCTGAGGTGAGGTGAGGTGAGGTGAG	GTGTC 1140
QY	1141	CCACTCTGCCCTGCCCTACCGCCCACTGAGGGTCAAGCAGCAGCCCTGGGCTT	CACCGTG 1200
Dd	1141	CCACTCTGCCCTGCCCTACCGCCCACTGAGGGTCAAGCAGCAGCCCTGGGCTT	CACCGTG 1200
QY	1201	GCCCTGGTGAATGAATCCTTCTGTTTCCCTGGTGGTGGTGGTGGTGGTGGTGG	TGGTGGT 1260
Dd	1201	GCCCTGGTGAATGAATCCTTCTGTTTCCCTGGTGGTGGTGGTGGTGGTGGTGG	TGGTGGT 1260
QY	1261	TACTGTGACCTGCCCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATG	GTGAGGCAC 1320
Dd	1261	TACTGTGACCTGCCCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATG	GTGAGGCAC 1320
QY	1321	GTGGCCTGGCTCATCTTCGAGACGGGCTCCTCTACTGTCCCCTGGCTTCTC	CTCAGCTTC 1380
Dd	1321	GTGGCCTGGCTCATCTTCGAGACGGGCTCCTCTACTGTCCCCTGGCTTCTC	CTCAGCTTC 1380
QY	1381	GCCTCCATGTGGGCTTCTTCCCTGTACGCCCGAGGCCGTCAAGTCTGTCTG	TCTGGTG 1440
Dd	1381	GCCTCCATGTGGGCTTCTTCCCTGTACGCCCGAGGCCGTCAAGTCTGTCTG	TCTGGTG 1440
QY	1441	GTGCTGCCCTGCCCTGCTTCAACCCACTGTGTACCTGCTTCAACCCCTTCTC	AGCTTC 1500
Dd	1441	GTGCTGCCCTGCCCTGCTTCAACCCACTGTGTACCTGCTTCAACCCCTTCTC	AGCTTC 1500
QY	1501	CGGGATGACCTTCGGCGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTTAG	CCCTATGCT 1560
Dd	1501	CGGGATGACCTTCGGCGGCTTCGGCCCGCGCAGGGGACTCAGGGCCCTTAG	CCCTATGCT 1560
QY	1561	GCGCCCGGGAGCTGGAGAAGAGCTCCTGTGATTCACCCAGGCCCTGGTAG	CCCTTCTCT 1620
Dd	1561	GCGCCCGGGAGCTGGAGAAGAGCTCCTGTGATTCACCCAGGCCCTGGTAG	CCCTTCTCT 1620
QY	1621	GATGTGGATCTCATTTGGAAGCTTCTGAAGCTGGGGGGCCCCCTGGGCTG	GAGACCTAT 1680
Dd	1621	GATGTGGATCTCATTTGGAAGCTTCTGAAGCTGGGGGGCCCCCTGGGCTG	GAGACCTAT 1680
QY	1681	GGCTTCCCTCAGTGACCTCATCTCCTGTACAGCAGCGGGGGCCCCCAGG	CTGGAGG 1740
Dd	1681	GGCTTCCCTCAGTGACCTCATCTCCTGTACAGCAGCGGGGGCCCCCAGG	CTGGAGG 1740
QY	1741	AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTTCC	ATGGATGGA 1800
Dd	1741	AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTTCC	ATGGATGGA 1800
QY	1801	GAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGT	CAGGGGGTGGC 1860
Dd	1801	GAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGT	CAGGGGGTGGC 1860
QY	1861	GGCTTTCAGCCCTCTGGCTTGGCCCTTTGCTTCAACAGTG 1899	
Dd	1861	GGCTTTCAGCCCTCTGGCTTGGCCCTTTGCTTCAACAGTG 1899	

RESULT 4
AAI67922
ID AAI67922 standard; cDNA; 2486 BP.

XX AC AAI67922;
XX DT 13-MAR-2002 (first entry)
XX DE Human LGR6 polypeptide encoding cDNA (clone fahr).
XX KW Large G-protein coupled receptor 6; LGR6; GPCR; immunomodulator;
KW anti-HIV; cytostatic; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; neuroleptic; antidepressant; tranquilizer; antimigraine;
KW osteopathic; antiarteriosclerotic; vasotropic; hypotensive; cardiant;
KW antiarrhythmic; anorectic; gene therapy; human; ss.
XX OS Homo sapiens.
XX

Key Location/Qualifiers
CDS 2..1903
FT /*tag= a
FT /product= "LGR6 polypeptide"
FT /transl_except= (pos: 170..172, aa: Xaa)
FT /note= "Xaa = unknown"

PN WO200185768-A2.
XX
XX 15-NOV-2001.
XX
XX 08-MAY-2001; 2001WO-US015002.
XX
XX 08-MAY-2000; 2000US-00566588.
XX
XX (MILL-) MILLENNIUM PHARM INC.

XX Gu W;
PI WPI; 2002-055584/07.
XX P-PSDB; AAG66139.
DR

XX Novel isolated large G-protein coupled receptor 6 polypeptide, useful for
PT diagnosing and treating weight disorder, metabolic disorder, central
PT nervous system disorder, endocrine disorder and cardiovascular disorder.
XX
PS Example 1; Fig 4; 198pp; English.
XX

CC The invention provides isolated large G-protein coupled receptor 6 (LGR6)
CC polypeptides and polynucleotides encoding them. The LGR6 polypeptides and
CC polynucleotides are useful as targets for developing modulating agents
CC that regulate a variety of cellular process, e.g. neural and endocrine
CC processes, as well as thermogenesis. They are useful for developing novel
CC diagnostic and therapeutic agents for LGR6 associated disorders such as
CC weight disorders (anorexia, obesity), eating disorders, cancer-related wasting,
CC immunodeficiency syndrome (AIDS)-related wasting, acquired
CC metabolic disorders, central nervous system disorders (e.g. Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, Gilles de la
CC Tourette's syndrome, multiple sclerosis, amyotrophic lateral sclerosis,
CC epilepsy, Jakob-Creutzfeldt disease, depression, schizoprenia,
CC obsessive-compulsive disorder, anxiety, panic disorder, migraine),
CC endocrine disorders (hypo and hyperthyroidism, dwarfism, gigantism,
CC acromegaly), and cardiovascular disorders (atherosclerosis, restenosis,
CC hypertension, myocardial infarction, arrhythmia). The LGR6 polypeptides,
CC polynucleotides and antibodies are useful in screening assays, detection
CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials and pharmacogenomics), and in methods of
CC treatment (e.g. therapeutic and prophylactic). The present sequence
XX represents a human LGR6 polypeptide encoding cDNA

SQ Sequence 2486 BP; 455 A; 773 C; 692 G; 565 T; 0 U; 1 Other;

Query Match 99.9%; Score 1898; DB 6; Length 2486;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1899; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATACGACTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGGAATTCGGGG 60

Db ||||| 2 AATACGACTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGGAATTCGGGG 61
QY ||||| 61 TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCT 120
Db ||||| 62 TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCT 121
QY ||||| 121 CTTGCTGCCCTAGCGGCCTCCAAACACACCCGATCTGGGAAATTGGAGCTNGACACCTTC 180
Db ||||| 122 CTTGCTGCCCTAGCGGCCTCCAAACACACCCGATCTGGGAAATTGGAGCTNGACACCTTC 181
QY ||||| 181 AGCCAGCTGAGCTCCCTGCAAGCCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCAC 240
Db ||||| 182 AGCCAGCTGAGCTCCCTGCAAGCCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCAC 241
QY ||||| 241 CCTGAGGCCCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTG 300
Db ||||| 242 CCTGAGGCCCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTG 301
QY ||||| 301 ACCACACTGCCCTGGCTGGACTTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 360
Db ||||| 302 ACCACACTGCCCTGGCTGGACTTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 361
QY ||||| 361 GCTCTCTCCAGGCCTTCTCCAAGGACAGTTTCCAAAACTGAGGATCCTGGAGGTGCCT 420
Db ||||| 362 GCTCTCTCCAGGCCTTCTCCAAGGACAGTTTCCAAAACTGAGGATCCTGGAGGTGCCT 421
QY ||||| 421 TATGCCTACCACTGCTGTCCCTATGGGATGTGTCCAGCTTCTTCAAGGCCTCTGGGCAG 480
Db ||||| 422 TATGCCTACCACTGCTGTCCCTATGGGATGTGTCCAGCTTCTTCAAGGCCTCTGGGCAG 481
QY ||||| 481 TGGGAGGCTGAACACCTTCACCTTGATGATGAGGAGTCTTCAAAAAAGSCCCTTGGGCCTC 540
Db ||||| 482 TGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAAGSCCCTTGGGCCTC 541
QY ||||| 541 CTTGCCAGACAAGCAGAGAAACCACTATGACCAGGACCTGGATGAGTCCAGCTGGAGATG 600
Db ||||| 542 CTTGCCAGACAAGCAGAGAAACCACTATGACCAGGACCTGGATGAGTCCAGCTGGAGATG 601
QY ||||| 601 GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC 660
Db ||||| 602 GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC 661
QY ||||| 661 TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCTGGCCGTGTGGGCCATCGTGTGCTC 720
Db ||||| 662 TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCTGGCCGTGTGGGCCATCGTGTGCTC 721
QY ||||| 721 TCCGTGCTCTGCAATGGACTGGTGTGCTGACCCGTGTTTCGTGGCGGGCCTGCCCCCTG 780
Db ||||| 722 TCCGTGCTCTGCAATGGACTGGTGTGCTGACCCGTGTTTCGTGGCGGGCCTGCCCCCTG 781
QY ||||| 781 CCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGGGCGCCAAACACCTTGACTGGCATTTCC 840
Db ||||| 782 CCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGGGCGCCAAACACCTTGACTGGCATTTCC 841
QY ||||| 841 TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCC 900
Db ||||| 842 TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCC 901
QY ||||| 901 CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCCCTGGCACTTGGGTTCGGAG 960
Db ||||| 902 CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCCCTGGCAGTACTGGGTTCGGAG 961
QY ||||| 961 GCATCGGTGCTGCTGCTCACTCTGCGCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTC 1020
Db ||||| 962 GCATCGGTGCTGCTGCTCACTCTGCGCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTC 1021
QY ||||| 1021 CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTG 1080
Db ||||| 1022 CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTG 1081
QY ||||| 1081 GCACTGGCAGGGCTGGCCCGCGACTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCCTCC 1140

Db 1082 GCACTGGCAGGGCTGGCCGCGCACTGCCCTTGGCCCTCAGTGGGAGAATACGGGGCCCTCC 1141

Qy 1141 CCACCTCTGCCCTGCCCTACGCGGCACACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTG 1200
|||||

Db 1142 CCACCTCTGCCCTGCCCTACGCGGCACACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTG 1201

Qy 1201 GCCCTGGTGATGATGAACCTCTTCTGTGTTTCTGTGTCGTGGCCGGTGCCCTACATCAAACTG 1260
|||||

Db 1202 GCCCTGGTGATGATGAACCTCTTCTGTGTTTCTGTGTCGTGGCCGGTGCCCTACATCAAACTG 1261

Qy 1261 TACTGTGACCTGCCGCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCAC 1320
|||||

Db 1262 TACTGTGACCTGCCGCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCAC 1321

Qy 1321 GTGSGCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCCTTCCCTCAGCTTC 1380
|||||

Db 1322 GTGSGCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCGTGGCCCTTCCCTCAGCTTC 1381

Qy 1381 GCCTCCATGCTGGGCCCTCTTCCCTGTTCAGCCCGAGGCCGTCAAGTCTGTCTGCTGCTG 1440
|||||

Db 1382 GCCTCCATGCTGGGCCCTCTTCCCTGTTCAGCCCGAGGCCGTCAAGTCTGTCTGCTGCTG 1441

Qy 1441 GTGCTGCCCCCTGCCTGCCTGCCTCAACCCACTGTGTACTGTCTTCAACCCCCACTTC 1500
|||||

Db 1442 GTGCTGCCCCCTGCCTGCCTGCCTCAACCCACTGTGTACTGTCTTCAACCCCCACTTC 1501

Qy 1501 CGGATGACCTTCGGCGGCTTCGCGCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT 1560
|||||

Db 1502 CGGATGACCTTCGGCGGCTTCGCGCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT 1561

Qy 1561 GCGCGCGGGAGCTGGAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT 1620
|||||

Db 1562 GCGCGCGGGAGCTGGAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT 1621

Qy 1621 GATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGCGGCCCTGGGCTGGAGACCTAT 1680
|||||

Db 1622 GATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGCGGCCCTGGGCTGGAGACCTAT 1681

Qy 1681 GGCTTCCCCTCAGTGACCCCTCATCTCCTGTTCAGCAGCCAGGGCCCCCAGGCTGGAGGGC 1740
|||||

Db 1682 GGCTTCCCCTCAGTGACCCCTCATCTCCTGTTCAGCAGCCAGGGGCCCCAGGCTGGAGGGC 1741

Qy 1741 AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGA 1800
|||||

Db 1742 AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGA 1801

Qy 1801 GAACTGCTGTGAGGSCAGAGGGATCTAGCCAGCAGGTGAGGCTTGTCAAGGGGTGGC 1860
|||||

Db 1802 GAACTGCTGTGAGGSCAGAGGGATCTAGCCAGCAGGTGAGGCTTGTCAAGGGGTGGC 1861

Qy 1861 GGCTTTAGCCCTCTGGCCTTGGCCTTGGCTTCAACAGTG 1899
|||||

Db 1862 GGCTTTAGCCCTCTGGCCTTGGCCTTGGCTTCAACAGTG 1900
|||||

RESULT 5

ID ADN02242 standard; cDNA; 2486 BP.

XX AC ADN02242;

XX XX

DT 17-JUN-2004 (first entry)

XX Human partial large G protein-coupled receptor, LGR6, cDNA #1.

DE Human; ss; large G protein-coupled receptor 6; LGR6; heart failure;
XX ischaemic heart disease; myocardial infarction; hypertension;
KW pericarditis; atherosclerosis; hepatic failure; viral hepatitis; cancer;
KW intracerebral haemorrhage; brain abscess; Alzheimer's disease;
KW Pick disease; Parkinson's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; inflammatory bowel disease;
KW Crohn's disease; benign prostatic hypertrophy;
KW systemic lupus erythematosus.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 2..1903

FT /*tag= a

FT /partial

FT /note= "No start codon shown"

FT /product= "Partial LGR6"

XX US2003166047-A1.

PN 04-SEP-2003.

XX 08-MAY-2001; 2001US-00851595.

PF 06-MAY-1999; 99US-0132896P.

XX 08-MAY-2000; 2000US-00566588.

PR (MILL-) MILLENNIUM PHARM INC.

XX Gu W;

PI WPI; 2003-898067/82.

XX P-PSDB; ADN02243.

DR New isolated LGR6 nucleic acids and polypeptides, useful for diagnosing and treating LGR6-mediated disorders, such as myocardial infarction, hypertension, atherosclerosis, viral hepatitis, cancer and/or Alzheimer's disease.

DR Claim 1; SEQ ID NO 4; 145pp; English.

XX The invention relates to an isolated LGR6 (large G protein-coupled receptor) nucleic acid molecule comprising the mouse and human cDNA sequences appearing as ADN02239, ADN02241, ADN02242, ADN02244, ADN02245, ADN02247, ADN02248 and ADN02250. Also included are a host cell or a non-human mammalian host cell containing an LGR6 nucleic acid (and producing LGR6), an isolated LGR6 polypeptide appearing as ADN02240, ADN02243, ADN02246 and ADN02249, an antibody which selectively binds to LGR6, a method for detecting the presence of LGR6 in a sample, a kit (comprising a compound which selectively binds to LGR6, or hybridises to LGR6 nucleic acid, and instructions for use), a method for detecting LGR6 nucleic acid in a sample, a method for identifying a compound which binds to LGR6, a method for modulating the activity of LGR6 and a method for identifying a compound that modulates the activity of LGR6. The methods and compositions of the present invention are useful for diagnosing and treating large G-protein coupled receptor 6 (LGR6)-mediated or -related disorders, such as heart failure, ischaemic heart disease, myocardial infarction, hypertension, pericarditis, atherosclerosis, hepatic failure, viral hepatitis, cancer, intracerebral haemorrhage, brain abscess, Alzheimer's disease, Pick disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, inflammatory bowel disease, Crohn's disease, benign prostatic hypertrophy and systemic lupus erythematosus. The present sequence is a partial human cDNA for LGR6.

XX SQ Sequence 2486 BP; 455 A; 773 C; 692 G; 565 T; 0 U; 1 Other;

Query Match 99.9%; Score 1898; DB 11; Length 2486;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1899; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATACGACTCACTATAGGAAAGCTGGTACGCCCTGCAGGTACCGGTCCGGAAATTCCTCCGGG 60
|||||

Db 2 AATACGACTCACTATAGGAAAGCTGGTACGCCCTGCAGGTACCGGTCCGGAAATTCCTCCGGG 61
|||||

Qy 61 TCGACCCACGGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCT 120
|||||

Db 62 TCGACCCACGGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCT 121
|||||

Qy 121 CTTGCTGCCCTAGCGGCTCCAACAACCGCATCTGGGAAATTGGAGCTNGACACCTTC 180
|||||

Db 122 CTTGCTGCCCTAGCGGCTCCAACAACCGCATCTGGGAAATTGGAGCTNGACACCTTC 181
|||||

QY	181	AGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAAAGCCATCCGGTCCATCCAC	240
Db	182	AGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAAAGCCATCCGGTCCATCCAC	241
QY	241	CCTGAGGCCCTTCTCCACCTGCACTCCCTGGTCAAGCTGGACCTGACAGAACCAAGCTG	300
Db	242	CCTGAGGCCCTTCTCCACCTGCACTCCCTGGTCAAGCTGGACCTGACAGAACCAAGCTG	301
QY	301	ACCACACTGCCCTGGCTGGACTTGGGGCTTGAATGATCTGAAGCTCAAAAGGGAACCTT	360
Db	302	ACCACACTGCCCTGGCTGGACTTGGGGCTTGAATGATCTGAAGCTCAAAAGGGAACCTT	361
QY	361	GCTCTCTCCAGGCCCTTCTCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCT	420
Db	362	GCTCTCTCCAGGCCCTTCTCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCT	421
QY	421	TATGCCTACCAAGTGTGCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTTGGGCAG	480
Db	422	TATGCCTACCAAGTGTGCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTTGGGCAG	481
QY	481	TGGGAGGCTGAAGACCTTCAACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCTC	540
Db	482	TGGGAGGCTGAAGACCTTCAACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCTC	541
QY	541	CTTGCCAGACAAGCAGAGAAACCACCTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG	600
Db	542	CTTGCCAGACAAGCAGAGAAACCACCTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG	601
QY	601	GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC	660
Db	602	GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC	661
QY	661	TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCCCGTGTGGGCCATCGTGTGCTC	720
Db	662	TGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCCTGGCCCGTGTGGGCCATCGTGTGCTC	721
QY	721	TCCGTGCTCTGCAATGGACTGGTGTGCTGACCGGTTCGCTGGCGGGCCTGCCCCCTG	780
Db	722	TCCGTGCTCTGCAATGGACTGGTGTGCTGACCGGTTCGCTGGCGGGCCTGCCCCCTG	781
QY	781	CCCCCGGTCAAAGTTTGTGGTAGGTGCGATTGACGGCCCAACACCTTGACTGGCATTTCC	840
Db	782	CCCCCGGTCAAAGTTTGTGGTAGGTGCGATTGACGGCCCAACACCTTGACTGGCATTTCC	841
QY	841	TGTGGCCTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGACTACGGAGCC	900
Db	842	TGTGGCCTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGACTACGGAGCC	901
QY	901	CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGSGTTCTCTGGCAGTACTTTGGTCCGAG	960
Db	902	CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGSGTTCTCTGGCAGTACTTTGGTCCGAG	961
QY	961	GCATCGGTGCTGCTCACTCTGGCCGCGACTGCCCTGGCCTCAGTGCAGCGTCTCCGTCTCCTGTGTC	1020
Db	962	GCATCGGTGCTGCTGCTCACTCTGGCCGCGACTGCCCTGGCCTCAGTGCAGCGTCTCCGTCTCCTGTGTC	1021
QY	1021	CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTG	1080
Db	1022	CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTG	1081
QY	1081	GCACTGGCAGGGCTGGCCGCGCACTGCCCTGGCCTCAGTGGGAGATAACGGGGCCTCC	1140
Db	1082	GCACTGGCAGGGCTGGCCGCGCACTGCCCTGGCCTCAGTGGGAGATAACGGGGCCTCC	1141
QY	1141	CCACTCTGCCCTGACCCTACGGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTACCCGTG	1200
Db	1142	CCACTCTGCCCTGACCCTACGGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTACCCGTG	1201
QY	1201	GCCCTGGTGATGATGAATCCTTCTGTTTCCCTGGTGTGGCCGGTGCCTACATCAAACTG	1260
Db	1202	GCCCTGGTGATGATGAATCCTTCTGTTTCCCTGGTGTGGCCGGTGCCTACATCAAACTG	1261

QY	1261	TACTGTGACCTGCGCGGGCGAGCTTTGAGGCCGTGTGGACTGCGGCATGGTGAGGCAC	1320
Db	1262	TACTGTGACCTGCGCGGGCGAGCTTTGAGGCCGTGTGGACTGCGGCATGGTGAGGCAC	1321
QY	1321	GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCCTGGCCTCCTCAGCTTC	1380
Db	1322	GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCCTGGCCTCCTCAGCTTC	1381
QY	1381	GCCCTCCATGTGGGCCTCTTCCCTGTCAAGCCCGAGGCCGTCAAAGTCTGTCTGCTGGTG	1440
Db	1382	GCCCTCCATGTGGGCCTCTTCCCTGTCAAGCCCGAGGCCGTCAAAGTCTGTCTGCTGGTG	1441
QY	1441	GTGCTGCCCTGCCTGCCTGCCTCAACCCACTGTGTACCTGCTCTTCAACCCCACTTC	1500
Db	1442	GTGCTGCCCTGCCTGCCTGCCTCAACCCACTGTGTACCTGCTCTTCAACCCCACTTC	1501
QY	1501	CGGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT	1560
Db	1502	CGGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT	1561
QY	1561	GCGCCCGGAGCTGGAGAAGAGTCCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT	1620
Db	1562	GCGCCCGGAGCTGGAGAAGAGTCCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT	1621
QY	1621	GATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGCGGCCCCCTGGCTGGAGACCTAT	1680
Db	1622	GATGTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGCGGCCCCCTGGCTGGAGACCTAT	1681
QY	1681	GGCTTCCCCTCAGTGACCCCTCATCTCCTGTCAAGCCAGCCAGGGGCCCCCAGGCTGGAGGGC	1740
Db	1682	GGCTTCCCCTCAGTGACCCCTCATCTCCTGTCAAGCCAGCCAGGGGCCCCCAGGCTGGAGGGC	1741
QY	1741	AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGA	1800
Db	1742	AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGA	1801
QY	1801	GAACCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGTTGTTCAGGGGGTGGC	1860
Db	1802	GAACCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGTTGTTCAGGGGGTGGC	1861
QY	1861	GGCTTTCAGCCCTCTGGCTTGGCCTTGGCTTTCACACGTG	1899
Db	1862	GGCTTTCAGCCCTCTGGCTTGGCCTTGGCTTTCACACGTG	1900
RESULT 6			
ADK19407			
ID	ADK19407 standard; cDNA; 2486 BP.		
XX	ADK19407;		
XX			
DT	17-JUN-2004 (first entry)		
XX			
DE	cDNA encoding human LGR6 polypeptide #1.		
XX			
KW	G-protein coupled receptor; GPCR; large G-protein coupled receptor 6;		
KW	LGR6; weight disorder; neural disorder; endocrine disorder;		
KW	cardiovascular disorder; anorectic; anabolic; immunomodulator;		
KW	neuroprotective; nootropic; antiparkinsonian; anti-HIV; anticonvulsant;		
KW	antithyroid; osteopathic; cardiant; vasotropic; hypotensive;		
KW	antiarteriosclerotic; antiarrhythmic; human; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Location/Qualifiers		
FT	2. .1903		
FT	/*tag= a		
FT	/partial		
FT	/product= "LGR6 polypeptide #1"		
FT	/note= "This sequence lacks a start codon"		
FT	/transl_except= (pos:170. .172,aa:Xaa)		
FT	/note= "Xaa= Unknown"		
XX			

PN US2004058377-A1.
XX
PD 25-MAR-2004.
XX
PF 18-SEP-2003; 2003US-00664667.
XX
PR 06-MAY-1999; 99US-0132896P.
PR 08-MAY-2000; 2000US-00566588.
PR 08-MAY-2001; 2001US-00851595.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gu W;
XX
DR WPI; 2004-268789/25.
DR P-PSDB; ADKI9408.
XX
PT New large G-protein coupled receptor 6 nucleic acid molecules and
PT polypeptides, useful for diagnosing, preventing or treating diseases
PT associated with aberrant nucleic acid or protein activity, e.g. obesity,
PT anorexia or cachexia.
XX
PS Claim 2; SEQ ID NO 4; 145pp; English.
XX
CC The present invention relates to the isolation of novel members of the G-
CC protein coupled receptor (GPCR) family designated as large G-protein
CC coupled receptor 6 (LGR6), and the polynucleotide sequences encoding
CC them. The invention also discloses LGR6 fusion proteins, antigenic
CC peptides, anti-LGR6 antibodies, recombinant expression vectors, host
CC cells, and non-human transgenic animals in which an LGR6 gene has been
CC introduced or disrupted. The LGR6 polynucleotide sequences, polypeptide
CC sequences, and antibodies are useful for diagnosing, treating or
CC preventing diseases associated with aberrant LGR6 expression or activity,
CC such as weight disorders (e.g. obesity, anorexia nervosa or cachexia),
CC neural disorders (e.g. central nervous system disorder, including
CC Alzheimer's disease, Parkinson's disease, AIDS-related dementia, multiple
CC sclerosis and Huntington's disease), endocrine disorders (e.g.
CC hypothyroidism, hyperthyroidism or acromegaly), or cardiovascular
CC disorders (e.g. ischaemia-reperfusion injury, coronary artery disease,
CC myocardial infarction, arrhythmia, atherosclerosis, hypertension or
CC congestive heart failure). The LGR6 polynucleotide and polypeptide
CC sequences are also useful as targets for developing modulating agents
CC that regulate a variety of cellular processes, e.g. neural and endocrine
CC processes and thermogenesis. They can be used in screening assays (e.g.
CC chromosome mapping, tissue typing or in forensic biology), or in
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials or pharmacogenomics). The present sequence
CC encodes a human LGR6 polypeptide.
XX
SQ Sequence 2486 BP; 455 A; 773 C; 692 G; 565 T; 0 U; 1 Other;
Query Match 99.9%; Score 1898; DB 12; Length 2486;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1899; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATACGACTCACTATAGGGAAGCTGGTACGCCCTGCAGGTACCGGTCCGGAATTCCCGGG 60
Db 2 AATACGACTCACTATAGGGAAGCTGGTACGCCCTGCAGGTACCGGTCCGGAATTCCCGGG 61
QY 61 TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCCTGCCGGCTCATCCAGCCTCT 120
Db 62 TCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCCTGCCGGCTCATCCAGCCTCT 121
QY 121 CTGTGTCCTTAGCGGGCTCCAAACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTC 180
Db 122 CTGTGTCCTTAGCGGGCTCCAAACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTC 181
QY 181 AGCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCCATCCGGTCCATCCAC 240
Db 182 AGCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCCATCCGGTCCATCCAC 241
QY 241 CTTGAGGCTTCTCCACCCCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTG 300
XX

Db 242 CCTGAGGCCCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTG 301
QY 301 ACCACACTGCCCCCTGGCTGGACTTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 360
Db 302 ACCACACTGCCCCCTGGCTGGACTTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTT 361
QY 361 GCTCTCTCCAGGCCCTTCTCCAAGGACAGTTTCCAAAAAAGCTGAGGATCCTGGAGGTGCT 420
Db 362 GCTCTCTCCAGGCCCTTCTCCAAGGACAGTTTCCAAAAAAGCTGAGGATCCTGGAGGTGCT 421
QY 421 TATGCCTACCAGTGTGTCCTTATGGGATGTGTGCGAGCTTCTTCAAGGCCCTCTGGGCAG 480
Db 422 TATGCCTACCAGTGTGTCCTTATGGGATGTGTGCGAGCTTCTTCAAGGCCCTCTGGGCAG 481
QY 481 TGGGAGGCTGAAGACCTTACACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTCTGGGCCTC 540
Db 482 TGGGAGGCTGAAGACCTTACACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTCTGGGCCTC 541
QY 541 CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG 600
Db 542 CTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATG 601
QY 601 GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC 660
Db 602 GAGGACTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCC 661
QY 661 TGTGAGTACCTCTTTGAAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTTGTGTC 720
Db 662 TGTGAGTACCTCTTTGAAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTTGTGTC 721
QY 721 TCCGTGCTCTGCAATGGACTGGTGTGCTGACCCGTGTGCTGGCGGGCTGCCCCCTG 780
Db 722 TCCGTGCTCTGCAATGGACTGGTGTGCTGACCCGTGTGCTGGCGGGCTGCCCCCTG 781
QY 781 CCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCCAACACCTTGACTGGCATTTCC 840
Db 782 CCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCCAACACCTTGACTGGCATTTCC 841
QY 841 TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCC 900
Db 842 TGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCC 901
QY 901 CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTTGGTTCTCTGGCAGTACTTGGGTCCGAG 960
Db 902 CGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTTGGTTCTCTGGCAGTACTTGGGTCCGAG 961
QY 961 GCATCGGTGCTGCTGCTCACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCTCTGTGTC 1020
Db 962 GCATCGGTGCTGCTGCTCACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCTCTGTGTC 1021
QY 1021 CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCTCTAGGCTGCTG 1080
Db 1022 CGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCTCTAGGCTGCTG 1081
QY 1081 GCATGGCAGGGCTGCGCCGCGCACTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCTCTCC 1140
Db 1082 GCATGGCAGGGCTGCGCCGCGCACTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCTCTCC 1141
QY 1141 CCACCTCTGCCCTGCCCTAGCGGCCACCTGAGGGTACGAGCAGCCCTGGGCTTCAACGCTG 1200
Db 1142 CCACCTCTGCCCTGCCCTAGCGGCCACCTGAGGGTACGAGCAGCCCTGGGCTTCAACGCTG 1201
QY 1201 GCCCTGGTGATGATGAATCCTTCTGTTTCCCTGGTCCGTGGCCGGTCCCTACATCAAACTG 1260
Db 1202 GCCCTGGTGATGATGAATCCTTCTGTTTCCCTGGTCCGTGGCCGGTCCCTACATCAAACTG 1261
QY 1261 TACTGTGACCTGCCCGGGGGCGACTTTGAGGCCGTTGGGACTGCGCCCATGGTGAGGCAC 1320
Db 1262 TACTGTGACCTGCCCGGGGGCGACTTTGAGGCCGTTGGGACTGCGCCCATGGTGAGGCAC 1321
QY 1321 GTGGCCTGGCTCATCTTCGACAGCGGGCTCCTTACTGTCCCCTGGCCCTTCTCAGCTTC 1380
Db 1322 GTGGCCTGGCTCATCTTCGACAGCGGGCTCCTTACTGTCCCCTGGCCCTTCTCAGCTTC 1381

QY 1381 GCCTCCATGCTGGGCCCTCTTCCCTGTCTACGCCCGAGGCCGCTCAAGTCTGTCTGCTGGTG 1440
|||||
Db 1382 GCCTCCATGCTGGGCCCTCTTCCCTGTCTACGCCCGAGGCCGCTCAAGTCTGTCTGCTGGTG 1441
|||||
QY 1441 GTGTCGCCCTGCTGCTGCTGCTCAACCCACTGTGTACTGTCTTTCAACCCCCACTTC 1500
|||||
Db 1442 GTGTCGCCCTGCTGCTGCTGCTCAACCCACTGTGTACTGTCTTTCAACCCCCACTTC 1501
|||||
QY 1501 CGGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT 1560
|||||
Db 1502 CGGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCT 1561
|||||
QY 1561 GCGGCGGGGAGCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT 1620
|||||
Db 1562 GCGGCGGGGAGCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCT 1621
|||||
QY 1621 GATGTGATCTCATTTCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTAT 1680
|||||
Db 1622 GATGTGATCTCATTTCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTAT 1681
|||||
QY 1681 GGCTTCCCCTCAGTGACCCCTCATCTCCTGTCTCAGCAGCCAGGGGCCCCCAGGCTGGAGGC 1740
|||||
Db 1682 GGCTTCCCCTCAGTGACCCCTCATCTCCTGTCTCAGCAGCCAGGGGCCCCCAGGCTGGAGGC 1741
|||||
QY 1741 AGCATTTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGA 1800
|||||
Db 1742 AGCATTTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGA 1801
|||||
QY 1801 GAACTGTCTGTAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTTCAGGGGGTGGC 1860
|||||
Db 1802 GAACTGTCTGTAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTTCAGGGGGTGGC 1861
|||||
QY 1861 GGCTTTTCAGCCCTCTGGCTTGGCTTGGCTTTCACACGTG 1899
|||||
Db 1862 GGCTTTTCAGCCCTCTGGCTTGGCTTGGCTTTCACACGTG 1900
|||||

RESULT 7

AAF98722
ID AAF98722 standard; DNA; 2322 BP.
XX
AC AAF98722;
XX
DT 02-JUL-2001 (first entry)
XX
DE Human late stage ovarian tumour polynucleotide marker 37.
XX
KW Human; ovarian cancer; identification; detection; characterisation;
KW tumour; kinase; marker; cytostatic; antisense gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200118542-A2.
XX
PD 15-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-US024199.
XX
PR 03-SEP-1999; 99US-0152547P.
PR 16-MAR-2000; 2000US-0190347P.
PR 21-MAR-2000; 2000US-0191321P.
PR 31-MAY-2000; 2000US-0208382P.
PR 20-JUL-2000; 2000US-00220467.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lee J, Thompshe P, Lillie J;
XX
DR WPI; 2001-211428/21.
XX
PT Detection, assessment, prevention and therapy of ovarian cancer,
PT comprises detecting changes in the expression of a variety of markers.

XX
PS Claim 1; Page 1188-1189; 1198pp; English.
XX
CC The present invention describes a method for assessing whether a patient
CC is afflicted with ovarian cancer by comparing: (1) the expression of a
CC marker (I) (see AAF98594 to AAF98730), in a patient sample; and (2) the
CC normal level of expression of (I) in a control non-ovarian cancer sample,
CC where a significant difference between the level of expression in (a) and
CC (b) is an indication that the patient is afflicted with ovarian cancer.
CC (I) have cytostatic activities and can be used in antisense gene therapy.
CC The method, compositions and kits from the present invention can be used
CC for: (1) assessing and treating ovarian cancer; (2) making isolated
CC hybridoma, which produces an antibody useful for ovarian cancer
CC assessment; and (3) inhibiting ovarian cancer in a patient. AAF98573 to
CC AAF98593 represent human kinase marker primers and probes which are used
CC in the exemplification of the present invention
XX
SQ Sequence 2322 BP; 407 A; 733 C; 652 G; 530 T; 0 U; 0 Other;

Query Match 95.9%; Score 1820.4; DB 5; Length 2322;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1832; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 66 CCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGTCTATCCAGCCTCTCTTGC 125
|||||
Db 1 CCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGTCTATCCAGCCTCTCTTGC 60
|||||
QY 126 TGCCCTAGCGGCTCCAAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCA 185
|||||
Db 61 TGCCCTAGCGGCTCCAAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCA 119
|||||
QY 186 GCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTTGAAGCCCATCCGGTCCATCCACCCCTGA 245
|||||
Db 120 GCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTTGAAGCCCATCCGGTCCATCCACCCCTGA 179
|||||
QY 246 GGCCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTGACCAC 305
|||||
Db 180 GGCCTTCTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTGACCAC 239
|||||
QY 306 ACTGCCCTGGCTGGAATTGGGGGCTTGATGTCATCTGAAGCTCAAAGGGAACCTTGCTCT 365
|||||
Db 240 ACTGCCCTGGCTGGAATTGGGGGCTTGATGTCATCTGAAGCTCAAAGGGAACCTTGCTCT 299
|||||
QY 366 CTCCCAGGCCCTTCTCCAAGGACAGTTTCCAAAACCTGAGGATCCTGGAGTGCCCTTATGC 425
|||||
Db 300 CTCCCAGGCCCTTCTCCAAGGACAGTTTCCAAAACCTGAGGATCCTGAAGTGCCCTTATGC 359
|||||
QY 426 CTACCAGTGTCTCCCTATGGGATGTGTGCAGCTTCTTCAAGGCCCTCTGGGCAGTGGGA 485
|||||
Db 360 CTACCAGTGTCTCCCTATGGGATGTGTGCAGCTTCTTCAAGGCCCTCTGGGCAGTGGGA 419
|||||
QY 486 GGCTGAAGACCTTCACTTGTATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCCTCCTTGC 545
|||||
Db 420 GGCTGAAGACCTTCACTTGTATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCCTCCTTGC 479
|||||
QY 546 CAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGA 605
|||||
Db 480 CAGACAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGA 539
|||||
QY 606 CTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCCTGTGA 665
|||||
Db 540 CTCAAAGCCACACCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCCTGTGA 599
|||||
QY 666 GTACCTCTTTGAAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTCTCCGT 725
|||||
Db 600 GTACCTCTTTGAAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTCTCCGT 659
|||||
QY 726 GCTCTGCAATGGACTGGTGTGCTGACCCGTGTTGCTGGCGGGCCCTGCCCCCTGCCCCCC 785
|||||
Db 660 GCTCTGCAATGGACTGGTGTGCTGACCCGTGTTGCTGGCGGGCCCTGCCCCCTGCCCCCC 719
|||||
QY 786 GGTCAGTTTGTGGTAGGTGCGATTGACGGGCCCAACACCTTGACTGGCATTTCTGTGG 845
|||||

Db	720	GGTCAAGTTTGTGGTAGGTGCGAATTGCAGGCGCCAAACACCTTGACTGGCATTTCTCTGTGG	779
QY	846	CTTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTG	905
Db	780	CCTTCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTG	839
QY	906	GGAGACGGGGCTAGGCTGCCCGGCCACTGGCTTCCTGGCAGTACTTGGTCCGAGGCATC	965
Db	840	GGAGACGGGGCTAGGCTGCCCGGCCACTGGCTTCCTGGCAGTACTTGGTCCGAGGCATC	899
QY	966	GGTGCTGCTGCTACTCTTGGCCCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGC	1025
Db	900	GGTGCTGCTGCTACTCTTGGCCCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGC	959
QY	1026	CTATGGGAAGTCCCCCTCCCTGGGCAGCGTTGAGCAGGGGTCTTAGGCTGCCTGGGCACT	1085
Db	960	CTATGGGAAGTCCCCCTCCCTGGGCAGCGTTGAGCAGGGGTCTTAGGCTGCCTGGGCACT	1019
QY	1086	GGCAGGGCTGGCCGCGCACTGCCCTGGCCTCAGTGGGAGAATACGGGGCCTCCCCACT	1145
Db	1020	GGCAGGGCTGGCCGCGCACTGCCCTGGCCTCAGTGGGAGAATACGGGGCCTCCCCACT	1079
QY	1146	CTGCCTGCCCTACGGCGCCACCTGAGGGTCAGCCAGCAGCCCCCTGGGCTTCACCGTGGCCCT	1205
Db	1080	CTGCCTGCCCTACGGCGCCACCTGAGGGTCAGCCAGCAGCCCCCTGGGCTTCACCGTGGCCCT	1139
QY	1206	GGTGATGATGAATCCTTCTGTTTCTTGGTCGTGGCCGTGCGCATGGTGAGGCACGTGGC	1265
Db	1140	GGTGATGATGAATCCTTCTGTTTCTTGGTCGTGGCCGTGCGCATGGTGAGGCACGTGGC	1199
QY	1266	TGACCTGCCCGGGCGACTTTGAGGCCGTGTGSGACTGCGCCATGGTGAGGCACGTGGC	1325
Db	1200	TGACCTGCCCGGGCGACTTTGAGGCCGTGTGSGACTGCGCCATGGTGAGGCACGTGGC	1259
QY	1326	CTGGCTCATCTTCGACAGACGGGCTCCTCTACTGTCCCGTGGCCCTTCCTCAGCTTCGCCCTC	1385
Db	1260	CTGGCTCATCTTCGACAGACGGGCTCCTCTACTGTCCCGTGGCCCTTCCTCAGCTTCGCCCTC	1319
QY	1386	CATGCTGGGCTCTTCCCTGTACGCCCGAGGCCGTCAAGTCTGTCTCTGCTGGTGGTGT	1445
Db	1320	CATGCTGGGCTCTTCCCTGTACGCCCGAGGCCGTCAAGTCTGTCTCTGCTGGTGGTGT	1379
QY	1446	GCCCCCTGCCCTGCCTCAACCCACTGCTGTACTGCTCTTCAACCCCCACTTCCGGGA	1505
Db	1380	GCCCCCTGCCCTGCCTCAACCCACTGCTGTACTGCTCTTCAACCCCCACTTCCGGGA	1439
QY	1506	TGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGACTCAGGGCCCCCTAGCCTATGCTGCGGC	1565
Db	1440	TGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGACTCAGGGCCCCCTAGCCTATGCTGCGGC	1499
QY	1566	CGGGAGCTGGAGAAGAGCTCCTGTGATTCTACCGAGGCCCTGGTAGCCTTCTCTGATGT	1625
Db	1500	CGGGAGCTGGAGAAGAGCTCCTGTGATTCTACCGAGGCCCTGGTAGCCTTCTCTGATGT	1559
QY	1626	GGATCTCATTTCTGGAAGCTTCTGAAGCTGGGCGSCCCCTGGGCTGGAGACCTATGGCTT	1685
Db	1560	GGATCTCATTTCTGGAAGCTTCTGAAGCTGGGCGSCCCCTGGGCTGGAGACCTATGGCTT	1619
QY	1686	CCCCCTCAGTGACCCCTCATCTCCTGTGACGACGACGGGGCCCCCAGGCTGGAGGCAGCCA	1745
Db	1620	CCCCCTCAGTGACCCCTCATCTCCTGTGACGACGACGGGGCCCCCAGGCTGGAGGCAGCCA	1679
QY	1746	TTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGAGAACT	1805
Db	1680	TTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGAGAACT	1739
QY	1806	GCTGCTAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGGTGCGGCTT	1865
Db	1740	GCTGCTAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGGTGCGGCTT	1799
QY	1866	TCAGCCCTCTGGCTTGGCCCTTTGCTTCAACACGTG	1899
Db	1800	TCAGCCCTCTGGCTTGGCCCTTTGCTTCAACACGTG	1833

CC and conditions affecting the kidney. They may also be useful for treating
CC diseases and conditions involving cell proliferation and differentiation,
CC such as tissue damage and degeneration, ageing, wound healing, cancer,
CC hyperplasia and hypertrophy.

XX
SQ Sequence 3451 BP; 728 A; 1063 C; 920 G; 740 T; 0 U; 0 Other;

Query Match 95.4%; Score 1811.6; DB 12; Length 3451;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1825; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY	70	GCCTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCTCTTGCTGCC	129
Db	1066	GGGGCATGGAGCGGAGCCAGGGTCTGAGCCTGCCGGCTCATCCAGCCTCTCTTGCTGCC	1125
QY	130	CTAGCGCCTCCAACACACACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTG	189
Db	1126	CTAGCGCCTCCAACACACACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTG	1184
QY	190	AGCTCCCTGCAAGCCCTGGATCTTAGCTGGAAAGCCATCCGGTCCATCCACCCGTAGGCC	249
Db	1185	AGCTCCCTGCAAGCCCTGGATCTTAGCTGGAAAGCCATCCGGTCCATCCACCCGTAGGCC	1244
QY	250	TTCTCCACCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTGACCACTG	309
Db	1245	TTCTCCACCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCCAGCTGACCACTG	1304
QY	310	CCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCC	369
Db	1305	CCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCC	1364
QY	370	CAGGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGTGCCTTATGCCTAC	429
Db	1365	CAGGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGTGCCTTATGCCTAC	1424
QY	430	CAGTGTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGAGGCT	489
Db	1425	CAGTGTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGAGGCT	1484
QY	490	GAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCTCTTGCCAGA	549
Db	1485	GAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGGCCTCTTGCCAGA	1544
QY	550	CAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCA	609
Db	1545	CAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCA	1604
QY	610	AAGCCACACCCCAAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTAC	669
Db	1605	AAGCCACACCCCAAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTAC	1664
QY	670	CTCTTTGAAAGCTGGGGCATCCGCCTGGCCGTGTGGCCCATCGTGTGCTCTCCGTGCTC	729
Db	1665	CTCTTTGAAAGCTGGGGCATCCGCCTGGCCGTGTGGCCCATCGTGTGCTCTCCGTGCTC	1724
QY	730	TGCAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGCCCTGCCCCCTGCCCCCGGTC	789
Db	1725	TGCAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGCCCTGCCCCCTGCCCCCGGTC	1784
QY	790	AAGTTTGTGGTAGGTGCGATTGCAAGCGGCCCAACACCTTGACTGGCATTTCTCTGGCCCTT	849
Db	1785	AAGTTTGTGGTAGGTGCGATTGCAAGCGGCCCAACACCTTGACTGGCATTTCTCTGGCCCTT	1844
QY	850	CTAGCCTCAGTCGATGCCCTGACCTTTGGTCAAGTTCTCTGAGTACGGAGCCCGCTGGAG	909
Db	1845	CTAGCCTCAGTCGATGCCCTGACCTTTGGTCAAGTTCTCTGAGTACGGAGCCCGCTGGAG	1904
QY	910	ACGGGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGTCCGAGGCATCGGTG	969
Db	1905	ACGGGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGGTCCGAGGCATCGGTG	1964
QY	970	CTGCTGCTCACTCTGGCCGACGTGCAGCGTCTCCGTCTCCTGTGTCCGGCCCTAT	1029

Db	1965	CTGCTGCTCACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCTGTGTCCGGGCTAT	2024
QY	1030	GGGAAGTCCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCA	1089
Db	2025	GGGAAGTCCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCA	2084
QY	1090	GGGCTGGCCCGCCGCACTGCCCCCTGGCCCTCAGTGGGAGAAATACGGGGCCTCCCACTTGC	1149
Db	2085	GGGCTGGCCCGCCGCACTGCCCCCTGGCCCTCAGTGGGAGAAATACGGGGCCTCCCACTTGC	2144
QY	1150	CTGCCCTACGCGCCACCTGAGGGTCAGCCAGAGCCCTTGGGCTTCAACGTGGCCCTGGTG	1209
Db	2145	CTGCCCTACGCGCCACCTGAGGGTCAGCCAGAGCCCTTGGGCTTCAACGTGGCCCTGGTG	2204
QY	1210	ATGATGAACCTCCTTCTGTTTCTTGGTCTGGCCGTGCGACTGCGCCATGGTGAGGACGTGGCCTGG	1269
Db	2205	ATGATGAACCTCCTTCTGTTTCTTGGTCTGGCCGTGCGACTGCGCCATGGTGAGGACGTGGCCTGG	2264
QY	1270	CTGCCGCGGGCGACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGACGTGGCCTGG	1329
Db	2265	CTGCCGCGGGCGACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGACGTGGCCTGG	2324
QY	1330	CTCATCTTCGCAGACGGGCTCCTCTACTGTGCCGTGGCCCTTCTCAGCTTCGCTCCATG	1389
Db	2325	CTCATCTTCGCAGACGGGCTCCTCTACTGTGCCGTGGCCCTTCTCAGCTTCGCTCCATG	2384
QY	1390	CTGGGCCCTCTTCCCTGTCAAGCCGAGGCCGTCAAGTCTGTCTCTGCTGGTGGTGGCTGCC	1449
Db	2385	CTGGGCCCTCTTCCCTGTCAAGCCGAGGCCGTCAAGTCTGTCTCTGCTGGTGGTGGCTGCC	2444
QY	1450	CTGCTGCTGCTGCTCAACCCACTGCTGTACTGCTCTTCAACCCCACTTCCGGGATGAC	1509
Db	2445	CTGCTGCTGCTGCTCAACCCACTGCTGTACTGCTCTTCAACCCCACTTCCGGGATGAC	2504
QY	1510	CTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGCGGCCGG	1569
Db	2505	CTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGCGGCCGG	2564
QY	1570	GAGCTGGAGAAAGAGCTCCTGTGATTCTACCCAGGCCCTTGGTAGCCCTTCTCTGATGTGGAT	1629
Db	2565	GAGCTGGAGAAAGAGCTCCTGTGATTCTACCCAGGCCCTTGGTAGCCCTTCTCTGATGTGGAT	2624
QY	1630	CTCATTTCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCC	1689
Db	2625	CTCATTTCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCC	2684
QY	1690	TCAGTGACCCCTCATCTCCTGTGACGAGCCAGGGGCCCTCCAGGCTGGAGGGCAGCCATTGT	1749
Db	2685	TCAGTGACCCCTCATCTCCTGTGACGAGCCAGGGGCCCTCCAGGCTGGAGGGCAGCCATTGT	2744
QY	1750	GTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTG	1809
Db	2745	GTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTG	2804
QY	1810	CTGAGGCGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTGAGGGGTGGCGGCTTTTCAG	1869
Db	2805	CTGAGGCGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTGAGGGGTGGCGGCTTTTCAG	2864
QY	1870	CCCTCTGGCTTGGCCTTTGCTTCACACGTG	1899
Db	2865	CCCTCTGGCTTGGCCTTTGCTTCACACGTG	2894

RESULT 9
AAI67925
ID AAI67925 standard; cDNA; 2208 BP.
XX
AC AAI67925;
XX
DT 13-MAR-2002 (first entry)
XX
DE Human LGR6 polypeptide coding sequence.
XX

QY 552 AGCAGAGAACCACTATGACACGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 611
|||||
Db 861 AGCAGAGAACCACTATGACACGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA 920
|||||
QY 612 GCCACACCCAGTGTCAGTGACCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 671
|||||
Db 921 GCCACACCCAGTGTCAGTGACCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 980
|||||
QY 672 CTTTGAAGCTGGGGCATCCGCCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG 731
|||||
Db 981 CTTTGAAGCTGGGGCATCCGCCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG 1040
|||||
QY 732 CAATGGACTGGTGCTGCTGACCGTGTTCGCTGGCGGCTGCCCCCTGCCCCCGGTCAA 791
|||||
Db 1041 CAATGGACTGGTGCTGCTGACCGTGTTCGCTGGCGGCTGCCCCCTGCCCCCGGTCAA 1100
|||||
QY 792 GTTTGTGGTAGGTGCGATTGACGCGCCCAACACCTTGACTGGCATTTCTGTGGCCTTCT 851
|||||
Db 1101 GTTTGTGGTAGGTGCGATTGACGCGCCCAACACCTTGACTGGCATTTCTGTGGCCTTCT 1160
|||||
QY 852 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC 911
|||||
Db 1161 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC 1220
|||||
QY 912 GGGGTAGGCTGCCGGCCACTGGCTTCTTGGCAGTACTTGGGTGGAGGCATCGGTGCT 971
|||||
Db 1221 GGGGTAGGCTGCCGGCCACTGGCTTCTTGGCAGTACTTGGGTGGAGGCATCGGTGCT 1280
|||||
QY 972 GCTGTCACCTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGCCCTATGG 1031
|||||
Db 1281 GCTGTCACCTCTGGCCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGCCCTATGG 1340
|||||
QY 1032 GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGCTGCCCTGGCACTGGCAGG 1091
|||||
Db 1341 GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGCTGCCCTGGCACTGGCAGG 1400
|||||
QY 1092 GCTGCCGCCGCACTGCCCTTGGCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCT 1151
|||||
Db 1401 GCTGCCGCCGCACTGCCCTTGGCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGCT 1460
|||||
QY 1152 GCCCTACGCGCCACCTGAGGGTACGCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGAT 1211
|||||
Db 1461 GCCCTACGCGCCACCTGAGGGTACGCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGAT 1520
|||||
QY 1212 GATGAACCTCTTCTGTTTCCCTGGTGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCT 1271
|||||
Db 1521 GATGAACCTCTTCTGTTTCCCTGGTGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCT 1580
|||||
QY 1272 GCCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGTGTAGGCACGTGGCCCTGGCT 1331
|||||
Db 1581 GCCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGTGTAGGCACGTGGCCCTGGCT 1640
|||||
QY 1332 CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCCTTCTCAGCTTCGCCCTCCATGCT 1391
|||||
Db 1641 CATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCCTTCTCAGCTTCGCCCTCCATGCT 1700
|||||
QY 1392 GGGCTCTTCCCTGTACGCCCGAGGCCGTCAAGTCTGTCTGTGGTGGTGTGCCCT 1451
|||||
Db 1701 GGGCTCTTCCCTGTACGCCCGAGGCCGTCAAGTCTGTCTGTGGTGGTGTGCCCT 1760
|||||
QY 1452 GCCTGCTGCTCAACCCACTGCTGTACCTGTCTTCAACCCCACTTCCGGGATGACCT 1511
|||||
Db 1761 GCCTGCTGCTCAACCCACTGCTGTACCTGTCTTCAACCCCACTTCCGGGATGACCT 1820
|||||
QY 1512 TCGGCGGCTTCGGCCCCCGGCAGGGGACTCAGGGCCCCCTAGCTATGCTGCGGCCGGGA 1571
|||||
Db 1821 TCGGCGGCTTCGGCCCCCGGCAGGGGACTCAGGGCCCCCTAGCTATGCTGCGGCCGGGA 1880
|||||
QY 1572 GCTGAGAAAGAGCTCCTGTGATTTACCCAGGCCCTGGTAGGCTTCTCTGATGTGGATCT 1631
|||||
Db 1881 GCTGAGAAAGAGCTCCTGTGATTTACCCAGGCCCTGGTAGGCTTCTCTGATGTGGATCT 1940
|||||
QY 1632 CATCTGGAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCCTC 1691
|||||

Db 1941 CATCTGGAAGCTTCTGAAGCTGGCGGCCCTGGGCTGGAGACCTATGGCTTCCCTC 2000
|||||
QY 1692 AGTGACCCCTCATCTCCTGTCTCAGCAGCCAGGGGCCCAAGGCTGGAGGGCAGCATTGTGT 1751
|||||
Db 2001 AGTGACCCCTCATCTCCTGTCTCAGCAGCCAGGGGCCCAAGGCTGGAGGGCAGCATTGTGT 2060
|||||
QY 1752 AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTGCT 1811
|||||
Db 2061 AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTGCT 2120
|||||
QY 1812 GAGGGCAGAGGGATCTACCCAGCAGGTGGAGGCTTGTTCAGGGGGTGGCGCTTTTCAGCC 1871
|||||
Db 2121 GAGGGCAGAGGGATCTACCCAGCAGGTGGAGGCTTGTTCAGGGGGTGGCGCTTTTCAGCC 2180
|||||
QY 1872 CTCTGGCTTGGCCTTTGCTTCACACGTG 1899
|||||
Db 2181 CTCTGGCTTGGCCTTTGCTTCACACGTG 2208
|||||
RESULT 11
ADK19412
ID ADK19412 standard; cDNA; 2208 BP.
XX
AC ADK19412;
XX
DT 17-JUN-2004 (first entry)
XX
DE ORF of partial cDNA encoding human LGR6 polypeptide #2.
XX
KW G-protein coupled receptor; GPCR; large G-protein coupled receptor 6;
KW LGR6; weight disorder; neural disorder; endocrine disorder;
KW cardiovascular disorder; anorectic; anabolic; immunomodulator;
KW neuroprotective; nootropic; antiparkinsonian; anti-HIV; anticonvulsant;
KW antithyroid; osteopathic; cardiant; vasotropic; hypotensive;
KW antiarteriosclerotic; antiarrhythmic; human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2208
FT /*tag= a
FT /partial
FT /product= "LGR6 polypeptide #2"
FT /note= "This sequence lacks both start and stop codons"
XX
PN US2004058377-A1.
XX
PD 25-MAR-2004.
XX
PF 18-SEP-2003; 2003US-00664667.
XX
PR 06-MAY-1999; 99US-0132896P.
PR 08-MAY-2000; 2000US-00566588.
PR 08-MAY-2001; 2001US-00851595.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gu W;
XX
DR WPI; 2004-268789/25.
DR P-PSDB; ADK19411.
XX
PT New large G-protein coupled receptor 6 nucleic acid molecules and
PT polypeptides, useful for diagnosing, preventing or treating diseases
PT associated with aberrant nucleic acid or protein activity, e.g. obesity,
PT anorexia or cachexia.
XX
PS Claim 2; SEQ ID NO 9; 145pp; English.
XX
CC The present invention relates to the isolation of novel members of the G-
CC protein coupled receptor (GPCR) family designated as large G-protein
CC coupled receptor 6 (LGR6), and the polynucleotide sequences encoding

CC them. The invention also discloses LGR6 fusion proteins, antigenic
CC peptides, anti-LGR6 antibodies, recombinant expression vectors, host
CC cells, and non-human transgenic animals in which an LGR6 gene has been
CC introduced or disrupted. The LGR6 polynucleotide sequences, polypeptide
CC sequences, and antibodies are useful for diagnosing, treating or
CC preventing diseases associated with aberrant LGR6 expression or activity,
CC such as weight disorders (e.g. obesity, anorexia nervosa or cachexia),
CC neural disorders (e.g. central nervous system disorder, including
CC Alzheimer's disease, Parkinson's disease, AIDS-related dementia, multiple
CC sclerosis and Huntington's disease), endocrine disorders (e.g.
CC hypothyroidism, hyperthyroidism or acromegaly), or cardiovascular
CC disorders (e.g. ischaemia-reperfusion injury, coronary artery disease,
CC myocardial infarction, arrhythmia, atherosclerosis, hypertension or
CC congestive heart failure). The LGR6 polynucleotide and polypeptide
CC sequences are also useful as targets for developing modulating agents
CC that regulate a variety of cellular processes, e.g. neural and endocrine
CC processes and thermogenesis. They can be used in screening assays (e.g.
CC chromosome mapping, tissue typing or in forensic biology), or in
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials or pharmacogenomics). The present sequence
CC encodes a human LGR6 polypeptide.

XX
SQ Sequence 2208 BP; 396 A; 710 C; 631 G; 471 T; 0 U; 0 Other;

Query Match 92.4%; Score 1754.4; DB 12; Length 2208;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1766; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY	132	ACGGCCCTCCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG	191
Db	442	ATCGCCCTCCAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG	500
QY	192	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCTT	251
Db	501	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCTT	560
QY	252	CTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTGACCACTGCC	311
Db	561	CTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTGACCACTGCC	620
QY	312	CCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA	371
Db	621	CCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA	680
QY	372	GGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCA	431
Db	681	GGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCA	740
QY	432	GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGAGGCTGA	491
Db	741	GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGAGGCTGA	800
QY	492	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGSCCCCTGGGCCCTCCTTGCCAGACA	551
Db	801	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGSCCCCTGGGCCCTCCTTGCCAGACA	860
QY	552	AGCAGAGAACCACTATGACAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA	611
Db	861	AGCAGAGAACCACTATGACAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAA	920
QY	612	GCCACACCCCACTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTAGTACCT	671
Db	921	GCCACACCCCACTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTAGTACCT	980
QY	672	CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG	731
Db	981	CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTG	1040
QY	732	CAATGGACTGGTGTGCTGACCGTGTTCGCTGGGGGCTGCCCCCTGCCCCCGGTCAA	791
Db	1041	CAATGGACTGGTGTGCTGACCGTGTTCGCTGGGGGCTGCCCCCTGCCCCCGGTCAA	1100
QY	792	GTTTGTGGTAGGTGCGATTGACGGGCCCAACACCTTGACTGGCATTTTCCTGFGGCCTTCT	851

Db	1101	GTTTGTGGTAGTGGATTGCAGGGCGCAACACACTTGACTGGCAFTTCTGTGGCCTTCT	1160
QY	852	AGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	911
Db	1161	AGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGAC	1220
QY	912	GGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTTGGGTGGAGGCAATCGGTGCT	971
Db	1221	GGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTTGGGTGGAGGCAATCGGTGCT	1280
QY	972	GCTGCTCACTCTGGCCGCGCAGTGCAGTGCAGCCTCCGTCTCCTGTGTCCGGGCTATGG	1031
Db	1281	GCTGCTCACTCTGGCCGCGCAGTGCAGTGCAGCCTCCGTCTCCTGTGTCCGGGCTATGG	1340
QY	1032	GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGG	1091
Db	1341	GAAGTCCCCCTCCCTGGGCAGCGTTTCGAGCAGGGGTCTTAGGCTGCCTGGCACTGGCAGG	1400
QY	1092	GCTGGCCGCCGCACTGCCCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCCCACTCTGCCT	1151
Db	1401	GCTGGCCGCCGCACTGCCCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCCCACTCTGCCT	1460
QY	1152	GCCCTACGCCCACTGAGGGTGCAGCCAGCAGCCCTGGGCTTTCACCGTGGCCCTGGTGAT	1211
Db	1461	GCCCTACGCCCACTGAGGGTGCAGCCAGCAGCCCTGGGCTTTCACCGTGGCCCTGGTGAT	1520
QY	1212	GATGAACCTCCTTCTGTTTCTGGTCTGGCCGGTGCCTACATCAAACTGTACTGTGACCT	1271
Db	1521	GATGAACCTCCTTCTGTTTCTGGTCTGGCCGGTGCCTACATCAAACTGTACTGTGACCT	1580
QY	1272	GCCGCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT	1331
Db	1581	GCCGCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT	1640
QY	1332	CATCTTCGACACGGGCTCCTCTACTGTCCGTGGCCTTCCCTCAGCTTCGGCTCCATGCT	1391
Db	1641	CATCTTCGACACGGGCTCCTCTACTGTCCGTGGCCTTCCCTCAGCTTCGGCTCCATGCT	1700
QY	1392	GGGCTCTTCCCTGTCA CGCCGAGGCCGTCAAAGTCTGTCTCTGCTGGTGGTGGCTGCCCT	1451
Db	1701	GGGCTCTTCCCTGTCA CGCCGAGGCCGTCAAAGTCTGTCTCTGCTGGTGGTGGCTGCCCT	1760
QY	1452	GCCTGCCTGCCTCAAACCCACTGCTGTACCTGCTCTTCAACCCCCACTTCGGGATGACCT	1511
Db	1761	GCCTGCCTGCCTCAAACCCACTGCTGTACCTGCTCTTCAACCCCCACTTCGGGATGACCT	1820
QY	1512	TCGGCGGCTTCGSCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTCGGCCGGGA	1571
Db	1821	TCGGCGGCTTCGSCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTCGGCCGGGA	1880
QY	1572	GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGATCT	1631
Db	1881	GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGATCT	1940
QY	1632	CATTCTGGAAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCCTC	1691
Db	1941	CATTCTGGAAAGCTTCTGAAGCTGGGCGGCCCTTGGGCTGGAGACCTATGGCTTCCCCTC	2000
QY	1692	AGTGACCCCTCATCTCTGTGAGCTGGGCGGCCCTTGGGCTGGAGGAGCCATTTGTGT	1751
Db	2001	AGTGACCCCTCATCTCTGTGAGCTGGGCGGCCCTTGGGCTGGAGGAGCCATTTGTGT	2060
QY	1752	AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTCCATGGATGGAGAACTGTGCT	1811
Db	2061	AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCTCCATGGATGGAGAACTGTGCT	2120
QY	1812	GAGGCGAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGGTGGCGGCTTTCAGCC	1871
Db	2121	GAGGCGAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGGTGGCGGCTTTCAGCC	2180
QY	1872	CTCTGGCTTGGCCTTGTCTCACACGTG 1899	

Db 2181 CTCTGGCTTGGCCTTTGCTTCACACGTG 2208

RESULT 12

AAI67924

ID AAI67924 standard; cDNA; 2711 BP.

XX

AC AAI67924;

XX

DT 13-MAR-2002 (first entry)

XX

DE Partial cDNA of human LGR6 polypeptide (clone fahr).

XX

KW Large G-protein coupled receptor 6; LGR6; GPCR; immunomodulator;

XX

KW anti-HIV; cytosstatic; nootropic; neuroprotective; antiparkinsonian;

XX

KW anticonvulsant; neuroleptic; antidepressant; tranquilizer; antimigraine;

XX

KW osteopathic; antiarteriosclerotic; vasotropic; hypotensive; cardiant;

XX

KW antiarrhythmic; anorectic; gene therapy; human; ss.

XX

OS Homo sapiens.

XX

XX

FH Key Location/Qualifiers

FT CDS 1..2211

FT /*tag= a

FT /product= "LGR6 polypeptide"

XX

PN WO200185768-A2.

XX

XX

PD 15-NOV-2001.

XX

PF 08-MAY-2001; 2001WO-US015002.

XX

XX

PR 08-MAY-2000; 2000US-00566588.

XX

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

XX

PI Gu W;

XX

DR WPI; 2002-055584/07.

DR P-PSDB; AAG66140.

XX

XX

PT Novel isolated large G-protein coupled receptor 6 polypeptide, useful for

PT diagnosing and treating weight disorder, metabolic disorder, central

PT nervous system disorder, endocrine disorder and cardiovascular disorder.

XX

PS Claim 2; Fig 8; 198pp; English.

XX

CC The invention provides isolated large G-protein coupled receptor 6 (LGR6)

CC polypeptides and polynucleotides encoding them. The LGR6 polypeptides and

CC polynucleotides are useful as targets for developing modulating agents

CC that regulate a variety of cellular process, e.g. neural and endocrine

CC processes, as well as thermogenesis. They are useful for developing novel

CC diagnostic and therapeutic agents for LGR6 associated disorders such as

CC weight disorders (anorexia, obesity), eating disorders, acquired

CC immunodeficiency syndrome (AIDS)-related wasting, cancer-related wasting,

CC metabolic disorders, central nervous system disorders (e.g. Alzheimer's

CC disease, Parkinson's disease, Huntington's disease, Gilles de la

CC Tourette's syndrome, multiple sclerosis, amyotrophic lateral sclerosis,

CC epilepsy, Jakob-Creutzfeldt disease, depression, schizophrenia,

CC obsessive-compulsive disorder, anxiety, panic disorder, migraine),

CC endocrine disorders (hypo and hyperthyroidism, dwarfism, gigantism,

CC acromegaly), and cardiovascular disorders (atherosclerosis, restenosis,

CC hypertension, myocardial infarction, arrhythmia). The LGR6 polypeptides,

CC polynucleotides and antibodies are useful in screening assays, detection

CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),

CC predictive medicine (e.g. diagnostic assays, prognostic assays,

CC monitoring clinical trials and pharmacogenomics), and in methods of

CC treatment (e.g. therapeutic and prophylactic). The present sequence

CC represents a partial cDNA sequence of human LGR6 polypeptide

XX

SQ Sequence 2711 BP; 530 A; 837 C; 740 G; 604 T; 0 U; 0 Other;

Query Match

92.4%; Score 1754.4; DB 6; Length 2711;

		Best Local Similarity 99.9%; Pred. No. 0;				Matches 1766; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			
Qy	132	AGCGGCTCCAACACAACCGCATCTGGAAATTGGAGCTNGACACACCTTCAGCCAGCTGAG	191						
Db	442	ATCGGCTCCAACACAACCGCATCTGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG	500						
Qy	192	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTTGAGGCTT	251						
Db	501	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTTGAGGCTT	560						
Qy	252	CTCCACCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACACTGCC	311						
Db	561	CTCCACCTGCACTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACACTGCC	620						
Qy	312	CTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA	371						
Db	621	CTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCA	680						
Qy	372	GGCCTTCTCAAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCCTATGCCTACCA	431						
Db	681	GGCCTTCTCAAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCCTATGCCTACCA	740						
Qy	432	GTGCTGTCCCTATGGGATGTGTCCAGCTTCTTCAAGGCTCTGGGCAGTGGGAGGCTGA	491						
Db	741	GTGCTGTCCCTATGGGATGTGTCCAGCTTCTTCAAGGCTCTGGGCAGTGGGAGGCTGA	800						
Qy	492	AGACCTTCACCTTGATGATGATGAGGAGTCTTCAAAAAGGCCCTTGGCCAGACA	551						
Db	801	AGACCTTCACCTTGATGATGATGAGGAGTCTTCAAAAAGGCCCTTGGCCAGACA	860						
Qy	552	AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCAGCTGGAGATGGAGGACTCAA	611						
Db	861	AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCAGCTGGAGATGGAGGACTCAA	920						
Qy	612	GCCACACCCAGTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	671						
Db	921	GCCACACCCAGTGTCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	980						
Qy	672	CTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGSCCATCTGTGCTCTCCGTGCTCTG	731						
Db	981	CTTTGAAAGCTGGGGCATCCGCTGGCCGTGTGGSCCATCTGTGCTCTCCGTGCTCTG	1040						
Qy	732	CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGGGCTGCCCTTGGCCCGGTCAA	791						
Db	1041	CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGGGCTGCCCTTGGCCCGGTCAA	1100						
Qy	792	GTTTGTGGTAGGTGCGATTGCAGGCGCCAAACACTTGACTGGCATTTCTGTGGCCTTCT	851						
Db	1101	GTTTGTGGTAGGTGCGATTGCAGGCGCCAAACACTTGACTGGCATTTCTGTGGCCTTCT	1160						
Qy	852	AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGTGGAGAC	911						
Db	1161	AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCCGTGGAGAC	1220						
Qy	912	GGGGCTAGGCTGCCGGGCCACTGGCTTCCCTGGCAGTACTTGGGTCCGAGGCATCGGTCT	971						
Db	1221	GGGGCTAGGCTGCCGGGCCACTGGCTTCCCTGGCAGTACTTGGGTCCGAGGCATCGGTCT	1280						
Qy	972	GCTGCTCACTCTGGCCCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCCTATGG	1031						
Db	1281	GCTGCTCACTCTGGCCCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCCTATGG	1340						
Qy	1032	GAAGTCCCCCTCCCTGGGAGCGGTTTCGAGCAGGGGTCTTAGGCTGCCCTGGCACTGGCAGG	1091						
Db	1341	GAAGTCCCCCTCCCTGGGAGCGGTTTCGAGCAGGGGTCTTAGGCTGCCCTGGCACTGGCAGG	1400						
Qy	1092	GCTGGCCGCCGACTGCCCTGGCCCTCAGTGGGAGATACGGGGCCCTCCCACTCTGCCT	1151						
Db	1401	GCTGGCCGCCGACTGCCCTGGCCCTCAGTGGGAGATACGGGGCCCTCCCACTCTGCCT	1460						
Qy	1152	GCCCTACGGCCACCTGAGGGTCAGCCAGCAGCCCTTGGGCTTACCCGTGGCCCTGTGAT	1211						

Db 1461 GCCCTACGGGCCACCTGAGGGTCAGCCAGCAGCCCTGGGGCTTACCGTGGCCCTGGTGAT 1520

Qy 1212 GATGAATCCTTCTGTTTCTGTGTCGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCT 1271

Db 1521 GATGAATCCTTCTGTTTCTGTGTCGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCT 1580

Qy 1272 GCCGCGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGTGTGAGGCACGTGGCCCTGGCT 1331

Db 1581 GCCGCGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGTGTGAGGCACGTGGCCCTGGCT 1640

Qy 1332 CATCTTCGAGACGGGCTCCTCTACTGTCCCGTGGCCCTTCTCTCAGCTTCGCCCTCCATGCT 1391

Db 1641 CATCTTCGAGACGGGCTCCTCTACTGTCCCGTGGCCCTTCTCTCAGCTTCGCCCTCCATGCT 1700

Qy 1392 GGGCTCTTCCCTGTCAAGCCCGAGGCCCGTCAAGTCTGTCTGTGGTGGTGGTGGCCCT 1451

Db 1701 GGGCTCTTCCCTGTCAAGCCCGAGGCCCGTCAAGTCTGTCTGTGGTGGTGGTGGCCCT 1760

Qy 1452 GCCTGCTGCCCTCAACCCACTGTGTACTCTGTCTTCAACCCCACTTCCGGGATGACCT 1511

Db 1761 GCCTGCTGCCCTCAACCCACTGTGTACTCTGTCTTCAACCCCACTTCCGGGATGACCT 1820

Qy 1512 TCGCGGCTTCGGCCCCCGCGAGGGGACTCAGGGCCCCCTAGCCCTATGCTGCGGCCGGGA 1571

Db 1821 TCGCGGCTTCGGCCCCCGCGAGGGGACTCAGGGCCCCCTAGCCCTATGCTGCGGCCGGGA 1880

Qy 1572 GCTGAGAAAGAGCTCCTGTGTATTCTACCCAGGCCCTGTAGCCCTTCTCTGATGTGGATCT 1631

Db 1881 GCTGAGAAAGAGCTCCTGTGTATTCTACCCAGGCCCTGTAGCCCTTCTCTGATGTGGATCT 1940

Qy 1632 CATCTGGAAGCTTCTGAAGCTGGGGCGGCCCTGGGCTGGAGACCTATGGCTTCCCCTC 1691

Db 1941 CATCTGGAAGCTTCTGAAGCTGGGGCGGCCCTGGGCTGGAGACCTATGGCTTCCCCTC 2000

Qy 1692 AGTGACCCCTCATCTCCTGTACAGAGCCAGGGGCCCCCAAGGCTGGAGGCGAGCCATTGTGT 1751

Db 2001 AGTGACCCCTCATCTCCTGTACAGAGCCAGGGGCCCCCAAGGCTGGAGGCGAGCCATTGTGT 2060

Qy 1752 AGAGCCAGAGGGGAAACCATTGTGGGAACCCCAACCCTCATGGATGGAGAACTGTGCT 1811

Db 2061 AGAGCCAGAGGGGAAACCATTGTGGGAACCCCAACCCTCATGGATGGAGAACTGTGCT 2120

Qy 1812 GAGGCGAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGTGGCGGCTTTCAGCC 1871

Db 2121 GAGGCGAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGTGGCGGCTTTCAGCC 2180

Qy 1872 CTCTGGCTTGGCCTTTGCTTACACAGTG 1899

Db 2181 CTCTGGCTTGGCCTTTGCTTACACAGTG 2208

RESULT 13

ADN02245

ID ADN02245 standard; cDNA; 2711 BP.

XX AC ADN02245;

XX DT 17-JUN-2004 (first entry)

XX DE Human partial large G protein-coupled receptor, LGR6, cDNA #2.

XX KW Human; ss; large G protein-coupled receptor 6; LGR6; heart failure; ischaemic heart disease; myocardial infarction; hypertension; pericarditis; atherosclerosis; hepatic failure; viral hepatitis; cancer; intracerebral haemorrhage; brain abscess; Alzheimer's disease; pick disease; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; inflammatory bowel disease; Crohn's disease; benign prostatic hypertrophy; systemic lupus erythematosus.

OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 1. .2211

FT /*tag= a

FT /partial

FT /note= "No start codon shown"

FT /product= "Partial LGR6"

XX

PN US2003166047-A1.

XX 04-SEP-2003.

XX

PF 08-MAY-2001; 2001US-00851595.

XX

PR 06-MAY-1999; 99US-0132896P.

PR 08-MAY-2000; 2000US-00566588.

XX (MILL-) MILLENNIUM PHARM INC.

PA

XX Gu W;

PI

XX WPI; 2003-898067/82.

DR P-PSDB; ADN02246.

XX

PT New isolated LGR6 nucleic acids and polypeptides, useful for diagnosing and treating LGR6-mediated disorders, such as myocardial infarction, hypertension, atherosclerosis, viral hepatitis, cancer and/or Alzheimer's disease.

Claim 1; SEQ ID NO 7; 145pp; English.

The invention relates to an isolated LGR6 (large G protein-coupled receptor) nucleic acid molecule comprising the mouse and human cDNA sequences appearing as ADN02239, ADN02241, ADN02242, ADN02244, ADN02245, ADN02247, ADN02248 and ADN02250. Also included are a host cell or a non-human mammalian host cell containing an LGR6 nucleic acid (and producing LGR6), an isolated LGR6 polypeptide appearing as ADN02240, ADN02243, ADN02246 and ADN02249, an antibody which selectively binds to LGR6, a method for detecting the presence of LGR6 in a sample, a kit (comprising a compound which selectively binds to LGR6, or hybridises to LGR6 nucleic acid, and instructions for use), a method for detecting LGR6 nucleic acid in a sample, a method for identifying a compound which binds to LGR6, a method for modulating the activity of LGR6 and a method for identifying a compound that modulates the activity of LGR6. The methods and compositions of the present invention are useful for diagnosing and treating large G-protein coupled receptor 6 (LGR6)-mediated or -related disorders, such as heart failure, ischaemic heart disease, myocardial infarction, hypertension, pericarditis, atherosclerosis, hepatic failure, viral hepatitis, cancer, intracerebral haemorrhage, brain abscess, Alzheimer's disease, Pick disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, inflammatory bowel disease, Crohn's disease, benign prostatic hypertrophy and systemic lupus erythematosus. The present sequence is a partial human cDNA for LGR6.

Sequence 2711 BP; 530 A; 837 C; 740 G; 604 T; 0 U; 0 Other;

Query Match 92.4%; Score 1754.4; DB 11; Length 2711;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1766; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 132 AGCGGCTCCAAACACAAACCGCATCTGGGAATTGGAGCTNGACACCTTCAGCCAGCTGAG 191

Db 442 ATCGGCTCCAAACACAAACCGCATCTGGGAATTGGAGCT-GACACCTTCAGCCAGCTGAG 500

Qy 192 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCTT 251

Db 501 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCTT 560

Qy 252 CTCCACCCCTGCACTCCCTGGTCAAGCTGGAACCTGACAGACAACAGCTGACACTGCC 311

Db 561 CTCCACCCCTGCACTCCCTGGTCAAGCTGGAACCTGACAGACAACAGCTGACACTGCC 620

Qy 312 CCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTCTCTCCCA 371

Db 621 CCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTCTCTCCCA 680

QY	372	GGCCTTCTCCAAAGACAGATTTC	CCAAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCA	431
DB	681	GGCCTTCTCCAAAGACAGATTTC	CCAAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCA	740
QY	432	GTGCTGTCCCTATGGGATGTGTG	CCAGCTTCTTCAAGGCCCTCTGGGCAGTGGAGGCTGA	491
DB	741	GTGCTGTCCCTATGGGATGTGTG	CCAGCTTCTTCAAGGCCCTCTGGGCAGTGGAGGCTGA	800
QY	492	AGACCTTACCTTGATGATGAGGAGTCTT	CAAAAAGCCCCCTTGGGCCCTCCTTGGCCAGACA	551
DB	801	AGACCTTACCTTGATGATGAGGAGTCTT	CAAAAAGGCCCTTGGGCCCTCCTTGGCCAGACA	860
QY	552	AGCAGAGAACCACTATGACCAGGACCT	TGGATGAGCTCCAGCTGGAGATGGAGACTCAAA	611
DB	861	AGCAGAGAACCACTATGACCAGGACCT	TGGATGAGCTCCAGCTGGAGATGGAGACTCAAA	920
QY	612	GCCACACCCCAAGTGTCCAGTGTAGCCCT	ACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	671
DB	921	GCCACACCCCAAGTGTCCAGTGTAGCCCT	ACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	980
QY	672	CTTTGAAAGCTGGGGCATCCGCCCT	TGGCCGTGTGGCCCATCGTGTGCTCTCCGTGCTCTG	731
DB	981	CTTTGAAAGCTGGGGCATCCGCCCT	TGGCCGTGTGGCCCATCGTGTGCTCTCCGTGCTCTG	1040
QY	732	CAATGGACTGGTGTCTGACCGTGTTC	CGTGGGGCCCTGCCCCCTCGCCCGGTCAA	791
DB	1041	CAATGGACTGGTGTCTGACCGTGTTC	CGTGGGGCCCTGCCCCCTCGCCCGGTCAA	1100
QY	792	GTTTGTGTAGTGCAGTTGCAGGCGCC	CAACCTTGACTGGCATTTCTGTGGCCTTCT	851
DB	1101	GTTTGTGTAGTGCAGTTGCAGGCGCC	CAACCTTGACTGGCATTTCTGTGGCCTTCT	1160
QY	852	AGCCTCAGTCGATGCCCTGACCTTT	TGGTCAGTTCTTGAGTACGGAGCCCGTGGGAGAC	911
DB	1161	AGCCTCAGTCGATGCCCTGACCTTT	TGGTCAGTTCTTGAGTACGGAGCCCGTGGGAGAC	1220
QY	912	GGGGCTAGGTGCGGGCCACTGGCTT	CCTGGCAGTACTTGGGTCGGAGGCATCGGTGCT	971
DB	1221	GGGGCTAGGTGCGGGCCACTGGCTT	CCTGGCAGTACTTGGGTCGGAGGCATCGGTGCT	1280
QY	972	GCTGCTCACTCTGGCCCGCAGTGC	AGCGTCTCCGTCTCCTGTGTCCGGCCCTATGG	1031
DB	1281	GCTGCTCACTCTGGCCCGCAGTGC	AGCGTCTCCGTCTCCTGTGTCCGGCCCTATGG	1340
QY	1032	GAAGTCCCCCTCCCTGGGCAGCGTT	CGAGCAGGGTCTTAGGCTGCCCTGGCAGG	1091
DB	1341	GAAGTCCCCCTCCCTGGGCAGCGTT	CGAGCAGGGTCTTAGGCTGCCCTGGCAGG	1400
QY	1092	GCTGGCCGCGCACTGCCCTGGCCT	CAGTGGAGAAATACGGGGCCTCCCACTCTGCCT	1151
DB	1401	GCTGGCCGCGCACTGCCCTGGCCT	CAGTGGAGAAATACGGGGCCTCCCACTCTGCCT	1460
QY	1152	GCCCTACGCGCACCTGAGGGTC	AGCCAGCCTGGGCTTACCGTGGCCCTGGTGAT	1211
DB	1461	GCCCTACGCGCACCTGAGGGTC	AGCCAGCCTGGGCTTACCGTGGCCCTGGTGAT	1520
QY	1212	GATGAACTCCTTCTGTTTCCCTGGT	CGTGGCCGCTACATCAAACTGACTGTGACCT	1271
DB	1521	GATGAACTCCTTCTGTTTCCCTGGT	CGTGGCCGCTACATCAAACTGACTGTGACCT	1580
QY	1272	GCCGGGGGCGACTTTGAGGCCGT	TGGGACTGCGCCCATGGTGGGCACGTGGCCCTGGCT	1331
DB	1581	GCCGGGGGCGACTTTGAGGCCGT	TGGGACTGCGCCCATGGTGGGCACGTGGCCCTGGCT	1640
QY	1332	CATCTTCGACAGCGGCTCCTCT	ACTGTCCCGTGGCCTTCCCTCAGCTTCGCTCCATGCT	1391
DB	1641	CATCTTCGACAGCGGCTCCTCT	ACTGTCCCGTGGCCTTCCCTCAGCTTCGCTCCATGCT	1700
QY	1392	GGGCCTCTTCCCTGTACGCCCG	AGCCGTCAGTCTGTCTCCTGCTGGTGGTGTGCCCCCT	1451
DB	1701	GGGCCTCTTCCCTGTACGCCCG	AGCCGTCAGTCTGTCTCCTGCTGGTGGTGTGCCCCCT	1760

QY	1452	GCCTGCCTGCCTCAACCCCACTGCTGTACTCTGCTCTTTCAACCCCCCACTTCGCGGATGACCT	1511
Db	1761	GCCTGCCTGCCTCAACCCCACTGCTGTACTCTGCTCTTTCAACCCCCCACTTCGCGGATGACCT	1820
QY	1512	TCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGCGGCCGGGA	1571
Db	1821	TCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGCGGCCGGGA	1880
QY	1572	GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGATCT	1631
Db	1881	GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGATCT	1940
QY	1632	CATTCTGGAAGCTTCTGAAGCTGGCGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCCTC	1691
Db	1941	CATTCTGGAAGCTTCTGAAGCTGGCGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCCTC	2000
QY	1692	AGTGACCCCTCATCTCTGTCTGTCAGCAGCCAGGGGGCCCCCAGGCTGGAGGCGAGCCATTGTGT	1751
Db	2001	AGTGACCCCTCATCTCTGTCTGTCAGCAGCCAGGGGGCCCCCAGGCTGGAGGCGAGCCATTGTGT	2060
QY	1752	AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT	1811
Db	2061	AGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCCTCCATGGATGGAGAACTGCTGCT	2120
QY	1812	GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGTGGCGCTTTCAGCC	1871
Db	2121	GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGTGGCGCTTTCAGCC	2180
QY	1872	CTCTGGCTTGGCTTTGCTTCACACGTG	1899
Db	2181	CTCTGGCTTGGCTTTGCTTCACACGTG	2208
RESULT 14			
ADK19410			
ID	ADK19410 standard; cDNA; 2711 BP.		
XX	ADK19410;		
AC			
XX			
DT	17-JUN-2004 (first entry)		
XX			
DE	Partial cDNA encoding human LGR6 polypeptide #2.		
XX			
KW	G-protein coupled receptor; GPCR; large G-protein coupled receptor 6;		
KW	LGR6; weight disorder; neural disorder; endocrine disorder;		
KW	cardiovascular disorder; anorectic; anabolic; immunomodulator;		
KW	neuroprotective; nootropic; antiparkinsonian; anti-HIV; anticonvulsant;		
KW	antithyroid; osteopathic; cardiac; vasotropic; hypotensive;		
KW	antiarteriosclerotic; antiarrhythmic; human; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key		
FT	CDS		
FT	1. .2211		
FT	/*tag= a		
FT	/partial		
FT	/product= "LGR6 polypeptide #2"		
FT	/note= "This sequence lacks a start codon"		
XX			
PN	US2004058377-A1.		
XX			
PD	25-MAR-2004.		
XX			
PF	18-SEP-2003; 2003US-00664667.		
XX			
PR	06-MAY-1999; 99US-0132896P.		
PR	08-MAY-2000; 2000US-00566588.		
PR	08-MAY-2001; 2001US-00851595.		
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
PI	Gu W;		
XX			

DR WPI; 2004-268789/25.
DR P-PSDB; ADK19411.
XX
PT New large G-protein coupled receptor 6 nucleic acid molecules and
PT polypeptides, useful for diagnosing, preventing or treating diseases
PT associated with aberrant nucleic acid or protein activity, e.g. obesity,
PT anorexia or cachexia.
XX
PS Claim 2; SEQ ID NO 7; 145pp; English.
XX
CC The present invention relates to the isolation of novel members of the G-
CC protein coupled receptor (GPCR) family designated as large G-protein
CC coupled receptor 6 (LGR6), and the polynucleotide sequences encoding
CC them. The invention also discloses LGR6 fusion proteins, antigenic
CC peptides, anti-LGR6 antibodies, recombinant expression vectors, host
CC cells, and non-human transgenic animals in which an LGR6 gene has been
CC introduced or disrupted. The LGR6 polynucleotide sequences, polypeptide
CC sequences, and antibodies are useful for diagnosing, treating or
CC preventing diseases associated with aberrant LGR6 expression or activity,
CC such as weight disorders (e.g. obesity, anorexia nervosa or cachexia),
CC neural disorders (e.g. central nervous system disorder, including
CC Alzheimer's disease, Parkinson's disease, AIDS-related dementia, multiple
CC sclerosis and Huntington's disease), endocrine disorders (e.g.
CC hypothyroidism, hyperthyroidism or acromegaly), or cardiovascular
CC disorders (e.g. ischaemia-reperfusion injury, coronary artery disease,
CC myocardial infarction, arrhythmia, atherosclerosis, hypertension or
CC congestive heart failure). The LGR6 polynucleotide and polypeptide
CC sequences are also useful as targets for developing modulating agents
CC that regulate a variety of cellular processes, e.g. neural and endocrine
CC processes and thermogenesis. They can be used in screening assays (e.g.
CC chromosome mapping, tissue typing or in forensic biology), or in
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials or pharmacogenomics). The present sequence
CC encodes a human LGR6 polypeptide.
XX

SQ Sequence 2711 BP; 530 A; 837 C; 740 G; 604 T; 0 U; 0 Other;

Query Match		92.4%;	Score 1754.4;	DB 12;	Length 2711;
Best Local Similarity		99.9%;	Pred. No. 0;		
Matches 1766;		Conservative 0;	Mismatches 1;	Indels 1;	Gaps 1;
QY	132	AGCGGCCTCCAACACACACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG	191		
Db	442	ATCGGCCTCCAACACACACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG	500		
QY	192	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCTT	251		
Db	501	CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCCTT	560		
QY	252	CTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAAACCAGCTGACACACTGCC	311		
Db	561	CTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAAACCAGCTGACACACTGCC	620		
QY	312	CCTGGCTGGAATTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACTTGTCTCTCTCCCCA	371		
Db	621	CCTGGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACTTGTCTCTCTCCCCA	680		
QY	372	GGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCCTTATGCTTACCCA	431		
Db	681	GGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCTTACCCA	740		
QY	432	GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGAGGCTGA	491		
Db	741	GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGCAGTGGAGGCTGA	800		
QY	492	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGCCCTCCTTGGCAGACA	551		
Db	801	AGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTTGGCCCTCCTTGGCAGACA	860		
QY	552	AGCAGAGAACCACTATACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAA	611		
Db	861	AGCAGAGAACCACTATACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAA	920		

QY	612	GCCACACCCCACTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	671
Db	921	GCCACACCCCACTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT	980
QY	672	CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGGCGTGGGCCATCGTGTGCTCTCCGTGCTCTG	731
Db	981	CTTTGAAAGCTGGGGCATCCGCCCTGGCCGTGGCGTGGGCCATCGTGTGCTCTCCGTGCTCTG	1040
QY	732	CAATGGACTGGTGTCTGCTGACCCGTGTTGCTGGCGGGCCCTGCCCCCTGCCCCCGGTCAA	791
Db	1041	CAATGGACTGGTGTCTGCTGACCCGTGTTGCTGGCGGGCCCTGCCCCCTGCCCCCGGTCAA	1100
QY	792	GTTTGTGGTAGTGCAGATTGCAGGCGCCAAACACTTGACTGGCATTTCCTGTGGCCTTCT	851
Db	1101	GTTTGTGGTAGTGCAGATTGCAGGCGCCAAACACTTGACTGGCATTTCCTGTGGCCTTCT	1160
QY	852	AGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCGCTGGGAGAC	911
Db	1161	AGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCGCTGGGAGAC	1220
QY	912	GGGGCTAGGCTCGCGGGCCACTGGCTTCTCGGCAGTACTTGGGTCGGAGGCATCGGTGCT	971
Db	1221	GGGGCTAGGCTCGCGGGCCACTGGCTTCTCGGCAGTACTTGGGTCGGAGGCATCGGTGCT	1280
QY	972	GCTGCTCACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCCTATGG	1031
Db	1281	GCTGCTCACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCCTATGG	1340
QY	1032	GAAGTCCCCCTCCCTGGGCAGCGTTTCAGCAGGGGTCTTAGGTCGCTGGCACTGGCAGG	1091
Db	1341	GAAGTCCCCCTCCCTGGGCAGCGTTTCAGCAGGGGTCTTAGGTCGCTGGCACTGGCAGG	1400
QY	1092	GCTGGCCGCCGCACTGCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCCCACTCTGCCT	1151
Db	1401	GCTGGCCGCCGCACTGCCCTGGCCTCAGTGGGAGAAATACGGGGCCTCCCACTCTGCCT	1460
QY	1152	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT	1211
Db	1461	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT	1520
QY	1212	GATGAACCTCTTCTGTTTCTGGTCTGTGGSCGGTGCCCTACATCAAACTGTACTGTGACCT	1271
Db	1521	GATGAACCTCTTCTGTTTCTGGTCTGTGGSCGGTGCCCTACATCAAACTGTACTGTGACCT	1580
QY	1272	GCCGGGGGGGCACTTTGAGGCCGTGTGGACTGCGCCCATGGTGAGGCACGTGGCCCTGGCT	1331
Db	1581	GCCGGGGGGGCACTTTGAGGCCGTGTGGACTGCGCCCATGGTGAGGCACGTGGCCCTGGCT	1640
QY	1332	CATCTTCGACAGCGGCTCCTCTACTGTCCCGTGGCCCTTCTCAGCTTCGCCCTCCATGCT	1391
Db	1641	CATCTTCGACAGCGGCTCCTCTACTGTCCCGTGGCCCTTCTCAGCTTCGCCCTCCATGCT	1700
QY	1392	GGGCCCTTCCCTGTACGCCCCGAGGCCGTCAAGTCTGTCTCTGTGGTGGTGTGCCCT	1451
Db	1701	GGGCCCTTCCCTGTACGCCCCGAGGCCGTCAAGTCTGTCTCTGTGGTGGTGTGCCCT	1760
QY	1452	GCCTGCCCTGCCCTCAACCCCACTGCTGTACCTGCTCTTCAACCCCCCACTTCGGGGATGACCT	1511
Db	1761	GCCTGCCCTGCCCTCAACCCCACTGCTGTACCTGCTCTTCAACCCCCCACTTCGGGGATGACCT	1820
QY	1512	TCGGGGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGCGGCCGGGA	1571
Db	1821	TCGGGGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCCTATGCTGCGGCCGGGA	1880
QY	1572	GCTGGAGAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGATCT	1631
Db	1881	GCTGGAGAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGTGGATCT	1940
QY	1632	CATTCTGGAAGCTTCTGAAGCTGGCGGCCCTTGGGCTGGAGACCTATGCGCTTCCCCTC	1691
Db	1941	CATTCTGGAAGCTTCTGAAGCTGGCGGCCCTTGGGCTGGAGACCTATGCGCTTCCCCTC	2000
QY	1692	AGTGACCCCTCATCTCCTGTGACGACGCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGT	1751

Db 2001 AGTACCCTCATCTCTGTACAGACCAGGGGCCCCAGGCTGGAGGGCAGCCATTGTGT 2060
Qy 1752 AGAGCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCATGGATGGAGAACTGCTGCT 1811
Db 2061 AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCATGGATGGAGAACTGCTGCT 2120
Qy 1812 GAGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGGTGGCGGCTTTCAGCC 1871
Db 2121 GAGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACAGGGGGTGGCGGCTTTCAGCC 2180
Qy 1872 CTCTGGCTTGGCCTTTGCTTCACACGTG 1899
Db 2181 CTCTGGCTTGGCCTTTGCTTCACACGTG 2208

RESULT 15
AAI67927
ID AAI67927 standard; cDNA; 2901 BP.
XX
AC AAI67927;
XX
DT 13-MAR-2002 (first entry)
XX
DE Human LGR6 polypeptide coding sequence (clone Fbh150881).
XX
KW Large G-protein coupled receptor 6; LGR6; GPCR; immunomodulator;
KW anti-HIV; cytostatic; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; neuroleptic; antidepressant; tranquilizer; antimigraine;
KW osteopathic; antiarteriosclerotic; vasotropic; hypotensive; cardiant;
KW antiarrhythmic; anorectic; gene therapy; human; ss.
XX

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1. .2901
FT /*tag= a
FT /product= "LGR6 polypeptide"
XX
PN WO200185768-A2.
XX
PD 15-NOV-2001.
XX
PF 08-MAY-2001; 2001WO-US015002.
XX
PR 08-MAY-2000; 2000US-00566588.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gu W;
XX
DR WPI; 2002-055584/07.
DR P-PSDB; AAG66141.
XX
PT Novel isolated large G-protein coupled receptor 6 polypeptide, useful for
PT diagnosing and treating weight disorder, metabolic disorder, central
PT nervous system disorder, endocrine disorder and cardiovascular disorder.
XX
PS Claim 2; Fig 14; 198pp; English.
XX

CC The invention provides isolated large G-protein coupled receptor 6 (LGR6)
CC polypeptides and polynucleotides encoding them. The LGR6 polypeptides and
CC polynucleotides are useful as targets for developing modulating agents
CC that regulate a variety of cellular process, e.g. neural and endocrine
CC processes, as well as thermogenesis. They are useful for developing novel
CC diagnostic and therapeutic agents for LGR6 associated disorders such as
CC weight disorders (anorexia, obesity), eating disorders, acquired
CC immunodeficiency syndrome (AIDS)-related wasting, cancer-related wasting,
CC metabolic disorders, central nervous system disorders (e.g. Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, Gilles de la
CC Tourette's syndrome, multiple sclerosis, amyotrophic lateral sclerosis,
CC epilepsy, Jakob-Creutzfeldt disease, depression, schizophrenia,
CC obsessive-compulsive disorder, anxiety, panic disorder, migraine),

CC endocrine disorders (hypo and hyperthyroidism, dwarfism, gigantism,
CC acromegaly), and cardiovascular disorders (atherosclerosis, restenosis,
CC hypertension, myocardial infarction, arrhythmia). The LGR6 polypeptides,
CC polynucleotides and antibodies are useful in screening assays, detection
CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials and pharmacogenomics), and in methods of
CC treatment (e.g. therapeutic and prophylactic). The present sequence
CC represents a human LGR6 polypeptide coding sequence

XX
SQ Sequence 2901 BP; 513 A; 973 C; 818 G; 597 T; 0 U; 0 Other;
Query Match 92.4%; Score 1754.4; DB 6; Length 2901;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1766; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 132 AGCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG 191
Db 1135 ATCGGCTCCAACACAAACCGCATCTGGGAAATTGGAGCT-GACACCTTCAGCCAGCTGAG 1193
Qy 192 CTCCTGCAAGCCCTGGATCTTAGCTGGAACGGCCATCCGGTCCATCCACCCCTGAGGCCTT 251
Db 1194 CTCCTGCAAGCCCTGGATCTTAGCTGGAACGGCCATCCGGTCCATCCACCCCTGAGGCCTT 1253
Qy 252 CTCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACTGCC 311
Db 1254 CTCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACACAGCTGACCACTGCC 1313
Qy 312 CCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAGGGAACCTTGCTCTCTCCCA 371
Db 1314 CCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAGGGAACCTTGCTCTCTCCCA 1373
Qy 372 GGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGTGCCCTTATGCTTACCA 431
Db 1374 GGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGTGCCCTTATGCTTACCA 1433
Qy 432 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCAGTGGAGGCTGA 491
Db 1434 GTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCAGTGGAGGCTGA 1493
Qy 492 AGACCTTCACTTGATGATGAGGAGTCTTCAAAAGGCCCTCTGGGCCTCTTGGCAGACA 551
Db 1494 AGACCTTCACTTGATGAGGAGTCTTCAAAAGGCCCTCTGGGCCTCTTGGCAGACA 1553
Qy 552 AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGACTCAAA 611
Db 1554 AGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGACTCAAA 1613
Qy 612 GCCACACCCCACTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 671
Db 1614 GCCACACCCCACTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCT 1673
Qy 672 CTTTGAAAGCTGGGGCATCCGCCTGGCCGTGGGCCCATCGTGTGCTCTCCGTGCTCTG 731
Db 1674 CTTTGAAAGCTGGGGCATCCGCCTGGCCGTGGGCCCATCGTGTGCTCTCCGTGCTCTG 1733
Qy 732 CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGGCCCTGCCCCCTGCCCCCGGTCAA 791
Db 1734 CAATGGACTGGTGTGCTGACCGTGTTCGCTGGCGGGCCCTGCCCCCTGCCCCCGGTCAA 1793
Qy 792 GTTTGTGGTAGTGCGATTGCAGGCGCCCAACACTTGACTGGCATTTCTGTGGCCTTCT 851
Db 1794 GTTTGTGGTAGTGCGATTGCAGGCGCCCAACACTTGACTGGCATTTCTGTGGCCTTCT 1853
Qy 852 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTTGAGTACGGAGCCCGTGGGAGAC 911
Db 1854 AGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTTGAGTACGGAGCCCGTGGGAGAC 1913
Qy 912 GGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTCCGAGGATCGGTGCT 971
Db 1914 GGGGCTAGGCTGCCGGGCCACTGGCTTCTTGGCAGTACTTGGGTCCGAGGATCGGTGCT 1973
Qy 972 GCTGCTCACTCTGGCCGCGAGTGCAGTGCAGCGTCTCCGTCTCTGTGTCCGGGCCTATGG 1031

Db	1974	GCTGCTCACTCTGGCCGAGTGCAAGTCAGCGTCTCCGTCTCCTGTGTCCGGGCTATGG	2033
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Db	2034	GAAGTCCCCCTCCCTGGGAGCGTTTCGAGCAGGGGTCTAGGCTGCCGTGGCACTGGCAGG	2093
Qy	1092	GCTGGCCCGCCGCACTGCCCTGGCCTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCT	1151
Db	2094	GCTGGCCCGCCGCACTGCCCTGGCCTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCT	2153
Qy	1152	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT	1211
Db	2154	GCCCTACGCGCCACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGAT	2213
Qy	1212	GATGAACCTCCTTCTGTTCCTGGTCGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCT	1271
Db	2214	GATGAACCTCCTTCTGTTCCTGGTCGTGGCCGGTGCCCTACATCAAACTGTACTGTGACCT	2273
Qy	1272	GCCGCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT	1331
Db	2274	GCCGCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCT	2333
Qy	1332	CATCTTCGACAGCGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCATGCT	1391
Db	2334	CATCTTCGACAGCGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCATGCT	2393
Qy	1392	GGGCTCTTCCCTGTCAAGCCCGAGGCCGTCAAGTCTGTCTCTGTGGTGGTGGCCCCCT	1451
Db	2394	GGGCTCTTCCCTGTCAAGCCCGAGGCCGTCAAGTCTGTCTCTGTGGTGGTGGCCCCCT	2453
Qy	1452	GCCTGCCTGCCCTCAACCCACTGCTGTACTCTCTCAACCCCCACCTTCGGGGATGACCT	1511
Db	2454	GCCTGCCTGCCCTCAACCCACTGCTGTACTCTCTCAACCCCCACCTTCGGGGATGACCT	2513
Qy	1512	TCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGGGCCGGGGA	1571
Db	2514	TCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTGGGCCGGGGA	2573
Qy	1572	GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT	1631
Db	2574	GCTGGAGAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCT	2633
Qy	1632	CATTCTGGAAGCTTCTGAAGCTGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCCTC	1691
Db	2634	CATTCTGGAAGCTTCTGAAGCTGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCCTC	2693
Qy	1692	AGTGACCTCATCTCCTGTCAACAGCCAGGGGCCCCAGGCTGGAGGGCAGCCATTTGTGT	1751
Db	2694	AGTGACCTCATCTCCTGTCAACAGCCAGGGGCCCCAGGCTGGAGGGCAGCCATTTGTGT	2753
Qy	1752	AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTGCT	1811
Db	2754	AGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTGCT	2813
Qy	1812	GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGTGGCGGCTTTTCAGCC	1871
Db	2814	GAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTACGGGGTGGCGGCTTTTCAGCC	2873
Qy	1872	CTCTGGCTTGGCCTTTGCTTTCACACGTG	1899
Db	2874	CTCTGGCTTGGCCTTTGCTTTCACACGTG	2901

GenCore version 5.1.6
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QM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 11:57:53 ; Search time 4096.82 Seconds
(without alignments)
17643.956 Million cell updates/sec

Title: US-10-664-667-6
Perfect score: 1899
Sequence: 1 aatacgactcactatagggg.....tggcctttgcttcacacgtg 1899

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1811.6	95.4	3509	3	BC038795 Homo sapi
2	1325	69.8	2822	3	AK052873 Mus muscu
3	1298.2	68.4	3583	3	AK085901 Mus muscu
4	537	28.3	982	2	BF159363 601770339
5	534.4	28.1	819	4	BG863804 602798701
6	516.2	27.2	812	4	BG916782 602816031
7	481.4	25.4	690	2	BB636845 BB636845
8	479.8	25.3	3855	3	AK040883 Mus muscu
9	465.8	24.5	680	7	CN258480 170005321
10	457.6	24.1	753	4	BG916963 602816251
11	424.4	22.3	869	2	BF158974 601766476
12	385.2	20.3	461	2	BE149368 RC1-HT025
13	362.4	19.1	2724	9	AY411734 Homo sapi
14	355.6	18.7	2724	9	AY411732 Homo sapi
15	322.4	17.0	640	7	CO351740 DR AOV NR
16	282.4	14.9	310	7	Z44115 HSC1SG111 n
17	274	14.4	2593	9	AY411733 Pan trogl
18	268.4	14.1	1719	2	BF144122 601788812
19	256.4	13.5	471	5	BX281802 BX281802
20	256.4	13.5	771	5	BQ425502 AGENCOURT
21	239.2	12.6	3006	3	AK033699 Mus muscu
22	237.6	12.5	3035	3	AK044357 Mus muscu
23	225.4	11.9	282	2	BF375245 QV0-ST021
24	209.4	11.0	515	6	CA034787 4000482 B

25	203	10.7	1212	4	BM543032	BM543032 AGENCOURT
26	200.6	10.6	671	4	BM795259	BM795259 K-EST0077
27	200.6	10.6	776	5	BU708439	UI-M-FC0-
28	195	10.3	1104	1	AL530798	AL530798 AL530798
c	29	189.2	10.0	467	4	BM673325 UI-E-CR1-
	30	169.2	8.9	448	1	AI596321 ve23f10.y
	31	166.2	8.8	651	2	BB621262 BB621262
	32	166	8.7	800	4	BG196708 RST15934
	33	159.2	8.4	798	4	BI143698 602907345
	34	157.2	8.3	557	1	AA435175 ve23f10.y
c	35	155.2	8.2	807	3	AK016357 Mus muscu
c	36	155.2	8.2	816	6	BY716002 BY716002
	37	153.8	8.1	695	6	BY731701 BY731701
	38	150.2	7.9	607	5	BQ572012 UI-M-FB0-
	39	138.2	7.3	880	5	BQ216343 AGENCOURT
c	40	126.4	6.7	181	7	Z38618 HSC01D122 n
c	41	125.6	6.6	865	9	AL221328 Tetraodon
	42	124.8	6.6	839	4	BI150746 602914834
c	43	122.8	6.5	386	6	CA035351 4001250 B
	44	122.2	6.4	494	7	CN683525 E0180A02-
c	45	121.2	6.4	391	8	B53762 CIT-HSP-201

ALIGNMENTS

RESULT 1	BC038795	3509 bp	mRNA	linear	HTC 19-NOV-2003
BC038795	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6, mRNA (cdna clone IMAGE:5220507), with apparent retained intron.				
LOCUS	BC038795.1	GI:24433474			
DEFINITION	Homo sapiens (human)				
ACCESSION	BC038795				
VERSION	BC038795.1				
KEYWORDS	HTC.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 3509)				
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettaman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
MEDLINE	22388257				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 3509)				
AUTHORS	Strausberg,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov				

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Akhter, N., Ayèle, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 64 Row: n Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis

This clone has the following problem: retained intron.

FEATURES	Location/Qualifiers
source	1..3509
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="IMAGE:5220507"
	/tissue_type="Pancreas, Spleen, adult pooled"
	/clone_lib="NIH MGC_120"
	/lab_host="DH10B"
	/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match	95.4%;	Score	1811.6;	DB	3;	Length	3509;
Best Local Similarity	99.7%;	Pred.	No. 0;				
Matches	1825;	Conservative	0;	Mismatches	4;	Indels	1;
						Gaps	1;
QY	70	CGGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCGGCTCATCCAGCCTCTCTTGCTGCC	129				
Db	1063	GGGGCATGGAGCGGAGCCAGGGTCTGAGCCTGCGGCTCATCCAGCCTCTCTTGCTGCC	1122				
QY	130	CTAGCGGCCTCCACACAAACCGCATCTGGGAATTGGAGCTNGACACCTTCAGCCAGCTG	189				
Db	1123	CTAGCGGCCTCCACACAAACCGCATCTGGGAATTGGAGCT-GACACCTTCAGCCAGCTG	1181				
QY	190	AGCTCCCTGCAAGCCCTGGATCTTAGCTGGAAACCGCATCCGGTCCATCCACCTGAGGCC	249				
Db	1182	AGTCCCTGCAAGCCCTGGATCTTAGCTGGAAACCGCATCCGGTCCATCCACCTGAGGCC	1241				
QY	250	TTCTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTGACCACTG	309				
Db	1242	TTCTCCACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCAAGCTGACCACTG	1301				
QY	310	CCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCC	369				
Db	1302	CCCCTGGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCC	1361				
QY	370	CAGGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTATGCCTAC	429				
Db	1362	CAGGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTATGCCTAC	1421				
QY	430	CAGTGTGTCCCTATGGGATGTGTGCCAGCTTCTTAAGGCCCTCTGGGAGTGGGAGGCT	489				
Db	1422	CAGTGTGTCCCTATGGGATGTGTGCCAGCTTCTTAAGGCCCTCTGGGAGTGGGAGGCT	1481				
QY	490	GAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGCCTCCTTGCCAGA	549				
Db	1482	GAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGCCTCCTTGCCAGA	1541				
QY	550	CAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCA	609				

Db	1542	CAAGCAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCA	1601				
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QY	850	CTAGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCGCTGGGAG	909				
Db	1842	CTAGCCTCAGTCGATGCCCTGACCTTTTGGTCAGTTCTCTGAGTACGGAGCCGCTGGGAG	1901				
QY	910	ACGGGGCTAGGTGTCGGGCCACTGGCTTCTCGGCAGTACTTGGGTCGGAGGATCGGTG	969				
Db	1902	ACGGGGCTAGGTGTCGGGCCACTGGCTTCTCGGCAGTACTTGGGTCGGAGGATCGGTG	1961				
QY	970	CTGCTGCTCACTGCGCCGCGAGTGCAGTGCAGCGCTCTCCGTCTCCTGTGTCGGGCCCTAT	1029				
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Db	2022	GGGAAGTCCCCCTCCCTGGGCAGCGTTCCAGCAGGGGTCTTAGGCTGCCTGGCAGTGGCA	2081				
QY	1090	GGGCTGGCCGCGCACTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGC	1149				
Db	2082	GGGCTGGCCGCGCACTGCCCTTGGCCTCAGTGGGAGAAATACGGGGCCTCCCCACTCTGC	2141				
QY	1150	CTGCCCTACGCGCCACTGAGGGTCAGCAGCAGCCCTGGGCTTACCGTGGCCCTGGTG	1209				
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QY	1270	CTGCCGCGGGCGCACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGCACGTGGCCTGG	1329				
Db	2262	CTGCCGCGGGCGCACTTTGAGGCCGTGTGGACTGCGCCATGGTGAGGCACGTGGCCTGG	2321				
QY	1330	CTCATCTTCGAGACGGGCTCCTCTACTGTTCCTGGGCTTCCCTCAGCTTCGCTCCCATG	1389				
Db	2322	CTCATCTTCGAGACGGGCTCCTCTACTGTTCCTGGGCTTCCCTCAGCTTCGCTCCCATG	2381				
QY	1390	CTGGGCTCTTCCCTGTCAAGCCGAGGCGGTCAAGTCTGTCTGCTGGTGGTGTGCCCC	1449				
Db	2382	CTGGGCTCTTCCCTGTCAAGCCGAGGCGGTCAAGTCTGTCTGCTGGTGGTGTGCCCC	2441				
QY	1450	CTGCCCTGCCTGCCTCAACCCACTGTGTACTGTCTTCAACCCCACTTCCGGGATGAC	1509				
Db	2442	CTGCCCTGCCTGCCTCAACCCACTGTGTACTGTCTTCAACCCCACTTCCGGGATGAC	2501				
QY	1510	CTTCGGCGGCTTCGGCCCCCGCGCAGGGGACTCAGGGCCCCCTAGCCTATGCTCGGCCGGG	1569				
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QY	1570	GAGCTGGAGAAAGAGCTCCTGTGATTTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGAT	1629				
Db	2562	GAGCTGGAGAAAGAGCTCCTGTGATTTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGAT	2621				
QY	1630	CTCATTTCTGGAAGCTTCTGAAGCTGGGGCCCCCTGGGCTGGAGACCTATGGCTTCCCC	1689				

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QY 1690 TCACTGACCCCTCATCTCCTGTCTCAGCAGCCAGGGGGCCCCCAGGCTGGAGGGCAGCCATTGT 1749
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|||||

QY 1750 GTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTG 1809
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Db 2742 GTAGAGCCAGAGGGGAACCACTTTGGGAACCCCAACCCCTCCATGGATGGAGAACTGCTG 2801
|||||

QY 1810 CTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTTCAGGGGGTGGCGGTTTCAG 1869
|||||

Db 2802 CTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTTCAGGGGGTGGCGGTTTCAG 2861
|||||

QY 1870 CCCTCTGGCTTGGCCCTTTGCTTCACACGTG 1899
|||||

Db 2862 CCCTCTGGCTTGGCCCTTTGCTTCACACGTG 2891
|||||

RESULT 2

AK052873

LOCUS

DEFINITION

AK052873 2822 bp mRNA linear HTC 03-APR-2004

Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830015D13 product:CDNA FLJ14471 FIS, CLONE MAMMA1001030, WEAKLY SIMILAR TO LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR homolog [Homo sapiens], full insert sequence.

AK052873

AK052873.1 GI:26095426

HTC; CAP trapper.

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

REFERENCE

AUTHORS

Carninci, P. and Hayashizaki, Y.

TITLE

High-efficiency full-length cDNA cloning

JOURNAL

Meth. Enzymol. 303, 19-44 (1999)

MEDLINE

99279253

PUBMED

10349636

2

REFERENCE

AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL

Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE

20499374

PUBMED

11042159

3

REFERENCE

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL

Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE

20530913

PUBMED

11076861

4

REFERENCE

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE

Functional annotation of a full-length mouse cDNA collection

JOURNAL

Nature 409, 685-690 (2001)

5

REFERENCE

AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL

Nature 420, 563-573 (2002)

6

REFERENCE

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.jp, URL:http://genome.gsc.riken.jp/, tel:81-45-503-9222, Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/

URL:http://fantom.gsc.riken.jp/.

Location/Qualifiers

1. .2822

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/mol_type="mRNA"

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/db_xref="taxon:10090"

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/tissue type="heart"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev stage="16 days neonate"

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misc_feature

1. .2822

ORIGIN

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Best Local Similarity 85.1%; Pred. No. 7.3e-289;

Matches 1503; Conservative 0; Mismatches 261; Indels 2; Gaps 2;

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Db 474 GGCCTCCGACATAACCGGATCAAGGAAATTGGTGC-AGATACCTTCAGCCAGCTGGGCTC 532
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QY 195 CCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGGCTTCTC 254
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Db 533 CTTGCAAGCTTTAGACCTGAGTTGGAATGCCATCCGTGCCATCCACCCCTGAGGCTTCTC 592
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QY 255 CACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACCAGCTGACCACACTGCCCT 314
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Db 593 AACCTTCGATCCTTGGTTAAGCTGGACCTGACTGACAACCAGCTGACCACACTGCCCT 652
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QY 315 GGCTGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACTTGTCTCTCCCAGGC 374
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Db 653 GGCTGGGCTGGGAGGCTGATGCACCTGAAGCTCAAAGGGAACTTGGCCCTGTCTCAGGC 712
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QY 375 CTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCTACCAGTG 434
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Db 713 CTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCCTACGCCATCAGTG 772
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QY 435 CTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTTGGGCAGTGGGAGGCTGAAGA 494
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Db 773 CTGTGCCTACGGCATCTGTGCCAGCTTCTTCAAGACCTCTTGGGCAGTGGCAGCCGAGGA 832
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QY      1452 GCCTGCCTGCCTCAACCCACTGCTGTACCTGCTCTTAACACCCCACTTCCGGGATGACCT 1511
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QY      1512 TCGGCGGCTTCGGCCCCCGCAGGGGACTCAGGGCCCTAGCCCTATGCTGCGGCCGGGA 1571
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QY      1572 GCTGGAGAAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCCTTCTCTGATGCGATCT 1631
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QY      1632 CATTCGGAAGCTTCTGAAGCTGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTC 1691
Db      2732 TATTCGGAAGCTTCTGAGGCTGGGCAGCCCTCCTGGGCTAGAGACCTATGGCTTCCCTTC 2791

QY      1692 AGTAGCCCTCATCTCCTGTAGCAGCCAGGGGGCCCCCAGGCTGGAGGCGAGCCATTGTGT 1751
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DEFINITION 601770339F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3989576 5',
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ACCESSION  BF159363
VERSION     BF159363.1  GI:11039462
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 982)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9199 row: n column: 09
            High quality sequence stop: 663.
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Best Local Similarity 82.2%; Pred. No. 1.3e-110;
Matches 629; Conservative 0; Mismatches 135; Indels 1; Gaps 1;

QY      1132 GGGGCCCTCCCACTCTGCCCTGCCCTACGGGCACCTGAGGGTCAGCCAGCAGCCCTGGGC 1191
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QY      1192 TTCACCGTGGCCCTGGTGATGATGAACCTCTTCTGTTTCCCTGGTCGTCGCGGTGCCCTAC 1251
Db      61      TTCGCTGTAGCCCTGGTGATGATGAACCTGCTCTGCTTCCCTGGTGGTGGCGGCCCTAC 120

QY      1252 ATCAAACTGTACTGTGACCTGCCCGGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATG 1311
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QY      1312 GTGAGGCACGTGGCCCTGGCTCATCTTTCGACAGCGGGCTCCTCTACTGTCCCGTGGCCTTC 1371
Db      181      GTGCGCCACGTGGCCCTGGCTCATCTTTGCAGATGGCCTCCTCTACTGCCCCGTGGCCTTC 240

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QY      1432 CTGCTGCTGCTGCTGCCCTGCCCTGCCCTGACCTCAACCCACACTGCTGTACCTGCTCTTCAAC 1491
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QY      1552 GCCTATGCTGCGGCCCGGGGAGCTGGAGAAAGACTCCTGTGATTCTATCCAGGCCCTGGTA 1611
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Db      541      GAGACCTATGGCTTCCCCTCAGTCAGTCAGCCCTCATCTCCCGACATCAGCCGGGGGCCACCAGG 600

QY      1732 CTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAAACCCCAACCCCTCC 1791
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QY      1852 GGGGTTGGCGGCTTTTCAGCCCTCTGGCTTGGCCTTTTGTCTTTCACAC 1896
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RESULT 5
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LOCUS      BG863804
DEFINITION 602798701F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4934280 5',
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ACCESSION  BG863804
VERSION     BG863804.1  GI:14214342
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

REFERENCE

1 (bases 1 to 819)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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High quality sequence stop: 758.

Location/Qualifiers

1. 819

/organism="Mus musculus"

/mol_type="mRNA"

/strain="NMRI"

/db_xref="taxon:10090"

/clone="IMAGE:4934280"

/tissue_type="tumor, gross tissue"

/dev_stage="5 months"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Mam4"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."

ORIGIN

Query Match 28.1%; Score 534.4; DB 4; Length 819;

Best Local Similarity 84.0%; Pred. No. 4.9e-110;

Matches 626; Conservative 0; Mismatches 117; Indels 2; Gaps 2;

QY 135 GGCTCCAAACAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAGCTC 194

DB 41 GGCTCCGACATAACAGGATCAAGGAAATTGGTGC-AGATACCTTCAGCCAGCTGGGCTC 99

QY 195 CTGTCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTC 254

DB 100 CTGTCAAGCTTTAGACCTGAGTTGGAATGCCATCCGTGCCATCCACCCTGAGGCTTTCTC 159

QY 255 CACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTGACCACACTGCCCT 314

DB 160 AACCTTCGATCCTTGGTTAAGCTGGACCTGACTGACAAACAGCTGACCACACTGCCCT 219

QY 315 GGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGC 374

DB 220 GGCTGGCTGGGAGGCCTGATGCACCTGAAGCTCAAAGGGAACCTTGGCCCTGTCTCAGGC 279

QY 375 CTCTCCAAGGACAGTTTCCAAAACTGAGGATCCTGGAGTG-CCTTATGCCTACCAGT 433

DB 280 CTCTCCAAGGACAGTTTCCAAAACTGAGGATCCTGGAGTGCCCCCTACGCCTACCAGT 339

QY 434 GCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCAGTGGGAGGCTGAAG 493

DB 340 GCTGTGCCTACGGCATCTGTGCCAGCTTCTTCAAGACCTCTGGGCAGTGGCAGGCCGAGG 399

QY 494 ACCTTCACCTTGATGATGAGGAGTCTTCAAAAGGCCCTTGGGCCCTCTTGCCAGACAAG 553

DB 400 ACTTTCATCCAGAAGAAGAGGAGGACCAAGAGGCCCTTGGGTCTCCTTGTGGACAAG 459

QY 554 CAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGC 613

DB 460 CTGAGAACCACTATGACCTAGACCTGGATGAGCTCCAGATGGGACAGAGGACTCAAAGC 519

QY 614 CACACCCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCCTGTGAGTACCTCT 673

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 819)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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High quality sequence stop: 758.

Location/Qualifiers

1. 819

/organism="Mus musculus"

/mol_type="mRNA"

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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."

ORIGIN

Query Match 28.1%; Score 534.4; DB 4; Length 819;

Best Local Similarity 84.0%; Pred. No. 4.9e-110;

Matches 626; Conservative 0; Mismatches 117; Indels 2; Gaps 2;

QY 135 GGCTCCAAACAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAGCTC 194

DB 41 GGCTCCGACATAACAGGATCAAGGAAATTGGTGC-AGATACCTTCAGCCAGCTGGGCTC 99

QY 195 CTGTCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTC 254

DB 100 CTGTCAAGCTTTAGACCTGAGTTGGAATGCCATCCGTGCCATCCACCCTGAGGCTTTCTC 159

QY 255 CACCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAACAGCTGACCACACTGCCCT 314

DB 160 AACCTTCGATCCTTGGTTAAGCTGGACCTGACTGACAAACAGCTGACCACACTGCCCT 219

QY 315 GGCTGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGC 374

DB 220 GGCTGGCTGGGAGGCCTGATGCACCTGAAGCTCAAAGGGAACCTTGGCCCTGTCTCAGGC 279

QY 375 CTCTCCAAGGACAGTTTCCAAAACTGAGGATCCTGGAGTG-CCTTATGCCTACCAGT 433

DB 280 CTCTCCAAGGACAGTTTCCAAAACTGAGGATCCTGGAGTGCCCCCTACGCCTACCAGT 339

QY 434 GCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCCTCTGGGCAGTGGGAGGCTGAAG 493

DB 340 GCTGTGCCTACGGCATCTGTGCCAGCTTCTTCAAGACCTCTGGGCAGTGGCAGGCCGAGG 399

QY 494 ACCTTCACCTTGATGATGAGGAGTCTTCAAAAGGCCCTTGGGCCCTCTTGCCAGACAAG 553

DB 400 ACTTTCATCCAGAAGAAGAGGAGGACCAAGAGGCCCTTGGGTCTCCTTGTGGACAAG 459

QY 554 CAGAGAACCACTATGACCAGGACCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGC 613

DB 460 CTGAGAACCACTATGACCTAGACCTGGATGAGCTCCAGATGGGACAGAGGACTCAAAGC 519

QY 614 CACACCCCAGTGTCCAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCCTGTGAGTACCTCT 673

Db 520 CAAACCCAGTGTCCAGTGCAGCCCTGTTCCAGGCCCTTCAAGCCCTGCAGCACCTCT 579

QY 674 TTGAAAGCTGGGCATCCGCCTGGCCGTGTGGCCATCGTGTGCTCTCCGTGCTCGCA 733

Db 580 TTGAGAGCTGGGCATCCGCCTGCTGTGTGGCCATCGTGTACTCTCCGTACTCTGA 639

QY 734 ATGGACTGGTCTGCTGACCGTGTTCGCTGGCGGGCCTGCCCCCTGCCCGGTCAGT 793

Db 640 ACGGCTGGTGTCTGCTGACAGTCTTTGCCAGCGGACCCAGCCCGCTGTCCCCCGTCAAGC 699

QY 794 TTGTGTAGGTGCGATTGCAGGCGCCAACACCTTGACTGGCATTCTCTGTGGCCTTAG 853

Db 700 TTGTGTGGTGGTGGATGGCAGGCGCCAACGCCCTGACGGGCATTCTGTGGGTCTCTGGG 759

QY 854 CCTCAGTCGATGCCCTGACCTTTGG 878

Db 760 CCTCGGTGACGGCCTTGACCTATGG 784

RESULT 6

BG916782

LOCUS

DEFINITION

BG916782 812 bp mRNA linear EST 05-JUN-2001

602816031F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4935343 5', mRNA sequence.

ACCESSION

BG916782

VERSION

BG916782.1 GI:14297258

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 812)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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High quality sequence start: 5

High quality sequence stop: 792.

Location/Qualifiers

1. 812

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/clone="IMAGE:4935343"

/sex="female, virgin"

/tissue_type="infiltrating ductal carcinoma"

/dev_stage="5 months"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Mam6"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match 27.2%; Score 516.2; DB 4; Length 812;

Best Local Similarity 81.3%; Pred. No. 6.4e-106;

Matches 635; Conservative 0; Mismatches 143; Indels 3; Gaps 3;

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Qy 1324 GCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGCTTCGCC 1383
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Qy 1384 TCATGCTGGGCCTCTTCCCTGTCACGCCCGAGGCCGTCAAGTCTGTCTCCTGCTGGTGGTG 1443
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Db 121 TCTATGCTGGGCCTCTTCCCTGTACCCCCGAGGCTGTCAAGTCAGTCCTTCTTGGTGGTG 180
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Qy 1504 GATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGACTCAGGGCCCCCTAGCCTATGCTGGG 1563
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Db 241 GATGACCTTCGGCGGCTCTGGCCAAGCCCTCGGTCCCCAGGGCCCCCTAGCCTACGCTGCA 300
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Qy 1564 GCCGGGAGCTGGAGAAAGCTCTCTGTGATTCTACCCAGGCCCCCTGGTAGCCTTCTCTGAT 1623
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Db 301 GCCGGTGAGCTGGAGAAAGCTCTCTGCGACTCCACCCCAAGCGCTGGTGGCTTCTCAGAT 360
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Qy 1624 GTGGATCTCATTTCTGGAAGCTTCTGAAGCTGGGGCGGCCCTGGGCTGGAGACCTATGGC 1683
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Db 361 GTGGATCTTATTCTGGAAGCTTCTGAGGCTGGGCAGCCTCTCTGGCTAGAGACCTATGGC 420
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Qy 1684 TTCOCCTCAGTGACCCCTCATCTCTGTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGCAGC 1743
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Db 421 TTCCCTTCAGTGACCCCTCATCTCCCGACATCAGCCGGGGGTACCAGGCTGGAGGGAAC 480
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Qy 1744 CATTTGTAGAGCCAGAGGGGAACCACTTTTGGGAACCCCCAACCCCTCCATGGATGGAGAA 1803
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Db 481 CATTTGTAGAGTCTGATGGAAACCAAGTTTGGGAACCCCAACCTCCCATGAAGGGAGAA 540
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Qy 1804 CTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTGTCAGGGGGTGGCGGC 1863
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Db 541 CTGCTGCTGAAGGCAGAGGGAGCCACTTTGGCAGGCTGTGGCTCTTCCGTGGGTGGAGCC 600
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Qy 1864 TTTACGCCCTCTGGCTTGGCCTTTTGCT 1890
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Db 601 CTCTGGCCCTCTGGCTCTCTCTTGCCCT 627
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RESULT 8
AK040883
LOCUS
DEFINITION
AK040883 3855 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male aorta and vein cDNA, RIKEN full-length
enriched library, clone:A530037C04 product:CDNA FLJ14471 FIS, CLONE
MAMMA1001030, WEAKLY SIMILAR TO LUTROPIN-CHORIOGONADOTROPIC HORMONE
RECEPTOR homolog [Homo sapiens], full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AK040883 GI:26088131
AK040883.1
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
2
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCE
3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCE
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

JOURNAL
REFERENCE
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
REFERENCE
6 (bases 1 to 3855)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Nunazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission

JOURNAL
TITLE
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES
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homolog [Homo sapiens] (SPTR|Q96K69, evidence: FASTY,
85.8%ID, 92.1%length, match=637)
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ORIGIN
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Best Local Similarity 85.4%; Pred. No. 1.4e-97;

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QY 1322 TGGCCTGGCTCATCTTCGACACGGGCTCCTCTACTCTCCGTGGCCTTCCTCAGCTTCG 1381
Db 61 TGGCCTGGCTCATCTTTCAGATGGCCTCCTCTACTGCCCCGTGGCCTTCCTCAGCTTTG 120
QY 1382 CCTCCATGCTGGGCCCTCTCCCTGTACGCCCGGAGCGCTCAAGTCTGTCTCTGCTGGTGG 1441
Db 121 CCTCTATGCTGGGCCCTCTCCCTGTACCCCCGAGGTGTCAAGTCAGTCTCTTCTGGTGG 180
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Db 181 TGCTGCCTCTGCCTGCCTGCCTCAACCCACTGCTTACCTGCTCTTCAACCCCTCACTTCC 240
QY 1502 GGGATGACCTTCGGCGGCTTCGGCCCCCGCGCAGGGACTCAGGG-CCCCTAGCCTATGCT 1560
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QY 1741 AGCCATTGTGTAGAGCCAGAGGGGAACCACTTTTGGGAACCCCAACCCCTCCATGGATGGA 1800
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Db 601 GCCCTCTGGCCCTCTGGCTCTCTCTTTGGCTCTCACTTG 639
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LOCUS 17000532179685 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN258480
VERSION CN258480.1 GI:47274894
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 680)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
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FEATURES
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and H9 (p26) maintained in feeder-free conditions"
ORIGIN
Query Match 24.5%; Score 465.8; DB 7; Length 680;
Best Local Similarity 99.2%; Pred. No. 1.6e-94;
Matches 489; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY 132 AGCGGCCTCCAAACACAAACCGCATCTGGGAAATTGGAGCTNGACACCTTCAGCCAGCTGAG 191
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QY 192 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCTGAGGCCTT 251
Db 248 CTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCATCCGGTCCATCCACCCGAGGCCTT 307
QY 252 CTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAAACCAGCTGACCACTGCC 311
Db 308 CTCCACCCCTGCACCTCCCTGGTCAAGCTGGACCTGACAGACAAACCAGCTGACCACTGCC 367
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QY 372 GGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCC-TGGAGGTGCCTTATGCCTACC 430
Db 428 GGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTTGGAGGTGCTTATGCCTACC 487
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Db 488 AGTGTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGGAGTGGGAGGCTG 547
QY 491 AAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCTCTTGCCAGAC 550
Db 548 AAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCCCTGGGCCTCTTGCCAGAC 607
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Db 668 AGCCACACCCCCAG 680
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DEFINITION mRNA sequence.
ACCESSION BG916963
VERSION BG916963.1 GI:14297439
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 753)
NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
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/db_xref="taxon:7955"
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synthesized from adult ovary poly(A)+ RNA with ZAP-cDNA
Synthesis Kit (Stratagene). Size-fractionated cDNA (mainly
0.5-3kb in length) were directionally cloned into Uni-ZAP
XR vector. The cDNA clones were excised from Uni-ZAP
vector using ExAssist helper phage. Excised pBluescript
phagemids were used to transform E coli XL1-Blue cells.
The plasmid library was normalized by using a
reassociation-kinetics-based approach according to Bonaldo
et al., (Genome Research 6: 791-806,1996) with minor
modifications. The insert from randomly selected white
colonies was PCR amplified using M13 forward and reverse
primers and partially sequenced by using M13 reverse
primer."

ORIGIN

Query Match		17.0%;	Score 322.4;	DB 7;	Length 640;
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Qy	911	CGGGCTAGGCTGCCGGGCCACTGGGCTTCCTGGCAGTACTTGGGTGGAGGCATCGGTGC	970		
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Dd	553	TAAGCTCTTTCCGGTAAGTAGGAGGTTGTCAAATCTGTCTCTCTAGTGTCTTTTGCTC	612		
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